```
28-DEC-2001; 2001US-0346299P
                                                                                                                                                                                                                    RESULT 1
                                                                                                                                                                                                                             ADC99773
                                                                                                                                                                                                                                      Anti-plat
Anti-plat
Anti-plat
Light cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-plat
Anti-IGF-
Anti-plat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human pro
Kappa cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-plat
Human ant
Human ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pho
Humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kappa cha
Murine-ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-plat
Anti-plat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid hu
                                                   1; Search time 64.2353 Seconds (without alignments) 674.351 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                        1 DIVMTQSPLSLPVTPGEPAS..........CMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                       Add05377
Adf20815
Ade28441
Ade28451
Adi22127
Adi22127
Adi22121
Adi22123
Adi22123
Adi22128
Adi22128
Adi22128
Adi22128
Adi22128
Adi22128
Adi22128
Adi892
Adi22128
Adi892
Adi22128
Adi893
Adi22128
Adi893
Adi22128
Adi893
                                                                                                                                                                       2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                    2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                    November 16, 2005, 21:35:48
                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO07297
ADJ80417
ADP47297
ABG76926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ76892
ADI22128
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD05377
ADF09815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW53586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI22118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE28441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP03893
                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                 geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                       geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
                                                                                                                                                                                                                                                    A_Geneseq_16Dec04:*
                                                                                                                                                                                                                                                                 geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                           geneseqp2004s:*
                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                      US-10-660-357A-2
                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                   Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                       Database
                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
```

A Anti-plat B Human CD4 O Human CD4 O Anti-hED8 O Anti-plat Human pho I Anti-plat A Anti-plat A Anti-plat A Anti-plat A Anti-plat C Anti-plat A Anti-plat A Human ant	Human CD4
Adi22129 Adi325114 Adi325114 Adi33560 Adi25119 Adi22119 Adi25119 Ady95120 Ady95120 Ady95120 Ady95186 Ade28487 Ade28487 Ade28483 Ade28483 Ade28483 Ade28483 Ade28483	Ad193654
AD122129 AD122114 AD193568 AD193668 AD193650 AD192119 AD847300 AD795187 AAY95220 AAY95220 AAY95220 AAY95220 AAY95240 AAY95240 AAY95186 AAY95240 AAY95186 AAY95286 AAY95186	ADL93654
@@@@4@@MMMMM\\\\\\\\\\\\\\\\\\\\\\\\\\\	80
231122 2332 2332 2332 2332 2311 2311 23	238
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	95.
2 222222222222222222222222222222222222	542
00000000000000000000000000000000000000	45

ALIGNMENTS

```
anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                          Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 2.
ADC99773 standard; protein; 112 AA
                                                                                                                                                               01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003057838-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
```

26-DEC-2002; 2002WO-US041581. 17-JUL-2003.

(ABGE-) ABGENIX INC

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99775.

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 2; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

N

```
The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the monoclonal antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytosteric and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumoure, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastesis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastetic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                 ö
                                                                                                                                                     9
                                                                                                                                                                             1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                     DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-MUC18 antibody light chain variable region protein, SEQ ID No 2.
                                                                                                                 Gaps
                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                     SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                 ö
                                                                       ; Score 584; DB 7; Length 112;
; Pred. No. 4e-40;
0; Mismatches 0; Indels (
light chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; SEQ ID NO 2; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                   ADD05377 standard; protein; 112 AA
                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-2001; 2001US-0346460P.
                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein of the invention.
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-577496/54.
N-PSDB; ADD05379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABGE-) ABGENIX INC.
                                                                       Query Match
Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastatic tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003057006-A2
                                       Sequence 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                         ADD05377;
                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                         ប្ដង្គន
                                                                                                                                                                                       a
                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                 ద
                                                                                                                                                       ò
```

100.0%; Score 584; DB 7; Length 112;

Sequence 112 AA;

Query Match

```
ö
                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     associated with expression of WC18 tumour antigen. The method involves administering anti-WUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastrasis. The method carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                              1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLRSNGYNYLDWYLDWYLCKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                 DIVMTOSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGOSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                         anti-MUC18 monoclonal antibody, tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; light chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises a method for inhibiting cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGGGTRLEIK 112
                                                                                                                                          61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 584; DB 7; Length 112; 100.0%; Pred. No. 4e-40; ive 0; Mismatches 0; Indels (
100.0%; Pred. No. 4e-40; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           cell proliferation inhibition; MUC18 tumour antigen;
                                                                                                                                                                                                                                                                                                                                           Human anti-MUC18 monoclonal antibody light chain #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 3; SEQ ID NO 2; 83pp; English.
                                                                                                                                                                                                                                          ADF09815 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2002; 2002WO-US041580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 112; Conservative
Best Local Similarity 100.
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-598367/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADF09817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                             12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                          ADF09815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gudas J;
                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                             ADF0981
                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                   원
                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                      ઠ
                                                                                                                        ò
```

ო

```
The present invention describes a method (M1) for identifying an antipatelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that conducing an antibody phage of interest to detect a phage that the mammal, and screening the library to detect a phage that is pacific comportively cell-comporties panning. Also described: (I) an autoantibody identified by (M1); (2) an isolated mucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombotic thrombocycopenic purpura in a mammal; (B) inhibiting (MN) and thrombotic thrombocycopenic purpura in a mammal; (B) inhibiting (MN) chrombotic thrombocycopenic purpura in a mammal; (B) inhibiting (MN) blatelet function; (II) inhibiting (MN) platelet autoantibody, or its biologically active fragment with a cantiplatelet autoantibody, (IS) treating (M2) applatelet autoantibody, with a platelet; (I3) a peptide that inhibiting platelet autoantibody, or its biologically active fragment that cantibody, or its biologically active fragment that comprise and inhibiting platelet activation comprising on derived from an H4414 corting inhibiting platelet aggregation, inhibiting platelet activation comprising an amount of an antiplatelet autoantibody, or its biologically active fragment that contribody, or its biologically active fragment that contribody, or its biologically active fragment that antiplatelet autoantibody, or its biologically active fragment that cantibody, or its biologically active fragment that antiplatelet autoantibody, or its biologically active fragment comprising with glycoprotein IIb/IIIa, where the autoantibody, or its biologically active fragment antiplatelet autoantibody, or its biologically active fragment antiplatelet autoantibody, or its biologically active 
                                                                                                                                                                                                         thrombus; platelet adhesion inhibition;
thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
                                                                                                                                             Anti-platelet autoantibody related light chain amino acid L54 SEQ:93.
                                                                                                                                                                                       anti-platelet autoantibody; autoantibody; blood clotting inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; SEQ ID NO 93; 232pp; English.
               ADI22130 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-2002; 2002US-0411694P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUL-2003; 2003WO-US021304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-2002; 2002US-0394352P
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                            thrombolytic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-142998/14.
N-PSDB; ADI22077.
                                                                                                                                                                                                                                                                                                                                                                                   WO2004005890-A2.
                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                    22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siegel DL;
                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                          ADI22130;
ADI22130
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder such as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length light chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
                                                                                                                                                                                                    1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                        1 DIVMTOSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEI 111
                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDIGVYYCMQAQDSPVTFGQGTRLDI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human anti-CD40 antibody 21-4-1 full length light chain protein.
                                                                                                                                                              ô
                                                                                                                         Length 112;
                                                                                                                  Query Match
95.2%; Score 556; DB 8;
Best Local Similarity 94.6%; Pred. No. 7.6e-38;
Matches 105; Conservative 3; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; SEQ ID NO 48; 177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corvalan J,
                                                                                                                                                                                                                                                                                                                                                                                                                           ADE28441 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-NOV-2001; 2001US-0348980P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38-NOV-2002; 2002WO-US036107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; light chain; 21-4-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER PROD INC (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bedian V, Gladue RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-441521/41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADE28440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viral infections
                                                                                 Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003040170-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE28441;
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                        ADE28441
    8X3333
                                                                                                                                                                                                                                                                                 ò
```

Sequence 112 AA;

DIVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 80

SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112

61

ò

```
The invention relates to a novel chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40. The anti-CD40 antibody of the invention demonstrates cytostatic, virucide, antibacterial, immunostimulant and anti-HIV activities and may be useful for treating a hyperproliferative disorder souch as cancer, viral and bacterial infection or genetic, primary or combined immunodeficiency conditions including neutropenia or HIV infection. The anti-CD40 antibodies may also be useful for detecting CD40 in a biological sample in vitro or in vivo, as well as during gene therapy procedures. The current sequence is that of the human anti-CD40 antibody full length light chain protein of the invention.
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                               anti-CD40 monoclonal antibody, CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; light chain; 23-28-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or
                                                                        9
                                                                                      1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                     Gaps
                                                                                                                                                          SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPRTFGQGTKVEIK 112
                                                                                                                                        SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                  Human anti-CD40 antibody 23-28-1 full length light chain protein.
                                     ô
   Length 112;
                                    3; Indels
 Score 554; DB 7;
Pred. No. 1.1e-37;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corvalan J, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; SEQ ID NO 72; 177pp; English.
                                                                                                                                                                                                                                                               Ā
                                                                                                                                                                                                                                                             ADE28465 standard; protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2002; 2002WO-US036107.
 94.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-2001; 2001US-0348980P
                                                                                                                                                                                                                                                                                                                                  29-JAN-2004 (first entry)
Query Match
Best Local Similarity 94.6
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PFIZ ) PFIZER PROD INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bedian V, Gladue RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-441521/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADE28464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003040170-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                ADE28465;
                                                                                                                                                                                                                         셤
                                                                                                                                                                  වූ
                                                                                                                                       ò
```

```
The present invention describes a method (M1) for identifying an anti-

C platelet autoantibody (1) in a mammal. The autoantibody is detected by

producing an antibody phage display library from B-lymphocytes obtained

from the mammal, and screening the library to detect a phage that

c preducing an antibody phage of library to detect a phage that

c specifically binds with a platelet component, where the screening

c surface panning the phage on intact platelets using competitive cell-

c surface panning. Also described: (1) an autoantibody identified by (M1);

C (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)

inhibiting (M2) blood clotting in a mammal having a thrombus or at risk

C (4) inhibiting of an anti-platelet autoantibody with a platelet component;

C (5) inhibiting of solatelet adhesion in a mammal; (7) treating (M7)

C (6) inhibiting (M5) platelet adhesion in a mammal; (1) reating (M7)

C (7) platelet aggregation; (9) inhibiting (M8) platelet activation; (10)

C (6) inhibiting (M3) platelet function; (11) inhibiting (M7)

C (7) platelet autoantibody, or its biologically active fragment with a conti-platelet autoantibody, (15) treating (M1) a peptide that inhibits binding of an anti-platelet autoantibody, (15) treating (M1) a peptide that inhibits binding of an anti-platelet autoantibody, or its biologically active fragment that

C platelet autoantibody, or its biologically active fragment that

C colotting, inhibiting platelet aggregation, inhibiting platelet function

C conting, inhibiting platelet aggregation, inhibiting a mammal;

C platelet autoantibody, or its biologically active fragment that

C platelet autoantibody, or its biologically active fragment that

C platelet autoantibody, or its biologically active fragment comprises an antigen binding region derived from an H414

C inhibitor of the binding with glycoprotein IIb/IIIa, where the autoantibody, the kit further comprised an applicator inhibitor of the binding with glycoprotein and an applicator inhibitor of th
                                                                                                                                                                                                                                                                                                          anti-platelet autoantibody; autoantibody; blood clotting inhibition;
thrombus; platelet adhesion inhibition;
thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
                                                                                                                                                                                                                                                                  Anti-platelet autoantibody related light chain amino acid L51 SEQ:90.
Claim 12; SEQ ID NO 90; 232pp; English.
                                                                                                                                ADI22127 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUL-2003; 2003WO-US021304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-0394352P.
2002US-0411694P.
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-142998/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AD122074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402004005890-A2.
                                                                                                                                                                                                                                                                                                                                                                                                           thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                       22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siegel DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                             ADI22127;
                                                                                                                                                     셤
```

ö

ö

Score 554; DB 7; Length 239; Pred. No. 2.3e-37; 3; Mismatches 3; Indels

94.98;

Matches 106; Conservative

Query Match Best Local Similarity 9

DIVMTQSPLSLPVTPGEPASISCRSSQSILRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA

വ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method (M1) for identifying an antipplatelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cellsurface panning. Also described: (I) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M4) binding of an anti-platelet autoantibody with a platelet component;
and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombocytopenic purpura and idiopathic thrombocytopenic purpura and idiopathic thrombocytopenic purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                        DIVMTQSPLSLPVTPGEPASISCRSSQSLLHTNGYNYLDWYLQKPGQSPQLLIYLGSHRA 60
                                                                                                                                                                                                                                                                                                  1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-platelet autoantibody; autoantibody; blood clotting inhibition; thrombus; platelet adhesion inhibition; thrombotic thrombocytopenic purpura; platelet aggregation inhibition; idiopsthic thrombocytopenic purpura; haemostatic; anticoagulant;
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-platelet autoantibody related light chain amino acid L36 SEQ:75.
                                                                                                                                                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                    Length 112
                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                  Score 553; DB 8;
Pred. No. 1.3e-37;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; SEQ ID NO 75; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI22112 standard; protein; 112 AA
                                                                                                                                                                                                                    94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2003; 2003WO-US021304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUL-2002; 2002US-0394352P.
18-SEP-2002; 2002US-0411694P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.6'
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-142998/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombolytic; human
                                                                                                                                        present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADI22059
                                                                                                                                                                               Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004005890-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Siegel DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI22112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
  8888888888
                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
thrombotic thrombocytopenic purpura in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7) charelet aggregation; (9) inhibiting (M8) platelet aggregation; (10) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibiting binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-compared (17P) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet activation comprising an amount of an anti-complatelet activation comprising a macunt of an anti-complatelet activations for the kit further comprising a peptide cand an instructions for use. (1) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (1) are useful for diagnosing cand for developing therapeutics for diseases mediated by autoantibody thrombolytic activities. The autoantibodies (1) are useful for treating thrombolytic purpura, respectively. (M2) and (M12) are useful for treating thrombolytic purpura, respectively. (M2) and (M13) are useful for inhibiting blood contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-platelet autoantibody; autoantibody; blood clotting inhibition; thrombus; platelet adhesion inhibition; thrombotic thrombocytopenic purpura; platelet aggregation inhibition; idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-platelet autoantibody related light chain amino acid L35 SEQ:74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 553; DB 8; Length 112; Pred. No. 1.3e-37; 2; Mismatches 4; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI22111 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUL-2003; 2003WO-US021304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002US-0394352P.
2002US-0411694P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombolytic; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MO2004005890-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UYPE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siegel DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI22111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADI22111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

03-JUL-2003; 2003WO-US021304.

WO2004005890-A2 Homo sapiens. Synthetic.

15-JAN-2004.

```
The present invention describes a method (MI) for identifying an antipoducing the autoantibody is detected by producing an antibody plage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that from the mammal, and screening the library to detect a phage that comprises panning the phage on intact platelets using competitive cellocomprises panning the phage on intact platelets using competitive cellocomprises panning the phage on intact platelets using competitive cellocomprises panning the phage on intact platelets using competitive cellocomprises panning the phage on intact platelets using competitive cellocomprises panning the phage on intact platelets using competitive cellocomprises panning the phage on intact platelet used into a mammal having a thrombus or at risk of thrombus formation; (3) inhibiting (M2) inhibiting (M3) inhibiting (M3) platelet defeated propers or a risk of thrombus formation; (6) inhibiting (M3) platelet autoantibody, or its biologically active fragment with a platelet autoantibody with a platelet; (13) identifying (M1) a peptide that specifically binds with an antiplatelet autoantibody with a platelet; (13) a peptide that specifically proper active fragment that the platelet autoantibody; (15) treating (M12) idiopathic thrombocycopenic platelet activation comprises an antiplatelet activation platelet activation comprising manner. The platelet activation comprising manner of an antiplatelet activation with a platelet activation comprising a peptide continuous inhibiting platelet activation comprising manner of the unition of the binding with glycoprotein IIb/IIIa, where the autoantibody, or its biologically active fragment that appeared the minimum or an H4414 and an instructions for use. (1) has haemoscatic, anticoagulant and and continuous manner or the binding with glycoprotein IIb/IIIa, where the autoantibody, the kit further comprising a peptide cond in instructions for use. (1) has haemoscatic, anticoagulant and antiplated tha
                                                                          Claim 12; SEQ ID NO 74; 232pp; English.
WPI; 2004-142998/14.
                          N-PSDB; ADI22058
```

Sequence 112 AA;

9 1 DIVMTÓSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60 1 DIVMIQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 0; Gaps SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112 Score 552; DB 8; Length 112; Pred. No. 1.6e-37; 2; Mismatches 4; Indels 94.5%; Conservative Similarity datches 106; 61 Query Match Local g ઠે

ADI22123 standard; protein; 112 AA. 22-APR-2004 (first entry) ADI22123; RESULT 10

Anti-platelet autoantibody related light chain amino acid L47 SEQ:86.

anti-platelet autoantibody; autoantibody; blood clotting inhibition; thrombus; platelet adhesion inhibition; thrombotic thromboxytopenic purpura; platelet aggregation inhibition; idiopathic thrombocytopenic purpura; haemostatic; anticoagulant; thrombolytic; human

The present invention describes a method (MI) for identifying an antipotation describes a method (MI) for identifying an antipody plage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that from the mammal, and screening the library to detect a phage that component, where the screening comprises panning the phage on intact platelets using competitive cell-specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cell-surface panning the phage on intact platelets using competitive cell-surface panning the phage on intact platelets using competitive cell-surface panning the phage on intact platelets using competition of an isolated mucleic acid encoding an auti-platelet autoantibody identified by (MI); inhibiting (M2) blood clotting in a mammal; (B) inhibiting in a mammal id inhibiting (M3) platelet autoantibody with a platelet activation; (IO) inhibiting (M3) platelet function; (II) inhibiting (M3) platelet function; (II) inhibiting (M3) platelet function; (II) inhibiting of an anti-platelet autoantibody of (II) inhibiting (M3) platelet function; (II) inhibiting of an anti-platelet autoantibody, (IS) treating (M1) a peptide that inhibits manning anti-platelet autoantibody (II) treating (M1) is a peptide that inhibits of anti-platelet autoantibody or its biologically active fragment with a nattice purpura (ITP) in a mammal; and (IA) a kit for reversibly inhibiting platelet activation comprising an amount of an anti-platelet autoantibody, or its biologically active fragment that capacitically binds with glycoprotein IID/IIIa, where the autoantibody or its biologically active fragment that autoantibody, or its biologically active fragment that an anti-platelet autoantibody, or its biologically active fragment that autoantibody, or its biologically active fragment comprises an antigen binding with platelet autoantibody, the kit further comprising a peptide and instructions for use under a 1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 0; Gaps Length 112; 4; Indels 94.5%; Score 552; DB 8; 95.5%; Pred. No. 1.6e-37; ive 1; Mismatches 4; Claim 12; SEQ ID NO 86; 232pp; English. 03-JUL-2002; 2002US-0394352P. 18-SEP-2002; 2002US-0411694P. (UYPE-) UNIV PENNSYLVANIA al Similarity 95.5 107; Conservative WPI; 2004-142998/14. present invention N-PSDB; ADI22070 Sequence 112 AA; Siegel DL; Query Match Best Local & Matches ò 셤

SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112

ô 9 9

61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGVYYCMQALQTPITFGQGTRLEIK 112

g ð

```
82668
                                                                                                                                                                             g
                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (MI) for identifying an antipatelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that from the mammal, and screening the library to detect a phage that from the mammal, and screening the phage on intact platelets using competitive cell-substitution and molecal conference of a ministring (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation; (8) inhibiting (M3) binding of an anti-platelet autoantibody with a platelet component; (6) inhibiting (M3) platelet function; (11) inhibiting (M3) platelet function; (13) inhibiting (M3) platelet function; (14) inhibiting (M3) platelet function; (11) inhibiting (M3) platelet autoantibody, or its biologically active fragment with a cantiplatelet autoantibody, or its biologically active fragment with a cantiplatelet autoantibody with a platelet; (13) a peptide that inhibiting blood clotting inhibiting platelet activation (M3) platelet autoantibody, or its biologically active fragment that antiplatelet autoantibody, or its biologically active fragment that copyriate autoantibody, or its biologically active fragment that copyriate autoantibody, or its biologically active fragment that copyriates an antigen binding region derived from an H44L4 articlated autoantibody, or its biologically active fragment that copyriates an antigen binding region derived from an inhibiting platelet autoantibody, or its biologically active fragment that antiplatelet autoantibody, or its biologically active fragment that comprises an antigen binding region derived from an inhibiting platelet autoantibody with glycoprotein IIb/IIIa, where the autoantibody or its further comprises an antigen binding vith platelet autoantibody with glycoprotein inhibitor and an instructions for 
                                                                                                                                                                                            thrombus; platelet adhesion inhibition;
thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
                                                                                                                                                 Anti-platelet autoantibody related light chain amino acid L48 SEQ:87.
                                                                                                                                                                             autoantibody; blood clotting inhibition;
inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; SEQ ID NO 87; 232pp; English.
                                                       ADI22124 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                03-JUL-2002; 2002US-0394352P.
18-SEP-2002; 2002US-0411694P.
                                                                                                                                                                                                                                                                                                                                                                                   03-JUL-2003; 2003WO-US021304
                                                                                                                                                                                 anti-platelet autoantibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                            chrombolytic; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-142998/14.
N-PSDB; ADI22071.
                                                                                                                                                                                                                                                                                                                       WO2004005890-A2.
                                                                                                                                                                                                                                                                          sapiens
                                                                                                                    22-APR-2004
                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004
                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siegel DL;
                                                                                      AD122124;
                            RESULT 11
```

```
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the light chain of a human antibody, and can be used in the humanised immunoglobulin of the invention. The humanised immunoglobulin reacts specifically with a region of a Pas ligand that is important in inhibiting apoptosis induced by cells with Pas expression. The immunoglobulin of the invention can inhibit applysiological reactions between a Pas ligand and Pas, typified by apoptosis. The humanised immunoglobulin is used for treatment of ADS, rejection following transplant surgery, autoimmune diseases such as SLE
                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQRPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunoglobulin or its active fragment specific for Fas ligand - treatment of AIDS, organ rejection, autoimmune diseases e.g. systemic lupus erythematosus and diabetes.
                                                                                                                                                                                                                                      Gape
purpura, respectively. (M2) and (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain; human; humanised immunoglobulin; NOK2; Fas ligand; inhibition; apoptosis; Fas expression; treatment; AIDS; rejection; transplant surgery; autoimmune disease; SLE; RA; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPTFGGGTRLEIK 112
                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 550; DB 2; Length 112;
Pred. No. 2.3e-37;
3; Mismatches 4; Indels
                                                                                                                                                                            Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maeda H,
                                                                                                                                                                            Score 551; DB 8;
Pred. No. 1.9e-37;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ushio Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 261; 348pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW53586 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okumura K, Nakata M, Higuchi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUME ) SUMITOMO ELECTRIC IND CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Light chain of a human antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96JP-00271546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96JP-00231742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.2%;
                                                                                                                                                                            Query Match
Best Local Similarity 94.6%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-JP002983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-193620/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or RA, and diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112 AA;
                                                                                                                         Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo gapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9810070-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW53586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW53586
```

```
The present invention describes a method (M1) for identifying an antipopate autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library from B-lymphocytes obtained from the mammal, and screening the library from B-lymphocytes obtained from the mammal, and screening the library from B-lymphocytes obtained from the mammal, and screening the library from B-lymphocytes obtained comprises panning the phage on intact platelets using competitive cell-caurface panning. Also described: (1) an autoantibody identified by (M1); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M3) platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet adhesion in a mammal; (8) inhibiting (M6) platelet dathesion in a mammal; (8) inhibiting (M7) platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M1) a peptide that inhibits binding of an anti-platelet autoantibody, or its biologically active fragment with a cani-platelet autoantibody, or its biologically active fragment that coperation or inhibiting platelet aggregation; (14) a peptide that specifically binds with an anti-coplatelet autoantibody, or its biologically active fragment that coplatelet autoantibody, or its biologically active fragment that coplatelet autoantibody, or its biologically active fragment that that the fragment comprises an antigen binding region derived from an H44L4 antigenent comprises an antigen binding region derived from an H44L4 antigenent that further comprising a peptide autoantibody, the kit further comprising a peptide
                        9
thrombotic thrombocytopenic purpura; platelet aggregation inhibition; idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                Anti-platelet autoantibody related light chain amino acid L50 SEQ:89.
                                                                                                                                                                                                                                                                                                                                                                                      anti-platelet autoantibody; autoantibody; blood clotting inhibition; thrombus; platelet adhesion inhibition;
                                                                                       SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK 112
                                                                  SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; SEQ ID NO 89; 232pp; English.
                                                                                                                                                                                                                   ADI22126 standard; protein; 113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2003; 2003WO-US021304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-2002; 2002US-0394352P.
18-SEP-2002; 2002US-0411694P.
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-142998/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chrombolytic; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADI22073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004005890-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                      22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L5-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siegel DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                  61
                                                                                                                                                                                                                                                            ADI22126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                      ò
```

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated antibody (Ab), and its functional fragments, that bind to human insulin-like growth factor-1 receptor (IGF-1R) and optionally: (i) inhibit natural binding of insulin-like growth factors (IGF)-1 and/or -2; and/or (ii) inhibit specifically tyrosine kinase activity of IGF-1R. Ab and its fragments are used to prevent or treat diseases associated with overexpression and/or abnormal activity of IGF-1R and/or epidermal growth factor receptor (EGFR) and/or with hyperactivity of signal transduction pathways mediated by interaction of these receptors with their ligands. Especially they inhibit
inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic purpura and idiopathic thrombocytopenic clotting. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDMYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; antipsoriatic; antibody; insulin-like growth factor-1 receptor; iGF-IR; tyrosine kinase activity; or epidermal growth factor receptor; BGFR; signal transduction pathway; or epidermal growth factor receptor; complementarity determining region; ligand; tumor; cancer; osteosarcoma; complementarity determining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies that bind to human insulin-like growth factor receptor, useful for treatment, prevention and diagnosis of cancers.
                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQS-PITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTRPVTFGGGTRLEIK 113
                                                                                                                                                                                                                                               DB 8; Length 113;
                                                                                                                                                                                                                                           Score 549.5; DB 8; Length Pred. No. 2.6e-37; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 58; 164pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leger 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADJ76892 standard; protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-IGF-1R related protein #9.
                                                                                                                                                                                                                                             Match 94.1%;
Local Similarity 94.7%;
hes 107; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8-JAN-2002; 2002FR-00000653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2002; 2002FR-00000654
07-MAY-2002; 2002FR-00005753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-2003; 2003WO-FR000178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corvaia N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-569653/53
                                                                                                                                                                                                         Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003059951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ното варіелв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soetsch L,
                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ76892;
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             සු
        888888888888888
                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
The present invention describes a method (M1) for identifying an antipplated autoantibody (1) in a mammal. The autoantibody is detected by platelet autoantibody (1) in a mammal. The autoantibody is detected by producing an antibody phage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that specifically binds with a platelet component, where the screening comprises panning the phage on intact platelets using competitive cellsurface panning. Also described: (1) an autoantibody identified by (M1); an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having an anti-platelet autoantibody is inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6) thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)
                                                                                                                                                                                                                             ö
transformation of normal cells to tumor cells, inhibit growth and/or proliferation of tumor cells, so are useful against cancers of the prostate, lung, breast, endometrium and colon, also osteosarcoma, and also for treating psoriasis. Ab are also used to diagnose diseases caused by abnormal expression of IGF-IR and/or EGFR. This sequence represents a protein sequence used to generate the Ab of the invention.
                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQXPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                   1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-platelet autoantibody; autoantibody; blood clotting inhibition; thrombus; platelet adhesion inhibition; thrombotic thrombocytopenic purpura; platelet aggregation inhibition; idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-platelet autoantibody related light chain amino acid L52 SEQ:91.
                                                                                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPQTFQGFTKVEIK 112
                                                                                                                                                                                 93.8%; Score 548; DB 7; Length 112; 93.8%; Pred. No. 3.4e-37; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; SEQ ID NO 91; 232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI22128 standard; protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2003; 2003WO-US021304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-0394352P.
2002US-0411694P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                        Best Local Similarity 93.8
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             API; 2004-142998/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombolytic; human
                                                                                                                                             Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADI22075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004005890-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Siegel DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI22128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI22128
  8888888888
                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                 8
```

```
contributing (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M11) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide that inhibits binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal, and (16) a kit for reversibly inhibiting blood clothing, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-continuity inhibiting platelet activation comprising an amount of an anti-continuity inhibiting platelet activation comprising an amount of an anti-continuity platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H4114 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator of thrombolytic activities. The autoantibodies (I) are useful for developing therapeutics for diseases mediated by autoantibody thrombolytic activities. (M6) and (M12) are useful for treating thrombolic thrombocytopenic purpura and idiopathic thrombocytopenic purpura and idiopathic thrombocytopenic purpura and idiopathic thrombocytopenic purpura and idiopathic thrombocytopenic cutting. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVWTQSPLSLPVTPGEPASISCRSGQSLLHSNGYNYLDWYLDKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIVMIQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGSGADFTLKISRVEAEDVGVYYCMQALQTPITFGQGTRLEIE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.8%; Score 548; DB 8; Length 112; 93.8%; Pred. No. 3.4e-37; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 16, 2005, 21:51:35 Job time : 66.2353 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112 AA;
            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

(CLCC) SIGNAGE TEMS CITAL

```
chain pre
chain V r
chain V r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain pre
chain pre
chain - m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain he cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain V-J
chain V r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoantib
                                                                                                                                                                                                     November 16, 2005, 21:37:48; Search time 13.3824 Seconds (without alignments) 805.260 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain
                                                                                                                                                                                                                                                                                                                                                   US-10-660-357A-2
584
1 DIVWIQSPLSLPVIPGEPAS........CMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa (Ig kap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283416
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $58207
$26882
$40342
$40342
$540340
$584036
$40313
$40317
$40317
$40317
$40317
$40317
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$4032
$403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S52028
S40340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9933.8
9933.8
9912.8
9912.8
9911.8
9911.8
9911.9
9911.9
9911.9
9911.9
9911.9
9911.9
9911.9
9911.9
9911.9
9911.9
9911.9
9911.9
                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
```

Ig kappa chain - h Ig light chain V r Ig kappa chain V r Ig kappa chain pre Ig kappa chain - h Ig kappa chain pre Ig kappa chain v r	ALIGNMENTS - human (fragment) on 19-Apr-1996 #text_change 21-Jan-2000 u, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, F July 1995 eavy and light chain immunoglobulin variable region c eavy and light chain immunoglobulin homology on; immunoglobulin homology ooy < IMM> ed: No. 4.5e-42; ed: No. 4.5e-4	61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMOAQOSPITFGGGTRLEIK 112 61 SGVPDRFSGSGGGTDFTLKISRVEAEDVGVYYCMOALOTPWTFGGGTKVEIK 112 6882 kappa chain V region (V607) - human Species: Homo sapiens (man) Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000 Accession: S26882 Weichhold, G M.; Klobeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G. Title: Megabase inversions in the human genome as physiological events. Reference number: S26882; MUID:90370099; PMID:2118596 Status: preliminary; translation not shown Wolecule type: DNA Molecule type: DNA Genetics: 1.13
---	--	--

~

```
ö
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 80
                                                                                                                                           21 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 73
                                                                                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V-J-C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Accession: S40357 R;Klein, R.; Jaenichen, R.; Zachau, H.G. R;Klein, R.; Jaenichen, R.; Zachau, H.G. A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341 A;Reference number: Lanslation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNCYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S40342
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Ru. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40342
A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q8NEKO; EMBL:X72452; NID:g441372; PID:g441373 C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Seywords: heterotetramer; immunoglobulin P;29-108/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPRTFGQGTKVEIK 125
                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                            ö
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.8%; Score 548; DB 2; Length 135; 93.8%; Pred. No. 5.5e-42; tive 3; Mismatches 4; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.8%; Score 548; DB 2; Length 136; 93.8%; Pred. No. 5.5e-42; ive 3; Mismatches 4; Indels
     Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Regidues: 1-136 <KLE>
A; Regidues: 1-136 <KLE>
A; Cross-references: UNIPROT:QBNEKO; EMBL:X72467
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>
                                                       4; Indels
Score 548; DB 2;
Pred. No. 5.3e-42;
3; Mismatches 4;
  93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.8:
Matches 105, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 93.8
Matches 105; Conservative
                                                    Matches 105; Conservative
                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-135 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                            ò
                                                                                                                                                g
                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                             g
```

```
A.Map position: 2p12-2p12

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lan

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>

F;2-17/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>

F;20-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                      Ig light chain V region anti-F(ab')2 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C;Accession: S58206
R;Welschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, I submitted to the RML Data Library, July 1995
A;Description: Characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization characterization of heavy and light chain immunoglobulin variable region characterization charac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Homo sapiens (man)
C.Jacestes: John-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C.Jacession: A01889; Bs4452
R.Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A.;Title: Contribution of human V-kappall germ-line genes to light-chain diversity.
A.;Reference number: A01889; MUID:84191506; PMID:6325927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIXLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X89054; NID:g929640; PIDN:CAA61441.1; PID:g929641
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                            81 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPWTFGQGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: the sequence was determined from the differentiated gene C;Genetics:
A;Gene: GDB:IGKV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.8%; Score 542; DB 2; Length 112; 92.0%; Pred. No. 1.5e-41; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain precursor V-II region (GM607) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 536; DB 1;
Pred. No. 5.5e-41;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 1-117 <KLO>
A,Cross-references: UNIPROT:P06309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.8%;
ilarity 92.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:136265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity ....
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: S58206
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-112 <WEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: A01889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                     g
ò
```

a case of primary amyloi

ઠે 셤

```
A)Cross-references: UNIPROT: P01617
A)Cross-references: UNIPROT: P01617
A)Note: this protein was isolated from the urine of a patient with plasma cell dyscragiagh A)Note: this crain of this chain has the Inv (1,2) marker
A)Note: the C region of this chain has the Inv (1,2) marker
B) Therry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osserman, E.F.; Glenner, G.G.
J. Clin. Invest. 52, 1276-1281, 1973
A)Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with A)Reference number: A2764; MUID:73166638; PMID:4700495
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004 C;Accession: A90370; A92764; A01888 R;Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N. Biochemistry 12, 3763-3796, 1973 A;Title: Amino acid sequence of a kappa Bence Jones protein from a case of IA;Reference number: A90370; MUID:74148480; PMID:4596149 A;Contents: Bence Jones protein Tew A;Accession: A90370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:136265
                                                                                                                                                                                                                                                                              A;Molecule type: protein A;Residues: 1-113 <PUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A92764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: IGKV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $4033
Every 1. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                    . North Species: Homo sapiens (man)
Species: Homo sapiens (man)
Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIVMTQSPLSLPVTPGEPASISCRSSQSLLHNNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHINGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X72449; NID:g441366; PIDN:CAA51117.1; PID:g441367
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                           CiSpecies: Homo sapiens (man)
CiDate: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-200
CiAccession: 84036
CiAccession: 84036
Rixlein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
Airitle: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: 840312; MUID:94080891; PMID:8258341
A; Accession: 840356
A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X72466; NID:g441400; PIDN:CAA51134.1; PID:g441401 CS.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: hererotetramer; immunoglobulin P;25-104/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                        65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMOGLQTPQTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQVLQIPLTFGGGTKVEIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 SGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCMQALQ-PWTFGQGTKVEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.3%; Score 527.5; DB 2; Length 126; 92.0%; Pred. No. 3.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.8%; Score 536; DB 2; Length 125; 91.1%; Pred. No. 5.9e-41; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V-II region (Tew) - human (tentative sequence)
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 91.13
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-126 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-125 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain - human
```

10 61

ò g ò g

Query Match

```
A;Molecule type: protein
A;Residues: 1-27 <TER>
A;Note: the major amyloid protein appears to be identical with the Bence Jones protein if
                                                                                                                                                                                                                      A,Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lan
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGFDYLNWYLQKPGQSPZLLIYALSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Of-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Ciscession: $40371
Rixlein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Reference number: $40371
A;Reference preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-121 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVMIQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTQSPLSLPVTPGEPASISCRSSQSLLXSTGYNYLDWYLQKPGKSPQLLIYLGSKRASGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MIOSPLSLPVIPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRASGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;13-92/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

89.9%; Score 525; DB 1; Length 11

Best Local Similarity 90.2%; Pred. No. 5.1e-40;

Matches 101; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, Indels
```

RESULT 9

셤 ò qq

ठ g

```
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHRYGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 DIVWIQSPLSLPVIPGEPASISCRSSQSLIHSNGYDYLDWYLQKPGQSPQLLIYLGSNRA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-II region (Inc) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S03876
                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840319
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
A;Accession: S40319
A;Accession: S40319
A;Accession: C;Accession: S40319
A;Accession: C;Accession: S40319
A;Accession: S40319
A;Accession: S40319
A;Accession: S40319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLRSNGYNYLDWYLOKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Residues: 1-123 «KLE».
A, Residues: 1-123 «KLE».
A, Cross-references: EMBL. X72429; NID: g441326; PIDN: CAAS1097.1; PID: g441327
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer: immunoglobulin
P;26-105/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F; 16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 SGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQALQTPSVTSAKG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSP-ITFGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 488; DB 2; L
Pred. No. 8.9e-37;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.6e-37; 5; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.2%; Score 497.5; Best Local Similarity 89.7%; Pred. No. 1.66 Matches 96; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Data Library, July 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 83.6%;
1 Similarity 94.0%;
94; Conservative
                                                                                                                                                                                                                                  Ig kappa chain V region – human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;van Es, J.H.
submitted to the EMBL Data L
A;Reference number: S24679
A;Accession: S24681
A;Actus: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Accession: S24681
                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S24681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KESULT 12
KZHUML

RIP KARDAD

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
C;Complex: An immunoglobulin heterotetramer subunit subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                              Ig kappa chain V-J region - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Accession: S40372
E; Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: S40312; MUID: 94080891; PMID: 8258341
A; Accession: S40372
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-131 < KLE>
A; Cross-references: EMRA
A; Residues: 1-131 < KLE>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 36-115/ Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIVMTQSPLSLPVTPGESASFSCKTSQSLLHSNGHNYLDWYLDWFQKPGQSPQLLIYLGSTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                61 PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPTTFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Residues: 1-112 < DRE>
A Cross-references: UNIPROT: P01616
A; Cross-references: UNIPROT: P01616
A; Note: the C region of this chain has the Inv (3) marker C; Comment: This is a Bence Jones protein.
C; Genetics:
A; Genetics:
A; Genetics:
A; Cross-references: GDB:136265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.3%; Score 514; DB 2;
88.3%; Pred. No. 5.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.5%; Score 499.5; DB 1
Best Local Similarity 82.1%; Pred. No. 9.5e-38;
Matches 92; Conservative 14; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 88.3
nes 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
```

g ò g

ઠે

1,

9

ö

g ò

ઠ

```
R;Ferri, G.; Stoppini, M.; Iadarola, P.; Bellotti, V.; Merlini, G.
Blochim. Biophys. Acta 995, 103-108, 1989
A;Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.
A;Recession: S03876; MUID:89194238; PMID:2495028
A;Accession: S03876
A;Molecule type: protein
A;Residues: 1-124 <FER>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.0%; Pred. No. 1.4e-36;
Matches 93; Conservative 9; Mismatches 10; Indels
```

a ò

ઠે g

. 0

Gaps

ô

Search completed: November 16, 2005, 22:04:06 Job time: 14.3824 secs

٠.

Color of Edward Color

.

Н

```
107
27
117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULPID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                          KV2E HUMAN
                                                                                                                                                                                                                                                                                                                 homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo Bapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus sp. b3(
                                                                                      November 16, 2005, 21:36:13; Search time 62.7941 Seconds (without alignments) 913.348 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a gcore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                    1 DIVMTQSPLSLPVTPGEPAS.........CMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01616 | P01615 | P01614 | Q652q7 | Q66491 | Q8tcd0 | P06310 | P06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PO1631
Q9ul80
Q65zc0
P01630
P01630
P03976
P01628
P01628
P01628
P01628
P01628
P01628
P01628
P01628
P016314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01627
P01620
P18136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09ul78
P06313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P06309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26pih6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8nek0
                                                                                                                                                                                                                                                                                                 1612378
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                1612378 seqs, 512079187 residues
 GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV2E HUMAN
QBNEKO
KV2D HUMAN
QGPIHG
KV2C HUMAN
KV2B HUMAN
KV2A HUMAN
QG5ZQ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OBTCDO
KV2F HUMAN
KV2G MOUSE
Q9ULE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O652CO
KV2F_MOUSE
KV2F_MOUSE
KV2F_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GELEMB
KV2C MOUSE
KV2A MOUSE
KV4A HUMAN
KV4C HUMAN
GEKBÖS
KV3D HUMAN
GOUL7B
KV3L HUMAN
KV3L HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV2B_MOUSE
KV3B_HUMAN
KV3M_HUMAN
                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CANFA
                                                                                                                                                                                                           Scoring table: .BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                      UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
                                                                                                                                                US-10-660-357A-2
584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
                Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.3
68.3
66.7
65.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405
399
389.5
381.5
378.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536
535
535
519.5
499.5
469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416
415.5
                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371
371
371
369
367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405
                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                       Sequence:
                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
```

	homo sapien												
	Q6p118												
KV3S MOUSE	Q6PIL8	KV3U MOUSE	KV3A HUMAN	Q920 <u>E</u> 9	KV3R MOUSE	KV3E_HUMAN	KV3G_HUMAN	Q6GMV9	KV3M MOUSE,	KV3N MOUSE	KV3T_MOUSE	KV3 F HUMAN	KV4D HUMAN
Н	~	-	-	~	-	-	٦	~	ч	7	-	٦	-
111	236	111	108	111	111	109	109	235	111	111	111	109	109
	9	4	e.	۲.	σ.	5.1	1.5	1.3	6.0	7.0	0.7	9.0	0.5
62.6	62.	62	62	62	6	6	9	9	ō	ĕ	ō	9	9
	365.5 62.												

ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                             Klobeck H.G., Solomon A., Zachau H.G.; "Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain V-II region GM607.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW; 92C57DC719E558B1 CRC64;
                                            01-JNN-1988 (Rel. 06, Created)
01-JNN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G Kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human).
117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, Q99M37, II91.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z00009; -; NOT ANNOTATED_CDS
PIR; A01889; K2HUGM.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=84191506; Pubmed=6325927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SWOO406, IGY; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12664
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Nature 309:73-76(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1117
27
43
58
65
65
97
106
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
```

N

ô

0; Gaps

5; Indels

6; Mismatches

```
101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                              JT 3
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
     Matches
                                                                                                                                                                                                                                                                                                                       KV2D
                                                                                                                                                                                                                                                                                                                                                        SOLUTION OF THE STANDARD OF TH
                                                                                                      g
                                                                                                                                                              ò
                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hepkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
A Attachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Scapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raba S., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Rabey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Dones S.J., Marra M.A.,
A Marra M.A.,
A Dones S.J., Marra M.A.,
A Marra M.A., Schmutz J., Myers R.M., Schein J.E.,
A Dones S.J., Marra M.A.,
A Marra M.A., Sodergren E.D., Dickson M.C.,
A Dones S.J., Marra M.A.,
A Marra M.A., Sodergren E.D., Dickson M.C.,
A Dones S.J., Marra M.A.,
A Marra M.A., Sodergren E.D., Dickson M.C.,
A Dones S.J., Marra M.A.,
A Marra M.A.,
A Marra M.A., Sodergren E.D., Dickson M.C.,
A Marra M.A., Sodergren E.D., Dickson M.C.,
A Dones S.J., Marra M.A.,
A Marra M.A., Sodergren E.D., Dickson M.C.,
A Marra M.A., Sodergren E.D., Schmerch A., Schein J.E.,
A Marra M.A., Sodergren E.D., Myers R.M., Butterfield M. S.,
A Marra M.A., Sodergren E.D., Myers R.M., Schein J.E.,
A Marra M.A., Sodergren E.D., Myers R.M., Schein J.E.,
A Marra M.A., Sodergren E.D., Schmutz J., Myers R.M., Schein J.E.,
A Marra M.A., Sodergren E.D., Schmutz J., Myers R.M., Schein J.E.,
A Marra M.A., Sodergren E.D., Schmutz J., Myers R.M., Schein J.E.,
A Marra M.A., Sodergren E.D., Schmutz J., Sodergren E.D., Schmutz J., Sodergren E.D., Schmutz J., Sodergren E.
                                                          ö
                                                                                                               9
                                                                                                                                                           64
                                                                                                         DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                              DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFQGFKVEIK 116
                                                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                          ó
Score 536; DB 1; Length 117;
Pred. No. 5.1e-48;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030814; AAH30814.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26024 MW; F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.6%; Score 535; DB 2; 90.2%; Pred. No. 1.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR007110; Ig-like.
Interpro; IPR00359; Ig_cl.
Interpro; IPR003596; Ig_MHC.
Interpro; IPR003596; Ig_WHC.
Interpro; IPR003596; Ig_v.
Pfam; PP07654; Cl-set; l.
PR031TE; PS06035; IG_LIKE; 2.
PROSITE; PS060290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
     Query Match
Best Local Similarity 92.0%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S23638; S23638.
PIR; S34091; S34091.
PIR; S40342; S40342.
PIR; S40357; S40357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al protein.
239 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01834; 117Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      QBNEKO;
                                                                                                                                                                                                                                                                                                                                                                                                          OBNEKO
                                                                                                                                                                                                                                                                                                                                                   RESULT 2
Q8NEKO
                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                  g
                                                                                                               8
                                                                                                                                                                                                                      ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
  9
                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                          21 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRA
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case of
                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                        81 SGVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQGLQTPQTFGQGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.9%; Score 525; DB 1; Length 113; larity 90.2%; Pred. No. 6.9e-47; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-1.
Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
MEDLINE=73166638; PubMed=4700495;
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman B.F.,
Glenner G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Amyloid; Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12316 MW; 0C3C38F81F1843CA CRC64;
                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
22-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-II region TEW
                                                                                                                                                                                                                                    113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, Q99M37; II9I.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
Sfan; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Framework-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Framework-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE (BENCE-JONES PROTEIN TEW).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primary amyloidosis.";
Biochemistry 12:3763-3780(1973)
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
39
54
61
102
112
93
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A90370; K2HUTW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Sim
Matches 101;
                                                                                                                                                                                                                                  KV2D HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

us-10-660-357a-2.rup

```
MEDLINE=76253627; PubMed=821524;
Riesen W.F., Jaton J.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A01887; KRHUML.
HSSP; Q99M37; 1191.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
38
38
101
1111
1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112
112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
92; Conserv
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                   KV2C HUMAN
P01616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                           81
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
KV2B HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV2B_
                                                                                                                                        유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
XX MEDINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
X Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Parmar A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
N Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
M. Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGFDYLNWYLQKPGQSPZLLIYALSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIVMAQSPLSLSVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIYWGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVMIQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQS-PITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGGGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 89.0%; Score 519.5; DB 2; Length 240; Best Local Similarity 90.3%; Pred. No. 6.3e-46; Matches 102; Conservative 2; Mismatches 8; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034142; AAH34142.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;
                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                 240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterProf. IPR003599; IG.
InterProf. IPR003109; IG-like.
InterProf. IPR003109; Ig_C1.
InterProf. IPR003006; Ig_MHC.
InterProf. IPR003966; IG_WHC.
InterProf. IPR00396; IG_V.
Pfam; PP07654; C1-set; I.
SMART; SM004007; IGC1; I.
SMART; SM004007; IGC1; I.
                                                                                                                                                                                                                                        05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, 16-JUL_2004 (TrEMBLrel. 27, 14) Thypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sednences."
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01837; 1KB5
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissue=Lung;
                                           61
                                                                                                                                                                                               О6РІН6
                                                                                                                                                   RESULT A

OF PINE

OF
유
                                           ò
                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVLTQSPLSLPVTPGEPASISCRSSQNLLZSBG-BYLDWYLZKPGZSPZLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dreyer W.J., Gray W.R., Hood L.E.;
The genetic, molecular, and cellular basis of antibody formation:
some facts and a unifying hypothesis.";
Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12055 MW; E5B22E2FA7ABE481 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.5%; Score 499.5; DB 1;
82.1%; Pred. No. 3.1e-44;
iive 14; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PP00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PSS0835; IG LIKE; 1. Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P016I5;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
25-UUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-II region FR.
                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
IG kappa chain V-II region MIL.
Homo sapiens (Human).
                                                                                                                                                                           Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Framework-4.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Framework-2.
```

ä 9 59 us-10-660-357a-2.rup

```
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=10095;
                                                        NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6P491
Q6P491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q6P491
ID Q6
AC Q6
DT 05
                                                                                                                                                                                            065207
                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
   SO F FF WAR DR.
                                                                                                                            g
                                                                                                                                             8
                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                            1 DVVMTQSPLFLPVTLGEPASIQCRSSQSLVYRBGBTYLBWYLQKPGQSPELLIYLSSYRD 60
                                                                                                                                                                                                                                                  1 DIVMTOSPLSLPVTPGEPASISCRSSOSLLRSNGYNYLDWYLOKPGOSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).",
                                                                                                                                                                                                                                                                                  SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                   DB 1; Length 113;
                                                                                                                                      Complementarity-determining-1.
                                                                                                                                              Framework-2.
Complementarity-determining-2.
                                                                                                                                                                    Complementarity-determining-3
                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                   OCODA39E46DB96BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
[2]
                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
DOMAIN V region.
                                                                                                                                                                                                                   80.3%; Score 469; DB 1; 79.5%; Pred. No. 4.8e-41; tive 9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         115 AA
                                                                                                                                                                                     By similarity.
                                                                                                                                                                              Framework-4
                                       PIR; A01886; KZHUFR.
HSSP; Q99M37; 1191.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR001596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 50; 52; 96 AND 97.
MEDLINE=70063440; PubMed=4188189;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=68242259; PubMed=5586923;
                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V-II region Cum
                                                                                                                                                                                                    12660 MW;
                                                                                                                                                                                                                           Best Local Similarity 79.5%;
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                           103
23
113
113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                       KV2A HUMAN
P01614;
                                                                                                                                                                                    DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                    Query Match
                                                                                                                                      DOMAIN
                                                                                                                                                     DOMAIN
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                 KV2A_HUMAN
                                                                                                                                                                                                                                                                  g
G
                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
ö
                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                  29
                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTOSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                      2 DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSGDGNTYLNWYLQKAGQSPQLLIYTLSYR
                                                                                                                                                                                                  1 DIVMTOSPLSLPVTPGEPASISCRSSOSLLRS-NGYNYLDWYLQKPGOSPHLLIYLGSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                             60 ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                            62 ASGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCMQRLEIPYTFGQGTKLEIR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                    1;
                                                                                                                                          Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.1%; Score 450; DB 2; Length 24 76.8%; Pred. No. 1.2e-38; ive 9; Mismatches 17; Indels
                                                                                                                                                                      Indels
                                                                                                115 115
115 AA; 12676 MW; 59E9F90A379569EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Pfar, PF00047; ig; 1.
SMART, SW00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
PTGTT.FID 24 95
                                                                                                                                       Score 464.5; DB 1
Pred. No. 1.4e-40;
7; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ź
                                                                                                                                                                                                                                                                                                                                                                    248 AA
                                                                                                                                                                                                                                                                                                                                                                065ZQ7
065ZQ7
25-OCT-2004 (TEMBLrel. 28, Cx
25-OCT-2004 (TEMBLrel. 28, La
25-OCT-2004 (TEMBLrel. 28, La
35-OCT-2004 (TEMBLrel. 28, La
B3 (Fv) - PE40 (Fragment).
                                                                                                                                          79.5%;
                                                                                                                          Query Match
Best Local Similarity 82.5.
Best Local 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 76.8
Les 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
```

```
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                      SEQUENCE FROM N.A
                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV2F HUMAN
P06310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
KV2F HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
 SETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                    **REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altausner R.D., Colline F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerdew K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caraninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
N. Hichards S., Worley K.C., Hale S., Garria A.M., Gay L.J., Hulyk S.W.,
N. Helton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Andrianski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIVMTQTPLSSPVTLGQPASISCRSSESLLHSNGNTYLSWLHQRPGQPPRLLIYKISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 SGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVSHFPRTFGQGTRVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 76.5%; Score 447; DB 2; Length 239; Local Similarity 78.6%; Pred. No. 2.3e-38; es 88; Conservative 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skin;
Straumberg R.;
Straumberg R.;
Submitted (GEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0631599; AAH631599.1; -.
HSSP; P01837; IKCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 239 AA; 26245 MW; CD73131DDFFD358B3 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PR07654; C1-set; 1.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                     Homo sapiens (Human)
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBTCD0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBTCD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
Q8TCD0
ID Q8TCD0
AC Q8TCD0
DT 01-JU
DT 01-MU
DT 01-MU
DE HYPOEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
```

```
Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altaubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McZwan P.J., McKernan R.J., Malek J.A., Gunzarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DVVWTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTOSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVPDRFSGSGSGTDFTLKITRVEAEDVGVXFCMQGTHWPSTFGQGTKLEIK 132
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Strausbergs,
Strausbergs,
Strausbergs,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databages.
R EMBL BC02362; AAH22362.1; -.
R PIR; S34095; S34095.
R PIR; S40374; S40334.
R PIR; S42267; S42267.
R PIR; S42267; S42267.
R RSPP PRO134; 1172.
R InterPro; IPR00110; Ig-like.
R InterPro; IPR003597; Ig_c1.
R InterPro; IPR003597; Ig_c1.
R InterPro; IPR003596; Ig_WHC.
R InterPro; IPR003596; Ig_V.
R Flam; PF07654; C1-set; I.
R SWART; SW0406; IGV; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 76.4%; Score 446; DB 2; Length 23 Local Similarity 76.8%; Pred. No. 2.9e-38; Local 86; Conservative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region RPMI 6410 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA
```

ö

g ò g

```
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HASP, POIGES, ILVE.
INCERPO, IPRO07110; IG-like.
INCERPO, IPRO0356; IG-V.
SMART; SMO0406; IGV; 1.
PROSITE; PS50835; IG-LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            23
39
54
61
112
112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; B49002; B49002.
PIR; S23638; S23638.
PIR; S34094; S34094.
PIR; S34095; S34095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 1
114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ULBO
Q9ULBO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fetus.",
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBTINGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V-II region RPMI 6410.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                     SEQUENCE FROM N.A. MEDLINE=86041852; PubMed=2997711; Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.; "Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%; Score 444; DB 1; Length 133; 77.7%; Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-2.
Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14707 MW; 513CCAF3673009EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A01890; KZHURP.
HSSP; Q9M37; I191.
GO; GO:00005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; I2-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SWART; SW00406; IGv; 1.
IMMUNOGlobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Framework-2
                                                                                                                                                                                                                                        Nucleic Acids Res. 13:6499-6513(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
STRAIN=A/J;
MEDLINE=83178921; PubMed=6404298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z00020; CAA77315.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
114
123
43
133
133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KV2G MOUSE
P01631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REAL SECTION OF THE S
     SOUCH THE TEST TO BE A DESCRIPTION OF THE TEST TO BE A DESCRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
```

```
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.8%; Score 437; DB 1; Length 113; 75.9%; Pred. No. 1e-37; ive 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                        Framework-3. Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12273 MW; F9F39CE949A84C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035034; AAD56270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
                                                                                                                                                                                                                                                                                                                         Framework-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Framework-4
```

ö

```
Search completed: November 16, 2005, 22:01:50 Job time : 63.7941 secs
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                              1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kipp B., Schlaak M., Becker W.M.; "Cloning and expression of a recombinant mouse Fab-fragment recognizing a defined linear epitope of Chironomus thummi thummi major allergen Chi t I."; Inc. Arch. Allergy Immunol. 110:348-353(1996).
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQ-SPITFGQGTRLEIK 112
                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPWTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ı,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                         Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 219;
                    Score 428.5; DB 2; Length
Pred. No. 8.1e-37;
9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.3%; Score 428; DB 2; Length 21
Best Local Similarity 75.0%; Pred. No. 2e-36;
Matches 84; Conservative 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23944 MW; 7E1B82A14EAF8445 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-II region 7834.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kappa light chain C region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Balb/c; TISSUE=Spleen;
MEDLINE=96319505; Pubmed=8768802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z37499; CAA85724.1; -...
INECPPCO; IPR003599; IG.
INICEPPCO; IPR0031599; IG.
INICEPPCO; IPR003597; IG.CI.
INICEPPCO; IPR003006; IG_MHC.
INICEPPCO; IPR003506; IG_V.
Pfam; PF007654; CI-set; I.
                    Query Match
Best Local Similarity 76.1%;
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00409; ĪG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV2F MOUSE
P01630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
KV2F_MOUSE
ID KV2F_MC
AC POL630;
DT 21-JUL-
DT 05-JUL-
DE 19 kapg
                                                                                                                                                                                                                                                                                                                                                                                         065ZC0
                                                                                                                                                                                                                                                                                                                                      RESULT 14
0652C0
AC 0652C0
DT 25-0C
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                           셤
                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
ö
                                                                                                                                                  Charge 12. The background of the variable region of kappa-
Thang J.-Y., Herbet H., Aebersold R., Braun D.G.;
Chang J.-Y., Herbet H., Aebersold R., Braun D.G.;
Chang J.-Y., Herbet H., Aebersold R., Braun D.G.;
I she wisotype sequence (V kappa 27) of the variable region of kappa-
Tight chains from a mouse hybridoma-derived anti-(streptococcal group
T plant of the dimethylaminoazobenzene isothiocyanate technique
T ppilication of the dimethylaminoazobenzene isothiocyanate technique
T for the isolation of peptides.
The for the isolation of peptides.
The STELLANEOUS: This chain is from a hybridoma-derived monoclonal
antibody against the streptococcal group A polysaccharide.
R PIRSP, Q99M37, 1191.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR007120; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMIQTAPSALVIPGESVSISCRSSKSLLHSNGNTYLYWFLQRPGQCPQLLIYRMSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLBIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.
Hybridoma; Immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-3. Framework-4. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity-determining-2. Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12496 MW; 42C019D10ADA3C91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 420; DB 1;
Pred. No. 6.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Hy
Monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
```

(C1327) 3. W. See 2. O. C. S. S. M.

```
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 113 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
  1008
1008
1008
1009
1009
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1251 Aver
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  10021
                                                                                                                                                                                                                                                US-09-025-769B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-025-769B-15
Query Match
  Sequence 8, Appli
Sequence 2, Appli
Sequence 30, Appl
Sequence 151, App
                                                                   November 16, 2005, 21:41:29; Search time 19.0441 Seconds (without alignments) 439.017 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45, Al
Sequence 29, Al
Sequence 45, Al
Sequence 178,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 178
Sequence 178
                                                                                                                               1 DIVMTQSPLSLPVTPGEPAS.......CMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-025-769B-45
US-09-490-070A-29
US-09-490-153-29
US-09-490-153-29
US-09-490-153-29
US-09-490-124-29
US-09-490-124-45
US-09-490-070A-178
US-09-490-070A-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-025-769B-15
US-09-490-070A-15
US-09-490-15-15
US-09-28-180-9
US-09-28-180C-9
US-08-311-397B-49
US-08-311-397B-49
US-08-75-804A-49
US-08-75-804A-49
US-08-75-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-488-113B-151
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-490-324-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-053-171-16
                                                                                                                                                                                  513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 protein search, using sw model
                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                        US-10-660-357A-2
584
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                    Copyright
                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                     Scoring table:
                                                 OM protein
                                                                                                                                  Sequence:
                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                    Database
                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                               Sequence
      Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09025769B

Sequence 15, Application US/09025769B

Batent No. 630064

GENERAL INFORMATION:
APPLICANT: Rnappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Red, Liming
APPLICANT: Pluckthuing
APPLICANT: Pluckthuin, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.7%; Score 553; DB 3; Length 113; larity 94.6%; Pred. No. 7.3e-47; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-PEB-1998
FILING DATE: 18-FEB-1998
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECPHONE: (212):596-9000
US-08-477-484B-151
US-08-107-669D-15
US-08-472-78B-15
US-08-477-531B-151
US-08-082-842A-15
US-08-082-842A-151
US-09-136-389-151
US-09-136-389-151
US-09-136-389-151
US-09-136-389-151
US-08-478-039-88
US-08-478-039-88
US-08-478-039-88
US-08-482-882-66
US-08-482-882-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-389-66
US-08-483-383-66
US-08-483-383-66
                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
```

```
JS-09-490-153-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-490-153-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                            1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK 112
                                                                                                                            SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK 112
                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 1DAPY disk
COMPUTER: 1DAPY disk
COMPUTER: 1DAP PC compatible
COMPUTER: 1DAP PC compatible
COMPUTER: 1DAP PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY'AGENT INFORMATION:
NAWE: COLIN G. SANGETCOCK, ESG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.7%; Score 553; DB 4; Length 113; 94.6%; Pred. No. 7.3e-47; Live 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                              Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-070A-15
                                                                                                                                                                                                                            US-00-490-070A-15
Sequence 15, Application US/09490070A
Patent No. 6696248
GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                                                                APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 94.6
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                 ilag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                       g
                                                                                                    ò
                                                                                                                                     원
```

RESULT 3

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EPS-1998
APPLICATION NUMBER: EPS-1998
APPLICATION NUMBER: EPS-1998
APPLICATION NUMBER: B-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

94.7%; Score 553; DB 4; Length 113;
Best Local Similarity 94.6%; Pred. No. 7.3e-47;
Matches 106; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-00-490-324-15
; Sequence 15, Application US/09490324
; Sequence 15, Application US/09490324
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Lilag, Vic
Ge, Liming
; Maxoney, Simon
Plueckthun, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)596-9000
TELERA: (212)596-9000
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
```

ö

```
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHNNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-08-331-398A-49
; Sequence 49. Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: FitzGeral, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Brinkmann, Ulrich
; TITLE OF INVENTION: and Their Uses (as amended)
; TITLE OF INVENTION: and Their Uses (AS ADDRESSER)
; CORRESPONDENCES: 68
; CORRESPONDENCES of Brinkmann and Townsend and Crew
; TIRET: One Market Plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                        Query Match

94.2%; Score 550; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.4e-46;
Matches 105; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATPONENT/AGENT INFORMATION:
AMADE: LARGE TO THE COMPATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5600
TELEPAX: (415) 543-5603
INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
; PRIOR FILING DATE: 1996-09-02; NUWBER OF SEQ ID NOS: 183; SOFTWARE: Patentin version 3.1; SEQ ID NO 9; LENGTH: 112; TYPE: PRT; TYPE: PRT; ORGANISM: Homo Bapiens US-09-254-180C-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OKUMURA, Ko

APPLICANT: OKUMURA, Ko

APPLICANT: EDA, Yasuyuki

APPLICANT: WAEDA, Hiroaki

APPLICANT: WAEDA, Hiroaki

APPLICANT: WAEDA, Hiroaki

APPLICANT: WINCHIO, Yoshitaka

APPLICANT: WAKAFA, Motcomi

TILLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or

TILLE OF INVENTION: Fragmente Thereof, and Apoptosis-Induced Site From Fas Ligand

TILLE OF INVENTION: Fragmente Thereof, and Apoptosis-Induced Site From Fas Ligand

TILLE OF INVENTION: Fragmente Thereof, and Apoptosis-Induced Site From Fas Ligand

FILE REFERENCE: 050006-0055

CURRENT APPLICATION NUMBER: PCT/JD97/02983

PRIOR PILING DATE: 1999-04-15

PRIOR PILING DATE: 1996-09-20

PRIOR PILING DATE: 1996-09-20

PRIOR APPLICATION NUMBER: 221246/1996

PRIOR PILING DATE: 1996-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMIQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVBAEDVGVYYCMOALOTPYTFGOGTKLEIK 112
                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDUIW TYPE: Floppy disk,
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSCYWARE: PATORIL Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: AND 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: AND 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: AND 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,
0
                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Score 553; DB 4; Length 113; 94.6%; Pred. No. 7.3e-47; Live 2; Mismatches 4; Indels
   TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09254180C
Patent No. 6777540
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.6%
Matches 106; Conservative
                                                                                                                                                  CITY: New York
STATE: New York
                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-254-180C-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-490-324-15
```

ઠ

ઠે

ô

0; Gaps

92.0%; Pred. No. 3.3e-45; tive 3; Mismatches 6; Indele

```
1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 60
                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
Best Local Similarity 92.0 Matches 103; Conservative
                                                                                                                                                                                          ò
                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-31-3978-49

US-08-31-3978-49

Sequence 49, Application US/083313978

Patent No. 5981726

GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Pastan, Ita
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STREET: ADDRESSE:
STREET: ADDRESSE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: ADDRESSE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: ADDRESSEE: Townsend and Townsend and Crew
STREET: ADDRESSEE: Townsend and Townsend and Crew
CITY: San Francisco
                                                                                                                                                                                                                                                                           1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                       61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                     SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFGQGTKVEIK 112
                                                                                                                                Score 536; DB 1; Length 112;
Pred. No. 3.3e-45;
3; Mismatches 6; Indels
                           /note= "Human IgM antibody GM607
Variable Light chain (V-L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Human IgM antibody GM607
Variable Light chain (V-L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION WHERE: US/07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/566,289
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015280-126120US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hunter, Tom
REGISCRATION UNUMBER: 38,498
REFRENCE/DOCKET NUMBER: 0152/
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   91.8%;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 112 amino acids
amino acid
                                                                                                                                   Query Match
Best Local Similarity 92.0°
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein LOCATION: 1..112 OTHER INFORMATION: OTHER INFORMATION:
LOCATION: 1..112
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-331-397B-49
                                                                                US-08-331-398A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                         원
```

91.8%; Score 536; DB 2; Length 112;

Query Match

```
91.8%; Score 536; DB 2; Length 112; 92.0%; Pred. No. 3.3e-45;
                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Tumor-Specific Antibody Fragments, TITLE OF INVENTION: Fusion Proteins, and Uses Thereof NUMBER OF SEQUENCES: 68
CORRESPONDENCES: ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Human IgM antibody GM607
Variable Light chain (V-L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/759,804A

FILING DATE: 03-DEC-1996

CLASSIFICATION NUMBER: US/08/739,31,398

FILING APPLICATION NUMBER: US 08/331,398

FILING DATE: 28-OCT-1994

PRIOR APPLICATION NUMBER: US 07/767,331

FILING DATE: 32-SEP-1991

PRIOR APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-OCT-1990

ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                 Sequence 49, Application US/08759804A
Patent No. 5990296
                                                                                                                                                                                                               APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1.112
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                         US-08-759-804A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-759-804A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
```

```
엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                        ઠે
     ö
                                                                          1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 60
                                                   1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PASTAN, Ira
APPLICANT: BENHAR, Itai
APPLICANT: BENHAR, Itai
APPLICANT: PADLAN, Eduardo A.
APPLICANT: UNG, Sun-Hee
APPLICANT: UNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: PRAGMENTS, FUSION PROTEINS, AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                         SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFGQGTKVEIK 112
                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 112
  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM GM607 VL region"
US-09-227-693-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.8%; Score 536; DB 3; L
Best Local Similarity 92.0%; Pred. No. 3.3e-45;
Matches 103; Conservative 3; Mismatches 6;
  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             Sequence 49, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 amino acids
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                JS-09-227-693-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH:
                                                                                                                                                ઠે
```

1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60

Indels

```
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMIQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLBIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQHYTTPPTFGGGTKVEIK 112
                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                       61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 532; DB 3; Length 114;
Pred. No. 8.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentION NATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATE: EP 95 11 3021.0

FILING DATE: 18-A0G-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794

REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                        GENERAL INPORMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plueckthun, Andreas
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esg. C/O Fish & Naave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 45, Application US/09025769B; Patent No. 6300064
                                                                                                                                                                                                                                                Sequence 29, Application US/09025769B Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELBFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.1<sup>1</sup>
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-025-769B-29
                                                                                                                                                                                                                            US-09-025-769B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-025-769B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
```

```
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45. Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 91.1%;
Best Local Similarity 91.1%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ilag,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-490-070A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-490-070A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 532; DB 3; Length 114;
Pred. No. 8.4e-45;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 7,794
REFERENCE/POCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                    STREET: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Knappik, Achim
Pack, Peter
11ag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
               APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Limino
APPLICANT: Ge, Limino
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-490-070A-29; Sequence 29, Application US/09490070A; Patent No. 6696248; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.1%;
91.1%;
Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212)590-5000
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.1<sup>1</sup>
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212)596-909(
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-025-769B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gарв
COMPUTE: C.C.

ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 31,298
ATTORNEY/AGENT INFORMATION:
REJERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELENGTH: 114 annino acids
LENGTH: 114 annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCQQHYTTPPTFGQGTKVEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ge, Liding
Moroney, Simon
Plueckthun, Andreas
Plueckthun, Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATURE: SM PC COMPATIBLE OPERATURE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 532; DB 4;
Pred. No. 8.4e-45;
3; Mismatches 7;
```

ô

```
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-490-153-45
                                                                                                                                         US-09-490-153-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-490-153-45
                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVXYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                        91.1%; Score 532; DB 4; Length 114; 91.1%; Pred. No. 8.4e-45; rive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: EP 95 11 3021.0 FILING DATE: 18-AUG-1995 ATTORNEY/AGENT INPORMATION:
                                                                 NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31.298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHOME: (202) 912-2020
INFORMATION FOR SEQ ID No: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-070A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.11
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-490-153-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
```

```
ö
                                                                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSILHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
91.1%; Score 532; DB 4; Length 114;
Best Local Similarity 91.1%; Pred. No. 8.4e-45;
Matches 102; Conservative 3; Mismatches 7; Indels
                                                                                                                                            Score 532; DB 4; Length 11:
Pred. No. 8.4e-45;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plueckinn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-F88-199B
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/09490153
Parent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                              Query Match
Best Local Similarity 91.1%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
```

```
6 6 6
```

Search completed: November 16, 2005, 22:07:17 Job time : 19.0441 secs

6, Appli 6, Appli 6, Appli 6, Appli 7, Appli 18, Appli 18, Appli 13, Appl 77, Appl 77, Appl 145, Appl 145, Appl 123, Appl

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

4, Appli 82, Appl 215, App

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Database

```
DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVBAEDVGVYYCWQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 584; DB 14; Length 112; 100.0%; Pred. No. 7.3e-46; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFRENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; RIOR APPLICATION NUMBER: 60/346299
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FRSELSQ for Windows Version 4.0
                                US-11.021.715.99

US-10.229.088-103

US-10.292.088-103

US-10.877.773.30

US-10.877.773.30

US-10.877.773.30

US-10.877.773.30

US-10.725.916A-58

US-10.726.332.212

US-10.726.332.212

US-10.726.332.212

US-10.726.332.226

US-10.269.805.18

US-10.269.805.18

US-10.212.715.81

US-11.021.715.81

US-11.021.715.81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
  Best Local Similarity 100.
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo Sapiens
  SEQ ID NO 2
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-330-613-2
JS-10-330-613-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2, Appli
2, Appli
93, Appli
52, Appl
52, Appl
104, App
75, Appl
74, Appl
74, Appl
                                                                                                                                 November 16, 2005, 22:02:09; Search time 68.7647 Seconds (without alignments) 681.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                  1 DIVMTQSPLSLPVTPGEPAS.......CMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-330-613-2
US-10-330-530-2
US-10-60-357-2
US-11-021-715-93
US-10-292-088-55
US-10-292-088-16
US-11-021-715-90
US-11-021-715-90
US-11-021-715-90
US-11-021-715-90
US-11-021-715-90
                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       1867879 seqs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                           US-10-660-357A-2
584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114
115
115
115
115
116
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1000.0
1000.0
1000.0
94.9
94.7
94.7
94.7
94.7
94.7
```

ö

Gaps

; 0

9

N RESULT

Result No.

```
US-10-292-088-52

US-10-292-088-52

Sequence 52, Application US/10292088

Publication No. US20030211100A1

GENERAL INFORMATION:

APPLICANT: GLADUE, RONALD P.

APPLICANT: GLADUE, RONALD P.

APPLICANT: CORVALAN, JOSE

APPLICANT: TIA, XIAO-CHI

APPLICANT: FENG, XIAO

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFRENCE: ABX-PF/3 US

CURRENT FILING DATE: 2003-03-14

PRIOR APPLICATION NUMBER: US/10/292,088

CURRENT APPLICATION NUMBER: 60/348,980

PRIOR APPLICATION NUMBER: 60/348,980

PRIOR APPLICATION NUMBER: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PATENTING DATE: 2001-11-09

MUMBER OF SEQ ID NOS: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 94.6
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-52
                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-021-715-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-292-088-56
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGGGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 584; DB 16; Length 112; Best Local Similarity 100.0%; Pred. No. 7.3e-46; Matches 112; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 584; DB 14; Length 112; Best Local Similarity 100.0%; Pred. No. 7.3e-46; Matches 112; Conservative 0; Mismatches 0; Indels 0
Sequence 2, Application US/10330530
Publication No. US20030152514A1
FUBLICANT: GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT APPLICATION NUMBER: US 60/346414
PRIOR FILING DATE: 2002-12-26
PRIOR PFLICHED DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:

APPLICANT: Green, Larry L.

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: ANTIGEN

TITLE OF INVENTION: ANTIGEN

FILE REFERENCE: ABGENIX.030C1

CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: 10/330,580

PRIOR FILING DATE: 2002-12-26

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 93, Application US/11021715;
Publication No. US20050208596A1;
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-11-021-715-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-660-357-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-330-530-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-660-357-2
```

엄

요 ð

요 ò 셤

```
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF FILE REPERBENCE: 053993-5050 CURRENT APPLICATION NUMBER: US/11/021,715 CURRENT APPLICATION NUMBER: US/11/021,715 PRIOR APPLICATION NUMBER: US/11/03/21304 PRIOR APPLICATION NUMBER: E0/394,352 PRIOR PILING DATE: 2002-07-03 PRIOR PILING DATE: 2002-07-03 PRIOR PILING DATE: 2002-09-18 PRIOR PILING DATE: 2002-09-18 NUMBER OF SEQ ID NOS: 153 SOFTWARE: PALCHING DATE: 2002-09-18 SOFTWARE: PALCHIN VETSION 3.2 SEQ ID NO 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKPGQSPHLLIXLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVATOSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.9%; Score 554; DB 15; Length 112; 94.6%; Pred. No. 4.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.2%; Score 556; DB 20; Length 1 Best Local Similarity 94.6%; Pred. No. 2.7e-43; Matches 105; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
```

```
GENERAL INFORMATION:
APPLICANT: 31.egel, Donald L.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
FILE REFERENCE: 053893-5050
CURRENT APPLICATION NUMBER: US/11/021,715
CURRENT FILING DATE: 2004-12-23
FRIOR FILING DATE: 2003-07-03
FRIOR FILING DATE: 2003-07-03
FRIOR FILING DATE: 2002-07-03
FRIOR APPLICATION NUMBER: 60/411,694
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2002-07-03
FRIOR FILING DATE: 2003-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 90, Application US/11021715
Sequence 90, Application US/11021715
Publication No. US20050208596A1
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
TITLE REPERENCE: 053893-505
CURRENT APPLICATION NUMBER: US/11/021,715
CURRENT APPLICATION NUMBER: PCT/US03/21304
PRIOR APPLICATION NUMBER: E0/394,352
PRIOR PILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/411,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVMTÓSPLSLPVTPGEPASISCRSSQSLLHTNGYNYLDWYLQKPGQSPQLLIYLGSHRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 553; DB 20; Length 112;
Pred. No. 5e-43;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 94.7%; Score 553; DB 20; Length 11 Best Local Similarity 94.6%; Pred. No. 5e-43; Matches 106; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
94.7%; Score 553; DB
Best Local Similarity 94.6%; Pred. No. 5e-4;
Matches 106; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin version 3.2
SEQ ID NO 90
LENGTH: 112
                                                  Publication No. US20050208596A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-11-021-715-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-021-715-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-021-715-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DIVWTQSPLSLPVTPGEPASISCRSSQSLLYSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHILIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPRTFGQGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
94.7%; Score 553; DB 15; Length 112;
Best Local Similarity 94.6%; Pred. No. 5e-43;
Matches 106; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.9%; Score 554; DB 15; Length 239; 94.6%; Pred. No. 9.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
APPLICANT: GLADUB, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: CORVALAN, JOSE
APPLICANT: JOSE NION TO THE SERVICE: TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 56
LENGTH: 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
ITILE OF INVENTION: ANTIBODIES TO CD40
ITILE REFERENCE: ABX-PF/3 US
CURRENT FILING DATE: 2003-03-14
FILING APPLICATION NUMBER: 60/348,980
PROR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 104
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 75, Application US/11021715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 94.63
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-292-088-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-292-088-104
```

JS-10-292-088-104

ઠે

ઠે

Gaps

ö

US-11-021-715-75 RESULT 8

ò

```
US-11-021-715-87

| Sequence 87, Application US/11021715
| Sequence 87, Application US/11021715
| Publication No. US20050208596A1
| GENERAL INFORMATION:
| APPLICANT: Siegel, Donald L. |
| TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF FILE REFERENCE: 053893-5050
| CURRENT FILING DATE: 2004-12-23 |
| PRIOR PRIOR APPLICATION NUMBER: PCT/US03/21304 |
| PRIOR PRIOR APPLICATION NUMBER: 60/394,352 |
| PRIOR FILING DATE: 2002-07-03 |
| PRIOR FILING DATE: 2002-07-03 |
| PRIOR FILING DATE: 2002-09-18 |
| PRIOR FILING DATE: 2002-09-18 |
| NUMBER OF SEQ ID NOS: 153 |
| SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQRPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 DVVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVWTOSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SGVPDRPSGSVSGTDFTLKISRVEAEDVGVYYCMQALQTPITFGQGTRLEIK 112
                                                                                                                                                                                                             APPLICANT: BASIL GARIG
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
TITLE OF INVENTION: AMYLOID PEPTIDE
FILE REFERENCE: ELM-0.28
CURRENT APPLICATION NUMBER: US/10/858,855
CURRENT PILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: 60/474654
PRIOR FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 552; DB 17;
Pred. No. 7.5e-43;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11arity 94.6%; Score 551; DB 20; 94.6%; Pred. No. 7.7e-43; Conservative 2; Mismatches 4;
                                                                                                                                 Sequence 8, Application US/10858855; Publication No. US20050118651A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.5%;
Best Local Similarity 93.8%;
Matches 105; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
US-10-858-855-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-021-715-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106;
                                                                                 RESULT 12
US-10-858-855-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                               Sequence 74, Application US/11021715

Publication No. US2005020856A1

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET

TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF

TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF

TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF

CURRENT FILING DATE: 2004-12-23

PRIOR FILING DATE: 2004-12-23

PRIOR FILING DATE: 2003-07-03

PRIOR FILING DATE: 2003-07-03

PRIOR FILING DATE: 2002-09-18

NUMBER OF SEQ ID NOS: 153

SEQ ID NO 74

LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
FILE REFERENCE: 053893-5050
CURRENT FILING DATE: 2004-12-23
CURRENT FILING DATE: 2003-07-03
PRIOR FILING DATE: 2003-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PATENTIAN OF SEQ ID NOS: 153
SOFTWARE: PATENTIAN OF SEQ ID NOS: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQXPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 552; DB 20; Length 112;
Pred. No. 6.2e-43;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

94.5%; Score 552; DB 20;
Best Local Similarity 94.6%; Pred. No. 6.2e-43;
Matches 106; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 86, Application US/11021715 Publication No. US20050208596A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.5%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-11-021-715-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-11-021-715-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-021-715-74
```

g ò

a ò

ö

S

```
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
셤
                                                     ઠે
                                                                                                                                                                       Sequence 89, Application US/11021715

Publication No. US20050208596A1

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET

TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF

TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF

TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF

CURRENT APPLICATION NUMBER: US/11/021,715

CURRENT FILING DATE: 2003-07-03

PRIOR FILING DATE: 2003-07-03

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-03

NUMBER OF SEQ ID NOS: 153

SEQ ID NOS: 153

SEQ ID NOS: 153

SEQ ID NOS: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLRSNGYNYLDWYLQKPGQSPHLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQAQQS-PITFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPTFGQGTRLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 94.7%; Pred. No. 1.1e-42;
Matches 107; Conservative 2; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
93.8%; Score 548; DB 15; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.4e-42;
Matches 105; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 103, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, ROMALD P.
APPLICANT: GLADUE, ROMALD P.
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
COURRENT FENG, XIAO-CHI
APPLICANT: FENG, XIAO-CHI
APPLICANT: PENG, XIAO-CHI
APPLICANT: PENG, XIAO-CHI
APPLICANT: PENG, XIAO-CHI
APPLICANT: ANTIBODIES TO CD40
FILE REFERENCE: ARX-PF/3 US
CURRENT APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2003-03-14
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-11-021-715-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-10-292-088-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-292-088-103
  ð
                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPWTFGQGTKVEIK 112
61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGTRLEIK 112
                                                                                                                                                                                  Search completed: November 16, 2005, 23:05:39 Job time : 69.7647 secs
```

OM protein - protein search, using sw model

November 16, 2005, 21:35:48; Search time 61.3676 Seconds (without alignments) 674.351 Million cell updates/sec Run on:

US-10-660-357A-6

Title: Perfect score:

1 EIVMTQSPATLSVSPGERAT......CQQYNNWPRTFGQGTKVEIK 107 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 0B 0B Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 16Deco4:*

1: geneseqp1990s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2001s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SOFTER	
Result No.	Score	Query Match	Length	DB	ID	Description
1	555	100.0	107	_	ADC99777	Adc99777 Anti-huma
7	555	100.0	107	7	ADD05381	Add05381 Anti-MUC1
e	555	100.0	107	7	ADF09819	Adf09819 Human ant
4	546	98.4		7	ADC99805	Adc99805 Anti-huma
ß	546	98.4		7	ADD05409	Add05409 Anti-MUC1
9	546	98.4	107	7	ADD05442	Add05442 Anti-MUC1
7	546	98.4	107	7	ADF09847	Adf09847 Human ant
80	543	97.8		9	ABR54896	Abr54896 Light cha
6	539	97.1		9	ABR54900	Abr54900 Light cha
10	536	9.96	107	9	ABR54897	Abr54897 Light cha
11	536	9.96	107	9	ABR54883	Abr54883 Light cha
12	536	9.96	107	8	ADP22404	
13	536	9.96	107	8	ADP22407	Adp22407 Human ant
14	536	9.96	107	œ	ADR43402	
15	536	9.96	107	æ	ADR31547	
16	534	96.2	107	9	ABR54891	Abr54891 Light cha
17	533.5	96.1	108	9	ABR54906	Abr54906 Light cha
18	533	96.0	107	9	ABR54893	Abr54893 Light cha
19	533	96.0	107	8	ADP22408	.
20	532	95.9	250	ß	ABP45941	Abp45941 Human BLy
21	532	95.9	250	7	ADG96768	Adg96768 Single ch
22	529.5	95.4	117	٣	AAY99557	
23	529.5	95.4	117	9	ABR42856	Abr42856 Tumour-sp
	529.5	95.4	117	ø	ABR42858	Abr42858 Tumour-sp
25	529.5	95.4	117	9	ABR42860	Abr42860 Tumour-sp

117 6 ABR42857 117 7 ABW02466 117 7 ABW02466 117 7 ABW02466 246 5 ABP42257 246 5 ABP42257 107 6 ABR54889 107 7 ADJ80364 1107 8 ADP22278 1107 8 ADC2110 1107 8 ADC21110 1107 8 ADC21110 1107 8 ADC21110 1107 8 ADC21110 1107 8 ABR42851 1117 6 ABR42851 1117 6 ABR42851 1117 7 ABW02460 1117 7 ABW02460	Abr42857 Tumour-sp Abw02466 Human mon Abw02466 Human mon Abw02465 Human mon Abp45257 Human Buy Adg96084 Single ch Abr54889 Light cha Adf80364 Human ant Adp22278 Human ant Adp22278 Human ant Adc61110 Human ant Adc61110 Human ant Adf25472 Human ant	Abr42849 Tumour-sp Abr42853 Tumour-sp Abw02460 Human mon Abw02462 Human mon Abw02459 Human mon
	ABR42857 ABW02446 ABW02466 ABW02465 ABP45257 ADG96084 ADC80364 ADC80364 ADC80364 ADC8110 ADC2110 ADC22778 ADC2110 ADC22778 ADC2110 ADC22778 ADC8110 ADC8110	ABR42849 ABR42853 ABW02460 ABW02462 ABW02459
		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	522.5 522.5 522.5 522.5 522.5
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 9 8 4 3 8 4 8 9 8 9 8 9 8 9 9 8 9 9 9 9 9 9 9 9	4 4 4 4 4 4 4 6 4 6

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 6. ADC99777 standard; protein; 107 AA (first entry) lung cancer; human. 01-JAN-2004 RESULT 1 ADC99777

Homo sapiens.

WO2003057838-A2.

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99779.

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 6; 78pp; English.

a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithal neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody comprising The invention relates to a novel isolated monoclonal antibody

õ

Gapa

. 0

Indels

9 9

SXS

61

셤 ò 원 ADD05381;

```
The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastesis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                  1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; light chain; human.
                                                                      1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLOSEDFAVYYCQOYNNWPRTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human anti-MUC18 monoclonal antibody light chain #2
100.0%; Pred. No. 4e-34; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 555; DB 7; Pred. No. 4e-34; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 6; 83pp; English.
                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                  ADF09819 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 107; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2002; 2002WO-US041580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2001; 2001US-0346414P
  al Similarity 100.
107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-598367/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADF09821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                 ADF09819;
  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gudas J;
    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                               ADF09819
                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                     셤
                                                                         ò
                                                                                                                                                                   ò
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                                                                                            9
                                                                                                                                                                                                                            1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel monoclonal antibody used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                            EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-MUC18 antibody light chain variable region protein, SEQ ID No
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                    Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 107;
                                                                                                                                             0; Indels
                                                                                               Score 555; DB 7;
Pred. No. 4e-34;
                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 555;
    light chain protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 6; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD05381 standard; protein; 107 AA
                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2001; 2001US-0346460P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein of the invention.
                                                                                                                                             Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-577496/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABGE-) ABGENIX INC
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metastatic tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADD05383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107 AA;
                                                   Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003057006-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUL-2003
```

RESULT 2
ADD05381
ID ADD05381
XXX
ADD DE ANT:
XXX
M MOD OF THE OF

```
1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQXPGQAPRLLIYGASTRATGIPA 60
                                                                                                 RESCSCTEFTLISSLOSEDFAVYYCQQYNNWPRIFGQGTKVEIK 107
                                                                     RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                      61
                                                                                                              g
```

Query Match

ô

Gaps

. 0

7; Length 107; Indels 9

RESULT 4

```
The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds WUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostetic and can be used in the production of a vaccine. The monoclonal antibodies against the WUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. mélanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-WUC18 antibody light chain, variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                              Anti-MUC18 antibody light chain variable region protein, SEQ ID No 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-MUC18 antibody light chain variable region L2 protein, SEQ ID
                                                                                        monoclonal antibody, tumour; MUC18; proliferation, cytostatic; antigen; tumour metastasis; melanoma; metastatic; human; light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RESGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.4%; Score 546; DB 7; 97.2%; Pred. No. 1.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 34; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD05442 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                        26-DEC-2002; 2002WO-US041582.
                                                                                                                                                                                                                                                                                                                                                    28-DEC-2001; 2001US-0346460P.
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-577496/54.
N-PSDB; ADD05411.
                                                                                                                                                                                                                                                                                                                                                                                                  (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastatic tumor.
                                                                                                                                                                                                           WO2003057006-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107 AA;
                                                                                                                                                                 Homo sapiens.
01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-2004
                                                                                                                                                                                                                                                       17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD05442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD05442
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WCI8. The monoclonal antibody of the invention demonstrates evrostatic activity and may be useful for treating a disease or condition associated with the expression of MUCI8 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUCI8 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                          anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated monoclonal antibody comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                   Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 546; DB 7; Length 107;
Pred. No. 1.9e-33;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 34; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 current sequence is that of the anti-
light chain protein of the invention.
                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD05409 standard; protein; 107 AA
                                                                                        ADC99805 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2002; 2002WO-US041581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-2001; 2001US-0346299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.2%;
Matches 104; Conservative
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-587113/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                      lung cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADC99807
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003057838-A2
                                                                                                                                                                                                                                                                                                                                                                                                     Ното варіепв.
                                                                                                                                                                                     01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-2003
                                                                                                                                      ADC99805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD05409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gudas J;
```

ADG9980S:

ö 9 9

Gaps

ö

Length 107; 1; Indels 67.

RESULT 5
ADD05409
ID ADD0
XX
AC ADD0
XX

셤 ઠે

ઠે 셤

```
The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting cell for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                           Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BIVMTQSPATLSVSPGBRATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Engineered template, single primer amplification; antibody library; nucleic acid amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.4%; Score 546; DB 7; Length 10 97.2%; Pred. No. 1.9e-33; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Light chain clone HBPAXK2d 3A9 SEQ ID NO:122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maruyama T,
                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID NO 34; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR54896 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowdish KS, Frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-2001; 2001US-0323455P
                                                        26-DEC-2002; 2002WO-US041580.
                                                                                                      28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2002; 2002WO-US029889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.2
Matches 104; Conservative
                                                                                                                                                                                                                                   WPI; 2003-598367/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody
                                                                                                                                                 (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                         N-PSDB; ADF09849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003025202-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2003
                  17-JUL-2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR54896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                            Gudas J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR54896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a menoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in chibited proliferation of the cells. The monoclonal antibody has cytosteric and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metaerasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; light chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
antigen; tumour metastasis; melanoma; metastatic; human; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human anti-MUC18 monoclonal antibody light chain #9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 546; DB 7;
Pred. No. 1.9e-33;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 67; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF09847 standard; protein; 107 AA
                                                                                                                                                                        26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                 28-DEC-2001; 2001US-0346460P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 97.2%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein of the invention.
                                                                                                                                                                                                                                                                                                       Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                            (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-577496/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                               metastatic tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107 AA;
                                                                                    WO2003057006-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2004
                                                                                                                            17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF09847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
```

ö 9 9

0; Gaps

Length 107;

Renshaw M;

Lin Y,

쉱 ð 셤

ð

ហ

```
The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered nucleic acid strand (S) acid strand. M1 comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence in the presence of a polymers or and nucleotides under conditions suitable for polymerisation of the nucleotides under conditions suitable for polymerisation of the nucleotides under conditions suitable for polymerisation of the nucleotides. Also described is an engineered and a sequence complementary to the predetermined sequence at the other end. M1 is useful for to the predetermined sequence at the other end. M1 is useful for complementary to the predetermined sequence at the other end. M1 is useful for products that can be used for products that can be used complementary in a susfable expression vector, where the vector can be used to transform an appropriate host organism to produce the polypeptide or protein encoded by the target sequence. M1 is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of antibody library M1 is useful not only for producing large amounts of confidered than one different target nucleic acid sequence located on the same or different nucleic acid sequence located on the same or different nucleic acid sequence and in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                           Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Engineered template, single primer amplification, antibody library, nucleic acid amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 543; DB 6; Length 107;
Pred. No. 3.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain clone HBPAXK2d 3D12 SEQ ID NO:126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.8%; Scor.
98.1%; Pred. No. 5...
1; Mismatches
                                                                                                                                                                                                                                                                                                         Example 3; Fig 8b-c; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR54900 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-SEP-2002; 2002WO-US029889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-2001; 2001US-0323455P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 98.1
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003025202-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR54900;
                                                                                                                                                                                                                                     seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
ABR54900
ABR54900
AC ABR5
XX
AC ABR5
XX
XX
DT 30-J
XX
XX
CO BC

ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other, and contacting (S) with a primer having the predetermined sequence in the presence of a polymers concletions under conditions suitable for polymerisation of the nucleotides. Also described is an engineered nucleic acid strand (I) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other end. M1 is useful for amplifying a nucleic acid. M1 can be used for producing an antibody library. M1 is useful for preparing amplified products that can be used to transform an appropriate host organism to produce the polypeptide or protein encoded by the target sequence. M1 is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of antibody library uncleic acid sequence, but also for amplifying simultaneously more than one different target nucleic acid sequence.

SECOND SECON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGTSTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                              Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Engineered template, single primer amplification, antibody library, nucleic acid amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
  Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPGTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
  Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 539; DB 6;
Pred. No. 6.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Light chain clone HBPAXK2d 3A12 SEQ ID NO:123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
     Maruyama T,
                                                                                                                                                                                                                           Example 3; Fig 8b-c; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR54897 standard; protein; 107 AA
Frederickson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-SEP-2001; 2001US-0323455P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2002; 2002WO-US029889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 104; Conservative
                                                 WPI; 2003-313359/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003025202-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2003
  Bowdish KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR54897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                               sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR54897
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
```

ö

(ALEX-) ALEXION PHARM INC.

```
The present invention describes a method (MI) for amplifying a nucleic acid strand. MI comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence in the presence of a polymers primer having the predetermined sequence in the presence of a polymers and nucleotides under conditions suitable for polymerisation of the nucleotides. Also described is an engineered nucleic acid strand (I) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other end. MI is useful for amplifying a nucleic acid. MI can be used for producin an antibody library. MI is useful for preparing amplified products that can be used ligated into a suitable expression vector, where the vector can be used to transform an appropriate host organism to produce the polypeptide or protein encoded by the target sequence. MI is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. MI is useful not only for producing large amounts of antibody library. MI is useful not only for producing large amounts of one target nucleic acid sequence, but also for amplifying similtaneously more than one different target nucleic acid sequence located on the same or different nucleic acid sequence acid not the exemplification of the present in the present and the present and an antibody library such as a constant and an antibody library such as a constant and a constant and a complex library such as a constant and a constant and a sequence and a sequence located on the same and and a constant and a sequence used in the exemplification of the present and an antibody library and an antibody library and an antibody library and an antibody library and a sequence used in the exemplification of the present and an antibody library and an antibody library and an antibody library and an antibody library and a sequence used in the sease
                                                                                                                                                                                                                     having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
                                                                                                                                                                                      Amplifying nucleic acid by contacting engineered nucleic acid strand
                                  Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 8b-c; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
```

```
9
                                                                              EIVMTQSPATLSVSPGERATLSCRASQSVSSNIAWYQQKPQQAPRLLIYGASTRATGIPA 60
                                                              1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                               Gaps
                               ;
0
                                                                                                                        61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                       Score 536; DB 6; Length 107;
                               2; Indels
                Pred. No. 1e-32;
                               2; Mismatches
             96.38;
                               Matches 103; Conservative
                Best Local Similarity
                                                                                             음
                                                                                                                          ઠે
                                                                                                                                                    g
                                                              ò
```

```
Engineered template; single primer amplification; antibody library; nucleic acid amplification.
                                                               Light chain clone HBPAXK1b 3A2 SEQ ID NO:109
                ABRS4883 standard; protein; 107 AA.
                                                                                                                                                             19-SEP-2002; 2002WO-US029889.
                                               (first entry)
                                                                                                                              WO2003025202-A2
                                                                                                       Homo sapiens.
                                                30-JUN-2003
                                                                                                               Synthetic.
```

19-SEP-2001; 2001US-0323455P

```
The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered nucleic acid strand (S) acid strand. M1 comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at the other, and contacting (S) with a primer having the predetermined sequence in the presence of a polymers or nucleotides. M1 as degenered in the presence of a polymers or nucleotides. M1 as described is an engineered nucleic acid strand (I) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other end. M1 is useful for the predetermined sequence at the other end. M1 is useful for proparing amplified products that can be used complementary. M1 is useful for preparing amplified products that can be used complementary m1 is useful for preparing where the vector can be used to transform an appropriate host organism to produce the polypeptide or protein encoded by the target sequence. M1 is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of antibody library m1 is useful not only for producing large amounts of antibody library uncleic acid sequence, but also for amplifying simultaneously or the than one different target nucleic acid sequence located on the same or wifferent nucleic acid molecules. Acc62635 to Acc62753 and ABR54841 to hand the present sequence used in the exemplification of the present
                                                                                                                                                                 Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
                                                      Renshaw
                                                   Lin Y,
                                                      Maruyama T,
                                                                                                                                                                                                                                                                                                                      Example 3; Fig 8b-c; 68pp; English.
                                                      Frederickson S,
                                                                                                                WPI; 2003-313359/30
                                                      Bowdish KS,
                                                                                                                                                                                                                                                                  sequence.
```

1; Indels Score 536; DB 6; Pred. No. 1e-32; 3; Mismatches 96.6%; Query Match Best Local Similarity 96.3 Matches 103; Conservative Sequence 107 AA;

Gaps

; 0

```
human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; eating-crisal; antiinflammatory; antipocratal; antinhemmatic; eating-disorder; immunomodulacor; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonis; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; bladder cancer; lung cancer; glioblastoma; stomach cancer; cancer; thing cancer; colon cancer; parcreatic cancer; prostrate cancer; immuno-mediated inflammatory disease; prostrate cancer; immuno-mediated inflammatory disease; restences; restencesis; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; multiple sclerosis.
                                                                                                                                                                                                                                                  Human anti-TNFa antibody light chain variable region SEQ ID NO:310
                                                                                                                ADP22404 standard; protein; 107 AA
                                                                                                                                                                                                         09-SEP-2004 (first entry)
                                                                                                                                                              ADP22404;
                                                                          RESULT 12
                                                                                                ADP22404
                                                                                                                                        셤
```

```
The present invention describes a human monoclonal antibody (1) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises: (a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined 5 amino acid sequence (13, ADP22417) or (82, ADP22421); and (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (83, ADP22421); and allow a hardown the sample, comprising contacting with (I), and detecting the level of binding between the antibody and TNFa in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and TNFa in composition comprising the antibody or its functional fragment and a cariter; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an emphasize of treatment for the disease by administering the human concolonal antibody of (1); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (1); and (4) inhibiting antiarthritic, antibacterial, antiinflammatory, antiarthritics, antiarthritics, and can be used as a TNFa antagonist. The antibody (I) is useful in the preparation of medicament for treating TNF induced apoptosis, neoplastic disease such as the managonist. The antibody (I) is useful in the preparation of the premach cancer, ondemetrial cancer, kidney cancer, colon cancer, endometrial cancer, kidney cancer, colon cancer, and prostrate cancer; or immuno-mediated inflammatory arbarance and arthritis, glomerial or frequence and restricting or immuno-mediated inflammatory arbarance and arthritis, glomerial or inflammatory arbarance and arthritis, glomerial or frequence and arthritis, glomerial or frequence and arthritis, and arthritis arthritis and arthritis arthritis and arthritis arthritis and arthritis arthritis arthritis and arthritis arthritis and arthritis arthritis arthritismina arthrit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                 Green L, Feng X, Klakamp
                                                                                                                                                                                                                                                                                                                                                  Haak-Frendscho M, Rathanaswami P, Pigott
Manchulencho K, Faggioni R, Senaldi G, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10; SEQ ID NO 310; 213pp; English.
                                                                                                                                                                                                                                                                                                                            Foord O,
                                                                                                                                                                                                                                                                                                        Babcook JS, Kang JS, Foord U,
                                                                                                                                                                02-DEC-2003; 2003WO-US038281.
                                                                                                                                                                                                                   02-DEC-2002; 2002US-0430729P.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-480601/45.
                                                                                                                                                                                                                                                                      (ABGE-) ABGENIX INC
                                                     WO2004050683-A2.
  Homo sapiens
                                                                                                           17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis.
```

Sequence 107 AA;

Gaps . 0 96.6%; Score 536; DB 8; Length 107; 96.3%; Pred. No. 1e-32; 1; Indels ive 3; Mismatches 1; Indels 103; Conservative Local Similarity Query Match Best Loca Matches

1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 1 EIVWTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA

> g ò

9 9

ADP22407 standard; protein; 107 AA.

ADP22407;

(first entry) 09-SEP-2004

Human anti-TNFa antibody light chain variable region SEQ ID NO:313.

human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antiacterial; antiinflammatory; antipsoriatic; antiarthritic; antibacterial; antiinflammatory; antipsoriatic; antirheumatic; eating-disorder; immunomodulator; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonist; TNF induced apoptosis, neoplastic disease; breast cancer; ovarian cancer; bladder cancer; lung cancer; clobustoma; stomach cancer; cancer; prostrate cancer; immuno-mediated inflammatory disease; prostrate cancer; immuno-mediated inflammatory disease; resemble; suctoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; multiple sclerosis.

ä

t C, Liang ML, Lee Qiaojuan JS;

Homo sapiens.

WO2004050683-A2.

17-JUN-2004.

02-DEC-2003; 2003WO-US038281.

02-DEC-2002; 2002US-0430729P.

(ABGE-) ABGENIX INC.

Feng X, Klakamp t C, Liang ML, Le Qiaojuan JS; Haak-Frendscho M, Rathanaswami P, Pigott Manchulencho K, Faggioni R, Senaldi G, C Green L, IS, Foord O, Rathanaswami Kang JS, Babcook JS,

WPI; 2004-480601/45.

New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid arthritis

Example 10; SEQ ID NO 313; 213pp; English.

The present invention describes a human monoclonal antibody (1) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined 5 amino acid sequence (81, ADP22417) or (82, ADP22411); and (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (83, ADP22418) or (84, ADP22424). Also described: (1) assaying (M1) the level of TNFa in a patient sample, comprising contacting with (1), and detecting the level of binding between the antibody and TNFa in Eragment and a carrier; (3) treating (M2) an animal suffering an enimal in need of treatment for the disease by administering the human animal in need of treatment for the disease by administering the human concolonal antibody of (1); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (1); and (4) inhibiting main in need of treatment for TNFa induced apoptosis by administering the human monoclonal antibody of (1); and (4) inhibiting contactivitic, antiarterior antiarterior antiarterior antiarterior antiarterior antibodicatic, antiarterior, antiarterior, antiarterior antiarefield antial antial antial antial antial antial antial antial an as a Trea antagonist. The antibody (I) is useful in the preparation of medicament for treating TNF induced apoptosis, neoplastic disease such as breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer, parcreatic cancer, and prostrate cancer; or immuno-mediated inflammatory diseases such as rheumatoid arthritis, glomerulonophitis, atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and

RESULT 13 ADP22407

SXSSS

g

ò

В

ò

```
61 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 16, 2005, 21:51:36
                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-604432/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foster C,
                                                                                                                                                                                                                                                                                                                                                                                                                                   (TANO-) TANOX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                   WO2004070010-A2
                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                   04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                           19-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                            ADR31547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Singh S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               made
                                                                                                                                                                                                                                      Key
Region
                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                  Region
                                                                          ADR31547
                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
  ò
                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to an antibody comprising a variable light chain region or a variable heavy chain region. The antibody and methods are useful for treating a disorder associated with an abnormally high IgE level, e.g. asthma, allergic rhinitis, eccama, urticaria, atopic dermatitis, or a food allergy. The present sequence represents human anti-IgE antibody light chain combined L16 and UK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                         9
                                                                                                                                               EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New high affinity human monoclonal antibodies, particularly those directed against isotypic determinants of immunoglobulin E, useful for asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                         EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
 a human anti-TNFa
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                          antibody; variable light chain; variable heavy chain; Antiallergic; Dermatological; Immunosuppressive; IgE; asthma; allergic rhinitis; eczema; urticaria; atopic dermatitis; food allergy; CDR.
                                                                                                  .;
0
                                                                                                                                                                                     RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIK 107
                                                                                                                                                                        RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.6%; Score 536; DB 8; Length 107; 97.2%; Pred. No. 1e-32;
                                                                          DB 8; Length 107
multiple sclerosis. The present sequence represents a human antibody light chain variable region, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                    Human anti-IgE antibody light chain L16 and JK4.
                                                                        Score 536; DB 8;
Pred. No. 1e-32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 2; 101pp; English.
                                                                                                                                                                                                                                                              ADR43402 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-2004; 2004WO-US002894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2003; 2003US-0444229P
                                                                        Query Match
Best Local Similarity 97.2%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ë
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Singh S, Foster C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-604433/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TANO-) TANOX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107 AA;
                                                Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004070011-A2
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                             04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                     ADR43402;
                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                  ADR43402
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for generating a humanised high affinity antibody from an antibody of interest. The method involves selecting a suitable human template as the framework for the H (heavy) and L (light) chain variable (V) domains of the high affinity antibody to be made. The method is useful for generating high affinity antibodies useful in diagnostics, prophlaxis and treatment of diseases. The present sequence is L16/JK4 human light chain consensus sequence template. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generating a humanized, high affinity antibody from an antibody of interest comprises selecting a suitable human template as the framework for the H and L chain variable domains of the high affinity antibody to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                 L16/JK4 human light chain consensus sequence template.
                                                                                                                                                                                                                                                                                                                                                                                     Antibody; diagnostic; prophylaxis; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 536; DB 8;
Pred. No. 1e-32;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 2; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Kabat CDR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Kabat CDR"
                                                                                                                                                                ADR31547 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Kabat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-2004; 2004WO-US002892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2003; 2003US-0444229P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.6%;
ilarity 97.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ï
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50. .56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24. .34
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
```

Job time : 62.3676 secs

Pg

Come of the feet of the contract

us-10-660-357a-6.rpr

```
Ig kappa chain - human
C;Species: Homo manior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          834005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kappa chain V r
kappa chain - h
kappa chain V-J
kappa chain V-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain - h
chain V r
chain V-I
chain V r
chain NIG
chain pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain V r
chain V-r
chain V r
chain pre
chain V-J
chain - h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chain V-I
chain V r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain V-I
chain V-I
chain V r
chain pre
                                                                                                                                                             November 16, 2005, 21:37:48; Search time 12.7849 Seconds (without alignments) 805.260 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain
chain
chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain
                                                                                                                                                                                                                                                                                                                                   1 EIVMTQSPATLSVSPGERAT......CQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kappa c Kappa 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kappa
kappa
kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283416 segs, 96216763 residues
GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         840343

K3HUPM

K3HUPM

A56701

B26555

B26555

B26264

JE0244

P10106

P10106

P10106

P10106

P10106

S14905

S14905
                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S34005
S40362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B30601
S20636
A32274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G30601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                 US-10-660-357A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      %
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111728
111731
111731
11175
11175
11175
11175
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
11176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
1176
11
                          Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 471
468
468
467.5
467.5
467.5
466.5
                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544
536
531
508.5
499.5
493.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491
490.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481
473.5
473
473
472.5
472.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
```

```
four human monoclonal )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V region - human
CiSpecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Obec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34005; S30524
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 46-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human mon A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Accession: S34005
A;Accession: B34005
A;Residues: preliminary
A;Moscule type: mRNA
A;Residues: 1-107 cMAR>
A;Cross-references: EMBL:218330
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Ig kappa chain V r
Ig kappa chain V-1
Ig kappa chain V-1
Ig kappa chain V-1
Ig kappa chain V-1
Ig kappa chain V r
anti-5m antibody V
Ig kappa chain V-1
Ig kappa chain pre
Ig kappa chain pre
Ig kappa chain N-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: $40362
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40362
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYRNWPRIFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 107,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X72472; NID:9441412; PID:9441413
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 544; DB 2; Length 10
Pred. No. 3.4e-39;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Keywords: heterotetramer; immunoglobulin;26-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                    SS7444
JE0242
PC4282
S40345
                                                                                 C30608
K3HUTI
PH0963
S49532
K3HUWL
A30608
                                                                                                                                                                                                                                                                                  529627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 98.0%;
Best Local Similarity 98.1%;
Matches 105; Conservative
        0000000000000000000
     464.5
4663.5
4663.5
4661.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461.5
461
```

Length 117;

DB 2;

96.6%; Score 536;

53

ద

ò q

ò

```
C;Accession: A56701
R;Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, B.A.
J. Biol. Chem. 270, 12457-12465, 1995
A;Title: Human and mouse monoclonal antibodies to blood group A substance, which are neamaly. Reference number: A56701; MUID:95279371; PMID:7759488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 BIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 EVVMTQSPATLSVSPGERATLSCRASQSVIHNLAWYQQKPGQAPRLLIYGAYTRATGVPA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region precursor (HuA) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                             C,Species: Homo sapiens (man)
C,Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                     EIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X72438; NID:g441344; PIDN:CAA51106.1; PID:g441345 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;35-109/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S40328
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 116.
Bur. J. Immunol. 23, 3248-3271, 116.
ByTitle: Expressed human immunoglobulin chi genes and their hypermutation. A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Accession: 840328
A;Status: preliminary; translation not shown
A;Residues: 1-131 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L41174; NID:g762823; PIDN:AAA64877.1; PID:g762824 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 RFSGSGSGTEFTLTISGLQSEDLATYYCQQYNDWPPWTFGQGTKVEIK 127
                                                                                                                                                                        61 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPTFGQGTRVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLOSEDFAVYYCQOYNNWPR-TFGQGTKVEIK 107
                                                                                                                                     60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 89.2%; Score 495; DB 2; Length 12
Best Local Similarity 88.8%; Pred. No. 5.3e-35;
Matches 95; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.0%; Score 499.5; DB 2;
89.8%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.8%; Pred. wv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 89.8 Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: A56701
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-128 <NIC>
                                                                                                                                                                                                                                                                                                                                     Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                        ò
                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P01624
C;Cross-references: UNIPROT:P01624
C;Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
C;Genetics:
A;Gene: GDB:IGKV3
A;Coross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Keywords: heterotetramer
C;Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V-III region (Pom) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01897
R;Klapper, D.G.; Capra, J.D.
Ann. Immunol. (Inst. Pasteur) 127C, 261-271, 1976
Ann. Immunol. (Inst. Pasteur)
A;Title: The amino acid sequence of the variable regions of the light chains from two A;Reference number: A01897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                     11 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 70
                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPTVLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                  1 EIVWTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C)Accession: 840343

R; Klein, R.; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3248-3271, 198

A; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: 840312; MUID: 94080891; PMID: 8258341

A; Accession: 840343

A; Status: preliminary; translation not shown

A; Molecule type: mRNA

A; Residues: 1-128 < KLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPYTFGQGTKLEIK 127
                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                  71 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 508.5; DB 1;
Pred. No. 3.4e-36;
4; Mismatches 4;
Pred. No. 1.7e-38;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 531; DB 2;
Pred. No. 5e-38;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;16-91/Domain: immunoglobulin homology <IMM>F;23-89/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 91.6%;
il Similarity 91.7%;
99; Conservative '
Best Local Similarity 97.2%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 95.3
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein A;Residues: 1-109 <KLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
K3HUPM
```

g

8

g

ò

1,

9

ö

9

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T submitted to JIFID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy A;Reference number: JE0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: 523628
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from A;Reference number: $23623; MUID:92156804; PMID:1740665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.; Kozin, F.; Carson, D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIVLTQSPATLSLSPGERATLSCRASOSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
Graphs chain V-III region (Ger) - human C, Species: Homo sapiens (man) C, Species: O-Jun-1988 #text_change 21-Jan-2000 C, Accession: B2655 R; Middaugh, C.R.; Litman, G.W. J. Biol. Chem. 262, 3671-3673, 1987 A, Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin. A, Reference number: A92630; MUD:87137666; PMID:3102493 A, Accession: B2655 A, Molecule type: protein A, Residues: 1-116 cMID. A, Residues: 1-116 cMID. C, Superfamily: immunoglobulin V region; immunoglobulin homology C, Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross.references: EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID:g1335190 C.S.Usperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: hererotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPR-TFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYDDWPPITFGQGTRLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                Score 493.5; DB 2
Pred. No. 6.5e-35;
7; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 491; DB 2;
Pred. No. 1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                88.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.5%;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9°
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.8°
Watches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-111 <OLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: JE0244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
```

```
Rijirik, F.R.; Sorge, J.; Fong, S.; Heitzmann, J.G.; Curd, J.G.; Chen, P.P.; Goldfien, R. Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A;Title: Choning and sequence determination of a human rheumatoid factor light-chain gene A;Reference number: A01898; MUID:86177570; PMID:3083417
A;Recession: A01898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AjGene: GDB:IGKV3
AjGene: GDB:I36266
AjCross-references: GDB:I36266
AjCross-references: GDB:I36266
Ajnatpons: 17/1
CjComplex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as ISA and IgM, the subunits associate into last cjSuperfamily: immunoglobulin V region; immunoglobulin homology
CjKeywords: autoantibody; chronic Iymphocytic leukemia; heterotetramer; immunoglobulin
Ej:1-20/Domain: signal sequence #status predicted < SIGS.
Ej:21-115/Product: rheumatoid factor, Ig kappa chain V-III region (CLL) #status predicted
                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQPPRLLIYGASTRATGIPA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain precursor V-III region (CLL) - human
NiAlternate names: rheumatoid factor
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C;Accession: A01898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A30553
Ig kappa chain precursor V-III region (Hah) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03.Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C;Accession: A30553
                                                                                                                                                                                                                                                                                                                                                                         1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFILTISSLQSEDFALYYCQQYNTWPPLTFGGGTKVBIK 108
                                                                                                                                                                                                    Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNW-PRTFGQGTKVEIK 107
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.2%; Score 484; DB 1; Length 11 97.9%; Pred. No. 4.1e-34; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                     Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: the sequence was determined from the germline gene
                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                88.4%; Score 490.5; DB 2, 88.9%; Pred. No. 2.1e-34; iive 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 RFSGSGSGTEFTLTISRLQSEDFAVYYCQQYNNWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RESGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;109-115/Region: complementarity-determining 3 F;43-108/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;21-115/Product: rheumatoid factor, Ig kappa of F;21-43/Region: framework 1 F;36-110/Domain: immunoglobulin homology cIMM> 744-54/Region: complementarity-determining 1 F;55-69/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;70-76/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.2.
Best Local Similarity 97.2.
And 93; Conservative
                                                                                                                                                                                                                               Best Local Similarity 88.9
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;77-108/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-115 <JIR>
```

```
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
                                                                                                                                                                                                                                             93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-23/Region: framework 1
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 93; Conserv
A, Accession: JE0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma secritates: Relationship of variable region genes expressed by a human B cell lymphoma secritates: PL0106
A;Reference number: PL0106; MUID:89235583; PMID:2541221
A;Recession: PL0106
A;Molecule type: mRNA
A;Residues: 1-144 <SILA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin predicted <SIG>F;1-20/Domain: signal sequence #status predicted <SIG>F;1-115/Domain: version <VRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amy
R;Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D. J. Immunol. 142, 688-694, 1989
A;Title: Characterization of four homologous L chain variable region genes that are rela A;Reference number: A30553; MUID:89093959; PMID:2492051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JE0243

Ig kappa chain NIG93 precursor - human
Ig kappa chain NIG93 precursor - human
Ig kappa chain NIG93 precursor - human
Is kappa chain wide aguence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Accession: JE0243
R; Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
B; Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.;
A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL am
A; Reference number: JE0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 BIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQRPGQAPRLLIYDASNRATGIPA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 EIVWMQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 144;
                                                                                                                                                                                                                                             A,Note: the sequence was determined from the differentiated gene C,Superfamily: immunoglobulin V region; immunoglobulin homology C,Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 483; DB 2; Length 115; 97.9%; Pred. No. 4.9e-34; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 86.8%; Score 482; DB 2; Length 14 Best Local Similarity 86.9%; Pred. No. 7.4e-34; Matches 93; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 RFSGSGSGTEFTLTISRLQSEDFAVYYCQQYNNWP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F,36-110/Domain: imminoglobulin homology <IMM>F;44-54/Region: complementarity-determining 1<br/>F;70-76/Region: complementarity-determining 2<br/>F;109-115/Region: complementarity-determining 3<br/>F;109-115/Domain: J region <IRG><br/>F;1128-144/Domain: C region (fragment) <CRB>
                                                                                                                                                                                                                                                                                                               C; Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93; Conservative
                                                                                                                                                                                                                   A; Residues: 1-115 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                              A;Status: preliminary A;Molecule type: DNA
                                                                                                                           A; Accession: A30553
A; Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
C;Accession 190601
C;Accession 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-95 < MAN>
A; Residues: 1-95 < MAN>
A; Note: the authors translated the codon CTC for residue 73 as Phe
C; Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: PH0868
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype A;Reference number: PH0862; MUID:92078875; PMID:1660528
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V region (anti-DNA, II-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-0cr-1992 #sequence_revision 09-0ct-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V-III region (Cur) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQXPGQAPRLLIYGASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EIVMTQSPATLSVSPGERATLSCRASQSVATNVVWYMQKLGQAPRLLIYDASTRATGVPA
                                                                                                                                                                                                                                                                                                                                                                Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLOSEDFAIYYCQHNNAWPPTFGQGTKVETK 107
                                                                                                                                                                                                                                                             Length 215;
A;Molecule type: protein
A;Residues: 1-215 ALI.>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;I6-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                        86.7%; Score 481; DB 2; Length 21
86.9%; Pred. No. 1.3e-33;
ive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 473.5; DB Pred. No. 3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.3%; Score 473.5; Best Local Similarity 86.1%; Pred. No. 3e-3 Matches 93; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;16-90/Domain: immunoglobulin homology
```

```
0, Gaps
                                                                                Query Match

85.2%; Score 473; DB 2; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.9e-33;
Matches 90; Conservative 3; Mismatches 2; Indels
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3
```

දු පු

ò

Search completed: November 16, 2005, 22:04:06 Job time: 12.7849 secs q

Cause sold and and and

Н

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FT FT FT SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapien
sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapien
sapien
sapien
sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapien
sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapien
                                                                                                                                                                 November 16, 2005, 21:36:13; Search time 59.9908 Seconds (without alignments) 913.348 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                      555
1 EIVMTQSPATLSVSPGERAT.......CQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                904207 homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGGMW0 P18135 P01620 P01622 P01623 P01623 P01623 P01623 P01623 P018136 P04206 P04206 P01619 P04433 P04433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6gmv9
Q6pjf2
P06311
P01605
Q6pi18
Q6p588
Q9u186
Q9u179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6gmw1
P01610
Q6pih7
Q6pit5
P01621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29n185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29ul70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0901.83

0901.83

0901.65

06GMMO

06GMMO

KV31 HUMAN

KV32 HUMAN

KV32 HUMAN

KV31 HUMAN

COUT.78

COEGEV

COEGEV

COEGEV

COEGEV

COEFI

COE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6PITS
KV3C_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV3H HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                          US-10-660-357A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513
508.5
508.5
508.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6460.5
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431
428.5
422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418
415.5
408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
```

32 40.5 72.5 13.1 70.24 140.8 10.15 10	32 402.5 72.5 13 34 402.5 72.5 13 35 400 72.1 10 36 400 72.1 10 37 400 72.1 10 39 400 72.1 23 39 400 72.1 23 41 395 71.2 24 42 394 71.0 22 44 393 70.8 10 44 44 393 70 44 44 30 44 44 30 44 44 30 44 44 10 44 1	Q72473 homo sapien P01599 homo sapien P01598 homo sapien P04430 homo sapien Q7234 homo sapien Q652C8 homo sapien Q652C9 homo sapien Q652C9 homo sapien Q652C9 homo sapien Q65C9 homo sapien Q65C09 homo sapien Q66C09 homo sapien	Heumatoid factor). Tebrata; Euteleostomi; G., Curd J.G., Chen P.P., man rheumatoid factor 1986).
32 402.5 72.5 13 34 402.5 72.5 13 35 402 72.4 10 35 400 72.1 10 36 400 72.1 10 37 400 72.1 10 39 400 72.1 24 41 39 77.5 12 42 39 77.5 12 42 39 77.5 12 43 39 70.8 10 44 30.0 10 44 30.0 10 44 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 50.0 10 44 44 54 44 54 44 50.0 10 44 44 54 44 10 44 54 44 10	32 402.5 72.5 13 34 402.5 72.5 13 35 400 72.1 10 36 400 72.1 10 37 400 72.1 10 39 400 72.1 23 39 400 72.1 23 41 395 71.2 24 42 394 71.0 22 44 393 70.8 10 44 393 70 44 393 70 40 401 10 40		PRT; 129 AA. ted) sequence update) annotation update) nn CLL precursor (Rheuma ta; Craniata; Vertebrat es; Catarrhini; Hominid 083417; S., Heitzmann J.G., Cu rmination of a human rh .A. 83:2195-2199(1986)O. 83:2195-2199(1986)I. is not removed. Usag e agreement (See http:/ e@isb.sib.ch) 10. 11. 11. 12 kappa chain V-III Framework-1. Complementarity-dete Framework-2. Complementarity-dete Framework-2. Complementarity-dete Framework-3. Complementarity-dete
32 402.5 72.5 13 34 402.5 72.5 13 35 400 72.1 10 36 400 72.1 10 37 400 72.1 10 39 400 72.1 22 41 39 71.5 12 42 39 71.2 24 42 39 71.2 24 43 39 71.2 24 44 39 71.2 24 44 39 71.2 24 44 39 70.8 10 44 40 70 40 70 70 70 70 40 70 70 70 40 70 70 70 40	32 402.5 72.5 13 34 402.5 72.5 13 35 400 72.1 10 36 400 72.1 10 37 400 72.1 10 39 400 72.1 22 41 39 71.5 12 42 39 71.2 24 42 39 71.2 24 43 39 71.2 24 44 39 71.2 24 44 39 71.2 24 44 39 70.8 10 44 40 70 40 70 70 70 70 40 70 70 70 40 70 70 70 40		D; Last Last Last Last Last Last Last Last
to H	EUGECCUCE OF A A A A A A A A A A A A A A A A A A	211222122	NDAR 116, 1 117, 1
to H	NE ENCHONING A 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	722.6 722.7 722.1 722.1 722.1 721.1 721.0 700.8 80.0 700.8	STP (Rel. (R
UNIC COUNTY A 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	UNIC COUNTY A 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 00 4 00 2 . 0 4 00 2 . 0 9 00 3 9 9 6 00 9 9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	HH HUMAN HH HUMAN HAR-1991 HAR-1999 HAR-1999 HAR-1999 HAR-1999 HAR-1999 HAR-1999 HAR-1999 HAR-1999 HAR-1999 HARN HARN HARN HARN HARN HARN HARN HARN
STITITITITITIES SHEET SOURCE STATE S	8 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	
			S T T T T T T T T T T T T T T T T T T T

Score 524.5; DB 1; Length 129;

94.5%;

```
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
Q9UL85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIVMIQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRAIGIPA 60
                                                                                             9
                                                                                                                                       21 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQPPRLLIYGASTRATGIPA 80
                                                                                             1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPR-TFGQGTKVEIK 107
                                                                                                                                                                                                                                                  81 RFSGSGSGTEFTLTISRLQSEDFAVYXCQQYNNWPPWTFGQGTRVEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.4%; Score 513; DB 2; Length 108; 93.5%; Pred. No. 4.5e-46; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
   95.4%; Pred. No. 3.4e-47;
iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Figure 1. | Fetue... | Clin. Immunopathol. 87:184-192(1998). | Clin. Immunol. Immunopathol. 87:184-192(1998). | EMBL, AF035031, AAD56267.1; -. | EMBL, A80609; B30609. | PIR; B30609; B30609. | PIR; B30609; B30609. | PIR; B30609; B30609. | PIR; S34099; S34099. | RIRSP; PO1625; 1LUE. | RSPR. PIRCO7110; IG-like. | InterPro; IPR003596; IG-v. | SMART; SM00406; IG-v; IRE; PS50835; IG-LIKE; I. | Lamber 1. | Lamber 2. | Lamber 3. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
15 kappa chain V-III region POM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last seq
01-OCT-2003 (TrEWBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
   Best Local Similarity 95.4
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV3F HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
KV3F HUMAN
                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
OGULB3
OGULB3
OGULB3
OGULB3
OGULB0
OGULD0
OGULD0
OGULD0
OGULB0

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                        g
                                                                                                                                                                                                                        ò
```

```
1;
                        M. Klapper D.G., Capra J.D.;

M. Klapper D.G., Capra J.D.;

M. Klapper D.G., Capra J.D.;

M. The amino acid sequence of the variable regions of the light chains if from two idiotypically cross reactive Igm anti-gamma globulins.";

M. Ann. Immunol. (Paris) 127C:261-271(1976).

M. HSCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

M. RISCELLANEOUS: This chain activity.

M. RISCELLANEOUS: Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.6%; Score 508.5; DB 1; Length 109; 91.7%; Pred. No. 1.3e-45; Live 4; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPFFGQGTRVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL85;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CAT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct protein sequencing, Immunoglobulin V region.
DISULFID 23 89 Similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
91.1%; Score 505.5; DB 2;
Best Local Similarity 91.7%; Pred. No. 2.8e-45;
Matches 99; Conservative 5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF035029; AAD56265.1; -.
PIR; D30609; D30609.
HSSP; P01625; 1EK3.
INTERPRO; IPR007110; Ig-like.
INTERPO; IPR003156; Ig-v.
SMART; SM00406; IG-v; I.-
PROSITE; PS50835; IG_LIKE; I.
MEDLINE=76276460; PubMed=60899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7%
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
```

m

```
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109
118
129
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
55
70
                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 1
129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986
21-JUL-1986
05-JUL-2004
                                                                                                RESULT 6
KV3L_HUMAN
ID KV3L_HUMAN
AC P18135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
NON TER
SEQUENCE
                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV3B HUMAN
ID KV3B HUM
AC P01620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444
                                                                                                                                  ઠે
                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Straubberg R.L., Faingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Moraten R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Andrigues A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and manage of the standard of the
 9
               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 EIVMTQSPATLSVSPGERATLSCRASQSISNNLAWYQQRPGQAPRLLIYGASSRVTGIPG 80
EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                             RFSGSGSGTEFILTISSLOSEDFAVYYCOOYNNW-PRIFGOGTKVEIK 107
                                                                               61 RFSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLFFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.3%; Score 495.5; DB 2; Length 235; 88.9%; Pred. No. 7.6e-44; ive 7; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberger R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Bublited (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Bublited (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Bublited (JUN-2004) ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R Pfam; PP00047; Ig. 2.
SWART; SW00409; IG; 2.
SWART; SW00406; IGv; 1.
R SWART; SW00406; IGv; 1.
R PROSITE; PS50835; IG_LIKE; 2.
R PROSITE; PS50835; IG_LIKE; 2.
R PROSITE; PS50835; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25765 MW; 4360C36B6D4133F5 CRC64;
                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                              Created)
                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 88.9
es 96; Conservative
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                            Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein SEQUENCE 235 AA;
                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissum-spleen;
                                                                                                                                                                                                                                                                             Homo sapiens
                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                             DEGMWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                            RESULT 5
                                                                                                                                                             Q6GMW0
                           g
                                                                                                                                                                              8
                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
21 EIVLTÓSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJNE-89171307.

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

"Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";

J. Exp. Med. 167:840-852 (1988).

-!- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                      81 RFSGSGSGTEFTLSISSLQSEDFAVYFCQQYNDWLLYTFGQGTKLEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V-III region HAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Framework-3.
Complementarity-determining-3.
RFSGSGSGTEFILTISSLOSEDFAVYYCOOYNNW-PRTFGOGTKVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.1%; Score 472.5; DB 1; Length 86.1%; Pred. No. 9.9e-42; ive 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                                                                                                                                  01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-III region HAH precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                     Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leukemia.
PIR; PLOG22; K2HUHA.
HSSP: PO1622; IEEQ.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Framework-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JK1 segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; i. --
MARAT; SM00406; IGV; i. -
PROSTTE; PSS6835; IG LIKE; i.
Immunoglobulin V regTon; Signal.
```

ä 29

```
NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                         NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
 SETEMBER
                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-72188439; PubMed=5027703;

Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

Immunoglobulin L-chain of Aspartype, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.';

HOPPE-Seyler's Z. Physiol. Chem. 353:189-208(1972).

-I- MISCELLANBOUS: The C region of this chain has the INV (3) marker.

-I- MISCELLANBOUS: This is a Bence-Jones protein.
                                                                                                                                                                 1 BIVMTOSPATLSVSPGERATLSCRASOSVSNN-LAWYQOKPGOAPRLLIYGASTRATGIP
                                                                                                                       Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
Ig kappa chain V-III region SiE.
Homo sapiens (Human).
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DRFSGSGGTDFTLTISRLEPDDFAVYXCQQYGSSPQTFGQGSKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.2%; Score 467.5; DB 1; Length 109;
84.3%; Pred. No. 2.7e-41;
ive 10; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 ARFSGSGSGTEFILIISSLQSEDFAVYYCQQYNNWPRIFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                  109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1. — SMART; SM00406; IGv; 1. SMART; SM50406; IGv; 1. Direct protein sequencing; Immunoglobulin V region. DISULFID 23 89 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
RAppa chain V-III region Ti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                         MEDLINE=82046598; PubMed=6794615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A01895; K3HUTI.
HSSP; P01625; 1LVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KV3D HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8

KV3D HUMAN

AC P016224

DT 21-JUL-

EN MEMBLINE

RX MEDLINE

RX MEDLINI

RX HIPP-

RX HIPP-

RX HOPP-

CC -1- MICC

DR HSSP; DR HTEPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
1 EIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP 59
                                                                                                                                                                                                                                                                                                                                                                                 1 BIVLTQSPGTLSLSPGERATLSCRASQSVSNSFLAWYQQKPGQAPRLLIYVASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 20:5816-5822(1981).
-!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.
PIR; A01896; K3HUWL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
                                                                                                                                                                                                                                                                                                                                                  1 BIVMTOSPATLSVSPGERATLSCRASOSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                    / Match 83.2%; Score 461.5; DB 1; Length Local Similarity 84.3%; Pred. No. 1.2e-40; nes 91; Conservative 8; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11746 MW; 566C115E6B9CBEEE CRC64;
                                                                                                                                                                                       109 AA; 11788 MW; 8C35058CDC7749BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PP00047; ig; 1.
SMART; SM0406; IGv; 1.
ProSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DISULFID 23 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.0%; Score 460.5; DB 1;
84.3%; Pred. No. 1.5e-40;
iive 7; Mismatches 9;
Pfam; PF00047; ig; 1.
SMART; SM00406; iGv; 1.
PROSTTE; PS50835; IG LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
DISULETD 129 109 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
IIG kappa chain V-III region WoL.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSRY, POIGSS, ILVE.

GO, GO:0005576; C:extracellular; NAS.
GO, GO:0003823; F:antigen binding; NAS.
GO, GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82046598; PubMed=6794615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 84.3 es 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
```

ഗ

```
F30608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PH0964
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                  B30607;
                                                                                                                                                                                                                                         C30601;
                                                                                                                                                                                                                                                                                                                                                                                                G30601;
G30608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PH0964;
                                                                                                                                                                                                                                                          C30607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            H3060B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H44151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PH0963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01625;
                                                                                                                                                                                                                                                                                                                                                                              F30608;
                                                                                                                                                                                                                                                                                                                                      D30608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; I PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV3G_HUMAN
                                                                                                                                                                                                                                                        PIR;
PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                              PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                              PIR;
    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 BIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                    or no somatic
                                                                                                                                                                                                                               MEDLINE=88171307; PubMed=3127527;
MEDLINE=88171307; PubMed=3127527;
MEDLINE=88171307; PubMed=3127527;
MEDLINE=88171307. Toughave E., Chen P.P., Carson D.A.;
Mutoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatimutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-i- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiene (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 459.5; DB 1; Length 129;
Pred. No. 2.3e-40;
8; Mismatches 8; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ARPSGSGSGTEFILIISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 DRFSGSGSGTDFTLTISRLEPXDFAVYYCQQYGSSPWTFGQTKVEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-III region HIC.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14070 MW; 7395528EA2BB74D6 CRC64;
                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-III region HIC precursor.
                    129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003596; IG-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 84.3
Matches 91, Conservative
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
129
43
43
70
70
109
118
109
                                                                                                                                        (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; PL0021; K3HUHI.
HSSP; P01625; 1EEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA;
                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                       leukemia.
                                                                                                                                        Homo sapiens
                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                    KV3M HU
P18136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UL78
Q9UL78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
020UL78
10 020UL7
AC 020UL7
DT 01-MA
DT 01-MA
DT 01-MA
DE MYOSI
DE (Frag
OS HOMO
OC BUKAR
OC MABMINA
OX MOBIL
                  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIVMTGSPATLSVSPGERATLSCRASQSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0; Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.; "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotypic group, in part predicted by its reactivity with antipeptide antibodies."; Mol. Immunol. 23:239-244(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                   'Myogin-reactive autoantibodies in rheumatic carditis and normal
MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DRPSGSGGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 109
109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KV3G HUMAN STANDARD; PRT; 109 AA.
P04206;
20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain. V-III region GOL (Rheumatoid factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.4%; Score 451.5; DB 2; Best Local Similarity 83.3%; Pred. No. 1.3e-39; Matches 90; Conservative 8; Mismatches 9;
                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; PH0965; PH0965.
PIR; S33988; S33988.
PIR; S34096; S34096.
```

ä 29

```
05-JUL-2004 (05-JUL-2004 (05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                   KV31 HUM
P04433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q6GMV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
             RESULT 14
KV31 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6GMV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44446
                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                  1 EIVMTQSPATLSVSPGERATLSCRASQSVSNN-LAWYQQKPGQAPRLLIYGASTRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                        1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.2%; Score 439.5; DB 1; Length 108; 76.9%; Pred. No. 2.4e-38; tive 13; Mismatches 11; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ARFSGSGSGTEFTLTISSLOSEDFAVYYCOOYNNWPRIFGOGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DRFSGSGSGADFTLTISRLZPEDFAVYYCQQYGSSPFTFGGGSKLEIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                     60 ARFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRSFGQGTKVEIK 108
                                                                                                                                                                                                                                                                                  79.7%; Score 442.5; DB 1; Length 109;
                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;
                                                                                                                                                                                                                                              109 AA; 11830 MW; 9349A5B1D9358BB6 CRC64;
                                                                                                                           PERM; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Direct protein sequencing; Immunoglobulin V region.
DISULFID 23 89 Similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                      Pred. No. 1.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
19 kappa chain V-III region B6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA
                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity
                               GO; GO:0005576; C:extracellular, NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A01891; K3HUB6.
HSSP; P01625; IEEQ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                      80.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Conservative
                                                                                                                                                                                                                                                                                                      Local Similarity 80.6
hes 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                 HSSP; P01625; 1EK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11946339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milstein C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KV3A_HUMAN
                                                                                                                                                                                                                          NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                    g
DR REAL DR REAL SOLUTION OF THE SOLUTION OF TH
                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80
                                                                                                                                                                                                                                                                                                                              MEDLINE-85087932; PubMed=6440122;
Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups are interdigitated within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V-III region VG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%; Score 438; DB 1; Length 115; 88.4%; Pred. No. 3.7e-38; ive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-2. Framework-3. Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12575 MW; 2DE47CDA3A17D555 CRC64;
                                                   13-AUC-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G kappa chain V-lil region VG precursor (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 AA
115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO, GO:000576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; CO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 12:9229-9236(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last seq
(TrEMBLrel. 27, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X01668; -; NOT_ANNOTATED_CDS.
PIR; A01900; K3HUVG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00047; ig, 1.
SMART, SM00406, IGv; 1.
PROSITE, PS50835; IG LIKE: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P01625; 1EEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                    the VK locus.";
```

```
TISSUE-Spleen,

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Astaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Astaplecon M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, BC073793, AAH73793.1; -
InterPro; IPR003599; IG. InterPro; IPR003599; IG. InterPro; IPR003599; IG. InterPro; IPR003599; IG. InterPro; IPR0031006; IG. InterPro; IPR003599; IG. InterPro; IPR003596; IG. InterPro; IPR00407; IG. InterPro; IG. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.6%; Score 436.5; DB 2
80.6%; Pred. No. 1.2e-37;
iive 7; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 80.6 es 87; Conservative
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

Search completed: November 16, 2005, 22:01:50 Job time : 59.9908 secs Carried Same 18 English Control

```
Sequence 82, Application US/09456090A

Patent No. 6680209

GENERAL INPORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunare
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
TITLE OF INVENTION: HUMAN ANTIBODIES
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 96.3
Matches 104; Conservative
US-09-456-090A-82
                                                                                                                                                                                                                       US-09-203-768A-4
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  November 16, 2005, 21:41:29 ; Search time 18.1939 Seconds (without alignments) 439.017 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                   1 EIVMTQSPATLSVSPGERAT.......CQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                    513545
                                                                                                                                                                                                                                                                    Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-456-090A-82
US-09-456-090A-82
US-09-453-234-82
US-09-453-234-88
US-09-453-234-90
US-09-453-234-90
US-09-456-090A-84
US-09-456-090A-84
US-09-456-090A-84
US-09-456-090A-84
US-09-456-090A-16
US-09-490-153-16
                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-490-153-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-490-324-47
                                                                                                                                                                 513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           protein search, using sw model
                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                             US-10-660-357A-6
555
                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyright
                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.4
87.2
887.2
885.6
885.0
885.0
885.0
                                                                                                                                                                                                                                                                              ........
                                                                                                 Title:
Perfect score:
                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4471.5
4471.5
4471.5
6471.5
6470.5
6470.5
6470.5
6470.5
6470.5
6470.5
6470.5
6470.5
                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                           OM protein
                                                                                                                                                                                                                                                                     Database :
                                                                                                                    Sequence:
                                                                                                                                                                 Searched:
                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
```

```
Sequence 4, Application US/09203768A
Fatent No. 67863B
Fatent No. 67863B
Fatent No. 67863B
Fatent No. 67863B
FAPLICANT: Huse, William D.
FAPLICANT: Warkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: 1987
CURRENT PLILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 117
THYE: PRT
CURRENT: 117
THYE: PRT
CURRENT: 117
SEQ ID NO 4
CENTRALLY SEQ ID NO 5
CENTRAL SEQ ID NO 5
CENTRALLY SEQ ID NO 5
CENTRALLY SEQ ID N
                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 EIVWIQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                      Sequence 86, Al
Sequence 150, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                              Sequence
Sequence
Sequence
                                                                                                                                                                                                        Sequence
Sequence
Sequence
                                    Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNW-PRIFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                US-09-438-954-40

US-08-107-768D-14

US-08-477-531B-14

US-08-477-531B-14

US-07-634-278-86

US-08-477-728-86

US-08-477-728-86

US-08-487-200-86

US-08-487-200-86

US-08-487-200-86

US-08-488-113B-150

US-08-465-50-150

US-08-446-537-86

US-09-136-138-150

US-09-136-138-150

US-09-136-138-150

US-09-136-138-150

US-09-136-138-150

US-09-136-138-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.4%; Score 529.5; DB 4.96.3%; Pred. No. 3.8e-40; tive 2; Mismatches 1.
3-08-232-081B-42
3-09-438-954-40
3-08-107-669D-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
```

```
SOFTWARE: Patentin Ver. 2.1
                                         Query Match
Best Local Similarity 89.7
Matches 96; Conservative
US-09-456-090A-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-453-234-88
                                                                                                                                                                                                                                                                                                                                                         US-09-453-234-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                           g
                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                     1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                              1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 90. Application US/09456090A; Sequence 90. Application US/09456090A; Patent No. 6680209; GENERAL INFORMATION:
APPLICANT: Buechler, Joe; APPLICANT: Userler, Gray, Jeff; APPLICANT: Cray, Jeff; APPLICANT: Lonberg, Nils; APPLICANT: Lonberg, Nils; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS; FILE REFERENCE: 020015-000200US; CURRENT APPLICATION NUMBER: US/09/456,090A; CURRENT FILING DATE: 1999-12-06; NUMBER OF SEQ ID NOS: 110; CURRENT PILING DATE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-456-090A-88

Squence 80, Application US/09456090A

Squence 80, Application US/09456090A

Squence 80, Application US/09456090A

GRNERAL INFORMATION:

APPLICANT: Buechler, Joe

APPLICANT: Buchler, Gunare

APPLICANT: Cray, Jeff

APPLICANT: Lonberg, Nils

TITLE OF INVENTION: UNDER NILS

TITLE OF INVENTION: UNDER: 120015-000200US

CURRENT APPLICATION NUMBER: US/09/456,090A

CURRENT FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 110

SOFTWARE: Patentin Ver. 2.1

LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGSGSGTDFTLTISSLEPEDFAVYYCQORTNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTWWPRTFGQGTKVEIK 107
                                                                                                          Score 498; DB 4; Length 224;
Pred. No. 4.8e-37;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 498; DB 4; Length 224;
Pred. No. 4.8e-37;
5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.78;
                                                                                                             89.7%;
                                                                                                      Ouery Match
Best Local Similarity 89.77
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.7<sup>3</sup>
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
OCHANISM: Homo mapiens
CTHER INFORMATION: M2-34L
US-09-456-090A-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-35L
; TYPE: PRT
, ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-09-456-090A-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 90
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                           à
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIVLIQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
                                                                                                                     1 EIVLIQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIXDASNRATGIPA 60
                                                                                           1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                 ô
                                                                                                                                                                                61 RFSGSGSGTEFILTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPRTFGQGTKVEIK 107
  Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6, Indels
                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 498; DB 4;
Pred. No. 4.8e-37;
5; Mismatches 6;
89.7%; Score 498; DB 4;
89.7%; Pred. No. 4.8e-37;
tive 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT PILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 82
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Conberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Bloatte Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                   Sequence 82, Application US/09453234
Patent No. 6794132
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Lonberg, Nils
APPLICANT: Enoberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genberg, Nils
APPLICANT: Genberg, Nils
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-0001100S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 88, Application US/09453234
Patent No. 6794132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.71
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
OCANISM: Homo sapiens
CTHER INFORMATION: M2-31L
US-09-453-234-82
```

```
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-453-234-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-453-234-36
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
                                                                                                                                                                                                                  1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTWWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPRTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 89.7%; Score 498; DB 4; Length 224; Best Local Similarity 89.7%; Pred. No. 4.8e-37; Matches 96; Conservative 5; Mismatches 6; Indels
                                                                                                                                        Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Buechler, Joe
APPLICANT: Buechler, Gunars
APPLICANT: Caray, Old
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFRENCE: 020015-00020003
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT PILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
                                                                                                                                                                             6; Indels
                                                                                                                                     Score 498; DB 4;
Pred. No. 4.8e-37;
                                                                                                                       89.7%; Scor.
89.7%; Pred. No. 4.c.
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Buechler, Joe
APPLICANT: Buechler, Joe
APPLICANT: Buechler, Gunars
APPLICANT: Caray, Jeff
APPLICANT: Comparent Caray, Jeff
APPLICANT: Gonetie Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36, Application US/09456090A Patent No. 6680209 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 90, Application US/09453234
Patent No. 6794132
GENERAL INFORMATION:
                                                                                                                               Query Match
Best Local Similarity 89.7
Matches 96; Conservative
                                     ; TYPE: PRT
OGNISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: M2-35L
US-09-453-234-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-456-090A-36
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-453-234-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 90
LENGTH: 224
SEQ ID NO 88
                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                          1 EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EIVLIQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
                                                                                                                                                                                                                                              1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EIVMTOSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLOSEDFAVYYCOOYNNWPRTFGGGTKVBIK 107
                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPRTFGQGTKVBIK 107
                                                                                                                                              Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 495; DB 4; Length 22
Pred. No. 8.9e-37;
6; Mismatches 6; Indels
                                                                                                                                           89.2%; Score 495; DB 4; Length 22
88.8%; Pred. No. 8.9e-37;
tive 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gray, Jeff
APPLICANT: Conberg, Mils
APPLICANT: Lonberg, Mils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFREENCE: 020015-00011003
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PATENT OF SEQ ID NOS: 112
SOFTWARE: ABLENTIN Ver. 2.1
SENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/456,090A CURRENT FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-456-090A-84; Sequence 84, Application US/09456090A; Patent No. 6680209; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Sequence 36, Application US/09453234
; Patent No. 6794132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Buechler, Joe APPLICANT: Valkirs, Gunars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.8
Matches 95; Conservative
                                                                                                                                                                                              95; Conservative
                                                                       ; OTHER INFORMATION: M1-1L
US-09-456-090A-36
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                              Query Match
Best Local Similarity
```

```
CURRENT FILING DATE: 1999-1
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-453-234-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-453-234-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-635-109-8
                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIVITQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIPA 60
                                                                                                                                                                                                                                                                                                                        1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIPA 60
                                                                                                                                                                                                                                                                                               1 EIVWTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRNNWPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 87.4%; Score 485; DB 4; Length 224; Best Local Similarity 87.9%; Pred. No. 6.9e-36; Matches 94; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                        ; DB 4; Length 224;
6.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46, Application US/09456090A
| Redence 46, Application US/09456090A
| GENERAL INFORMATION:
| APPLICANT: Buechler, Joe
| APPLICANT: Ualkirs, Genars
| APPLICANT: Carby, Jeff
| APPLICANT: Corberg, Nils
| TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
| TILE FERENCE: 0220015-000200US
| CURRENT APPLICATION NUMBER: US/09/456,090A
                                                                                                                                                                                                                                Pred. No. 6.96
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 84, Application US/09453234
Patent No. 6794132
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Unchery, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Gray, Jeff
APPLICANT: Geopherm International
ITILE OF INVENTION: Human Antibodies
ITILE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT FILING DATE: 1299-12-01
                                                                                                                                                                                                 Query Match

87.4%; Score 485;
Best Local Similarity 87.9%; Pred. No. 6.
Matches 94; Conservative 5; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
  NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 84
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-32L
                                                                                                             ORGANISM: Homo sapiens
OTHER INFORMATION: M2-32L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-456-090A-46
                                                                                                                                                            US-09-456-090A-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-453-234-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-453-234-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 84
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
ô
                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                         Gapв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08635109
; Sequence 8, Application US/08635109
; Patent No. 6538114
; GENERAL INFORMATION:
    APPLICANT: Persoon, Mats A. A.
    APPLICANT: Allander, Tobias E.
    ITILE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RESGSGSGTEFILTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 484; DB 4; Length 224;
Pred. No. 8.5e-36;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                        Length 224;
                                                                                                                                                                                                                                                     Query Match 87.2%; Score 484; DB 4; Length 22 Best Local Similarity 86.9%; Pred. No. 8.5e-36; Matches 93; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 224
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Gonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 46, Application US/09453234
Patent No. 6794132
GENERAL INFORMATION:
1999-12-06
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.9%;
Matches 93; Conservative 7
                                                                                                                             TYPE: PRT
OCHANISM: HOMO SADiens
CHER INFORMATION: M1-10L
US-09-456-090A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
OTHER INFORMATION: M1-10L
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LTQSPATLSVSPGERASLSCRASQSVGNNLAMYQQKPGQAPRLLIYGGNTRATGTPDRFS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 MTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPARFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16.747136

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: HEMAN MONOCLONAL ANTIBODIES SPECIFIC FOR TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN NUMBER OF SEQUENCES: ASSOCIATES

CORRESPONDENCE ADDRESS:

ADDRESSE: ROBINS & ASSOCIATES

STREET: 90 MIDDLEFIELD ROAD, SUITE 200

COTY: MENLO PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.6%; Score 475; DB 4; Length 106; Best Local Similarity 86.5%; Pred. No. 2.4e-35; Matches 90; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 GSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,109
FILING DATE: 19-APR-1996
CLESSIFICATION NUMBER: 38,548
FILING DATE: 19-APR-1996
TLASSIFICATION NUMBER: 38,548
REGISTRATION NUMBER: 300-6146
REGISTRATION NUMBER: 300-6146
TELEPHONE: (415) 327-3400
TELEPHONE: (415) 327-331
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENETHON FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17-APR-1997
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/635,109
FILING DATE: 19-APR-1996
ADDRESSEE: REED & ROBINS
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 106 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-635-109-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CILI:
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-844-215-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
```

```
### ATTORNEY/AGENT INFORMATION:
### MCRACKEN, THOMAS P.
### REGISTRATION NUMBER: 38,548
### RE
```

(complete state of the

```
RESULT 1
US-10-330-613-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-330-613-6
 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    App
App
App
App
                                                                                                                      November 16, 2005, 22:02:09; Search time 65.6949 Seconds (without alignments) 681.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126,
                                                                                                                                                                                                                                1 EIVMTQSPATLSVSPGERAT......CQQYNNWPRIFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/NSO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/RSO7_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
                 5.1.6
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-330-613-6
US-10-330-530-6
US-10-660-357-6
US-10-330-613-34
US-10-660-357-34
US-10-660-357-34
US-10-51-0858-122
US-10-737-252-125
US-10-737-252-126
US-10-737-252-126
US-10-737-252-126
US-10-737-252-126
US-10-737-252-126
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              1867879 segs, 418409474 residues
                 version:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                 GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-660-357A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1007
1007
1007
1007
1007
1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0
100.0
98.4
98.4
97.8
97.8
97.1
                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        •
                                                                                      OM protein
                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11098765432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š.
```

```
310, App
313, App
117, App
117, App
132, App
119, App
119, App
119, App
107, App
107, App
                                                                                                                                                                                                                            1952, Ap
1952, Ap
4, Appli
                                                                                                                                                                                                                                                                                                                                  1268, Ap
1268, Ap
115, App
115, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                           42, Appl
44, Appl
46, Appl
4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                      Sequence Sequence 1
                 Sequence 3
                                              Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                     Sequence 3
Sequence 3
Sequence 3
                                                                                                                                                                                                 Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                              Sequence (
Sequence (
Sequence (
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPSGSGSGTEFILIISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of Application US/10330613
Sequence of Application US/10330613
Sequence of Application US/2030147809A1
GENERAL INFORMATION:
APPLICANT Gudas, Jean
TITLE OF INVENTION:
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: 08/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 555; DB 14;
100.0%; Pred. No. 2.9e-40;
ive 0; Mismatches 0;
US-10-251-085B-123

US-10-737-252-109

US-10-737-252-123

US-10-727-155-313

US-10-727-155-313

US-10-251-085B-117

US-10-251-085B-117

US-10-251-085B-132

US-10-737-252-132

US-10-737-252-132

US-10-737-252-139

US-10-737-252-139

US-10-737-252-139

US-10-737-252-139

US-10-737-252-139

US-10-737-252-139

US-10-737-252-139

US-10-737-755-314

US-10-300-675-44

US-10-300-880-124

US-10-300-880-124

US-10-300-764-137

US-10-300-764-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo Sapiens
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAMYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EIVMTÓSPATLSVSPGERATLSCRASÓSVSNNLAWYQQKPGÓAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 107;
Sequence 6, Application US/10330530
Fublication No. US2030152514A1
GENERAL INFORMATION:
APPLICANT: GUAGA, Jean
TITLE OF INVENTION: WETHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
FRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PASESEQ for Windows Version 4.0
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 6, Application US/10660357
| Sequence 6, Application US/10660357
| Publication No. US20040115205A1
| GENERAL INFORMATION:
| APPLICANT: Bar-E11, Menashe
| APPLICANT: Bar-E11, Menashe
| TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
| TITLE OF INVENTION: ANTIGEN
| FILE REFERENCE: AGENIX.030C1
| CURRENT FILING NOWBER: US/10/660,357
| CURRENT FILING DATE: 2003-09-10
| PRIOR APPLICATION NUMBER: 10/330,580
| PRIOR PILING DATE: 2002-12-26
| NUMBER OF SEQ ID NOS: 40
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 555; DB 16;
100.0%; Pred. No. 2.9e-40;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 555; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-40;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/10330613
Publication No. US20030147809A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo Sapiens
US-10-330-530-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-10-660-357-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-660-357-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
1 EIVMTÖSPATLSVSPGERATLSCRASQSISNNFAMYQQKPGQAPRLLIFGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 BIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-330-530-34

Sequence 34, Application US/10330530

Publication No. US20303152514A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVERNION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

FILE REFERENCE: ABGENIX. 031A

CURRENT APPLICATION NUMBER: US/10/330,530

CURRENT FILING DATE: 2002-12-26

PRIOR APPLICATION NUMBER: US 60/346414

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SEQ ID NO 34

LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.4%; Score 546; DB 14; Length 107; 97.2%; Pred. No. 1.7e-39; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSSGTEFTLISSLQSEDFAVYYCQQYNNWPRFFGQGTKVBIK 107
                                                                                                                                                                                                                                                                                                                                                                             Score 546; DB 14; Length 107;
Pred. No. 1.7e-39;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWFRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/10660357
Publication No. US20040115205A1
Publication No. US20040115205A1
APPLICANT: Bar-Bli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 10/330,580
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.4%;
Best Local Similarity 97.2%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 97.29
Matches 104; Conservative
                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Homo Sapiens
US-10-330-613-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-660-357-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-330-530-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

ô

9

ò 셤 ઠ

```
APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Mark
APPLICANT: Renehaw, Mark
APPLICANT: Renehaw, Mark
APPLICANT: Maruyama, Toshiaki
TITLE OP INVENTION: ENINERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR APPLICATION NUMBER: US 60/323,455
SOFTWARE: PatentIn version 3.2
SEQ ID NO 126
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bowdish, Katherine S.
APPLICANT: Brederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Lin, Ying-Cohi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EIVWTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                97.8%; Score 543; DB 16; Length 107; 98.1%; Pred. No. 3.1e-39; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPGTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLÓSEDFAVYYCQÓYNNWPPTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 539; DB 15;
97.2%; Pred. No. 6.8e-39;
iive 1; Mismatches 2;
  PRIOR APPLICATION NUMBER: US 10/251,085
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR RILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.2
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 126, Application US/10251085B; Publication No. US20040072164A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 126, Application US/10737252; Publication No. US20040175736A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 98.1
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: human
US-10-251-085B-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-10-251-085B-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simil
Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-737-252-126
                                                                                                                                                                                                                                                               US-10-737-252-122
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 122, Application US/10251085B
Publication No. US20040072164A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Frederickson, Shana
APPLICANT: Marvyama, Toshiaki
APPLICANT: Marvyama, Toshiaki
TITLE OF INVERTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21
CURRENT APPLICATION UNMBER: US/10/251,085B
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,455
MINUSED OF CEA TE. WOOL -09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 122, Application US/10737252
Publication No. US20040175736A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Mark
APPLICANT: Frederickson, Mark
APPLICANT: Maruyama, Toshiaki
APPLICANT: Maruyama, Toshiaki
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
CURRENT APPLICATION NUMBER: US/10/737,252
CURRENT FILING DATE: 2003-12-15
                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                              1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                    Query Match 98.4%; Score 546; DB 16; Length 107; Best Local Similarity 97.2%; Pred. No. 1.7e-39; Matches 104; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.8%; Score 543; DB 15; Best Local Similarity 98.1%; Pred. No. 3.1e-39; Matches 105; Conservative 1; Mismatches 1;
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 122
                                                                                                                               TYPE: PRT
CAGANISM: Homo Sapiens
US-10-660-357-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: human
US-10-251-085B-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-251-085B-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-737-252-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
```

ઠે 음 ò g

```
Sequence 109, Application US/10/37252
; Sequence 109, Application US/10/37252
; Rublication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Brederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Marcham Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; TITLE OF INVERTION: DATE: 1003-12-15
; CURRENT FILING DATE: 2003-12-15
; PRIOR PRIOR DATE: 2001-09-19
; RRIOR FILING DATE: 2001-09-19
; RRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; LENGTH: 107
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21
CURRENT APPLICATION NUMBER: US/10/251,085B
CURRENT APPLICATION NUMBER: US/002-09-19
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR RILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 278
SOFTWARE PATENTIAL VERSION 3.2
SEQ ID NO 123
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPNTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPITFGQGTRLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.6%; Score 536; DB 16; Best Local Similarity 96.3%; Pred. No. 1.2e-38; Matches 103; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                    96.6%; Score 536; DB 15;
96.3%; Pred. No. 1.2e-38;
tive 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KESULT 14
US-10-737-252-123
Sequence 123, Application US/10737252
Publication No. US20040175736A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 96.3
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: human
US-10-251-085B-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: human
US-10-737-252-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 109, Application US/10251085B
Publication No. US20040072164A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Renshaw, Mark
APPLICANT: Maryama, Toshiaki
APPLICANT: Maruyama, Toshiaki
CURRENT MARUHON: ENGINEBRED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21
CURRENT APPLICATION NUMBER: US/10/251,085B
CURRENT FILING DATE: 2002-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGTSTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQSEDFAVYVCQQYNNWPGTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                            Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
96.6%; Score 536; DB 15;
Best Local Similarity 96.3%; Pred. No. 1.2e-38;
Matches 103; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 539; DB 16;
97.2%; Pred. No. 6.8e-39;
tive 1; Mismatches 2;
                   CURRENT APPLICATION NUMBER: US/10/737,252
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 10/251,085
PRIOR FILING DATE: 2002-09-19
PRIOR PLING DATE: 2002-09-19
PRIOR PLING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 123, Application US/10251085B
Publication No. US20040072164A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patentin version 3.2
SEQ ID NO 109
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: human
US-10-251-085B-109
                                                                                                                                                                                                                                                                                                                  ORGANISM: human
US-10-737-252-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-10-251-085B-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-10-251-085B-123
                                                                                                                                                                                                                                         SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

ហ

```
EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                            1 EIVMIQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                      61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
                                                                                                             61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPITFGGGTRLEIK 107
                                                                                                                                                                                                  Search completed: November 16, 2005, 23:05:40 Job time : 66.6949 secs
  -
                                            셤
                                                                                        ઠે
                                                                                                                              셤
                                                          APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REPERBNCE: 1087-21 CTP
CURRENT APPLICATION NUMBER: US/10/737,252
CURRENT FILING DATE: 2003-12-15
PRIOR PRILING DATE: 2002-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
SOFTWARE: Patentin version 3.2
SEQ ID NO 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIVWTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPKLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGGGTEFTLTISSLQSEDFAVYYCQQYNNWPNTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRIFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 96.6%; Score 536; DB 17; Length 107; Best Local Similarity 96.3%; Pred. No. 1.2e-38; Matches 103; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Giorgio Senaldi
APPLICANT: Giorgio Senaldi
ATTLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: APACTOR AND USES THEREOF
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR PILING DATE: 2003-12-02
PRIOR PILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.6%; Score 536; DB 16;
illarity 96.3%; Pred. No. 1.2e-38;
Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palaniswami Rathanaswami
Craig Pigott
Meina Liang
Rozanne Lee
Kathy Manchulencho
Raffaella Faggioni
Giorgio Sanaldi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 310, Application US/10727155; Publication No. US20050049402A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larry Green
Xiao Feng
Scott Klakamp
Mary Haak-Frendscho
                Frederickson, Shana
Renshaw, Mark
Bowdish, Katherine S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: John S. Babcook
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-727-155-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-727-155-310
                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-737-252-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

Case De la Level Entre

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

	Š
	Search time 62.5147 Se
	time
	Search
	•-
mode1	:35:48
8	21
using sw model	16, 2005, 21:35:48
۲,	ý
searc	ber 1
protein search,	November
•	
OM protein	Run on:

November 16, 2005, 21:35:48; Search time 62.5147 Seconds (without alignments) 674.351 Million cell updates/sec

Perfect score:

US-10-660-357A-10 566 1 DIQMTQSPSSLSASVGDRVT......QSYSTPPECSFGQGTKLEIK 109 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Aab46007 Human MUC Aab46008 Human TF Aab46006 Human MUC Aab46005 Human MUC Aab46005 Human MUC Ab595997 Human ser Ad192369 Human pha Ad77165 HSA Heavy Ad723122 Human cD7 Ad23322 Human cD7 Ad23326 Human ant Ad54107 Human ant Ad54107 Human pho Ad54107 Human pho Ad5439589 Human ant Aa93589 Human ant Aa93560 Human ant	Abo27396 Anti-Rh(D Adp47306 Human pho Aag65567 Amino aci
AAB46007 AAB46008 AAB46008 AAB46006 AAB46005 AAB46005 AAB45332 AD077165 AAC3322 AAC3322 AAC47107 AAC47305	ABO27396 ADP47306 AAG65567
4444460000000000001446	0 8 4
22440 2440 2440 2440 2440 2440 2440 244	108 111 107
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	89.3 89.3
511 511 511 511 511 511 510 500 508 508 508 508 508 508 508 508 50	505.5 505.5 505
00000000000000000000000000000000000000	4 4 4 6 4 4

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 10 ADC99781 standard; protein; 109 AA. (first entry) lung cancer; human. 01-JAN-2004 ADC99781; RESULT 1

Homo sapiens.

WO2003057838-A2.

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P

(ABGE-) ABGENIX INC

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99783.

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 10; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the call surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and centoral intraeptibelial neoplasis and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

N

SXS

ઠ g ठे g

```
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ното
                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                            ADF09823
                                                                                                                                                                                                                                          g
                                                                                                                      ð
                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                    8
                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                                      9
                                                                                                                                                          The invention relates to a novel monoclonal antibody used for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                      1 DIOMIQSPSSLSASVGDRVIITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-MUC18 antibody light chain variable region protein, SEQ ID No 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccin
antigen; tumour metastasis; melanoma; metastatic; human; light chain.
                                                                                                        Gaps
                                                                                                      ö
                                                                                                                                                                                                                            61 RESGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                     Length 109;
                                                                                                      0; Indels
                                                                Score 566; DB 7;
Pred. No. 9e-33;
; Mismatches 0;
light chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 10; 87pp; English.
                                                                                                                                                                                                                                                                                                                             ADD05385 standard; protein; 109 AA
                                                                100.0%; Sc
100.0%; Pr
:ive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-2001; 2001US-0346460P.
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                    Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-577496/54.
                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metastatic tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADD05387
                                  Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003057006-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gudas J,
                                                                                                                                                                                                                                                                                                                                                               ADD05385;
                                                                                                                                                                                                                                                                                             RESULT 2
ADD05385
```

100.0%; Score 566; DB 7; Length 109;

Query Match

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanome or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting tumour metastasis. The method carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
                                                                                                  9
                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                    1 DIOMIQSPSSLSASVGDRVIIICRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASOSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMIOSPSSISASVGDRVIITCRASOSISNYLNWYOOKPGKAPKLLIYGASSLOSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; light chain; human.
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                         61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQCTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human anti-MUC18 monoclonal antibody light chain #3.
9e-33;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 566; DB 7;
100.0%; Pred. No. 9e-33;
tive 0; Mismatches 0;
                   Pred. No. 9e-
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; SEQ ID NO 10; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Ź
                                                                                                                                                                                                                                                                                                                                                                                             ADF09823 standard; protein; 109
                ilarity 100.0%; P:
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2002; 2002WO-US041580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-598367/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADF09825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADF09823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gudas J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

Location/Qualifiers 1. .108 /label= V_region 109. .214 /label= C_region

Marissen WE;

```
New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated diseases, such as cancer or autoimmune disorders.
                                    Human, CD72, B-lymphocyte; receptor; scFv; antibody; cytostatic;
immunosuppressive; cancer; autoimmune disease; gene therapy.
           Human CD72-targeted IgG1 light chain.
                                                                                                                                                                                                                                                  27-JAN-2003; 2003WO-EP050004.
                                                                                                                                                                                                                          27-JAN-2003; 2003WO-EP050004
                                                                                                                                                                                                                                                                          (CRUC-) CRUCELL HOLLAND BV.
                                                                                                                                                                                                                                                                                                                           WPI; 2004-580978/56.
                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADR23359
                                                                                                                                                                           WO2004067569-A1
                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                  Bakker ABH,
                                                                                                                                                                                                  12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                             Region
                                                                                                                                      Region
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Alzhaeimer's disease, atherosclerosis, and restenceds. The present amino acid sequence represents the light chain from a monoclonal antibody that is specific for the human phospholipase A2 (PLA2) enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIOMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                         Human phospholipase A2-specific monoclonal antibody light chain #19.
                                                                                                                                                                                                                                                                                                                                                                                          Feng X;
                                                                                                                                                             inflammatory disorder; degenerative disorder; joint inflammatory reaction; skin inflammatory reaction; skin inflammatory rescue blood vessels inflammatory rection; arthritis; psoriasis; asthma; Alzheimer's disease; atherosclerosis; restenosis; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGOGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 108;
                                                                                                                                                                                                                                                                                                                                                                                          Liang ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                  human; monoclonal antibody; phospholipase A2; PLA2;
                                                                                                                                                                                                                                                                                                                                                                                        Lee YR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 520; DB 8;
Pred. No. 1.6e-29;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; SEQ ID NO 214; 128pp; English
                                                                                                                                                                                                                                                                                                                                                                                         Chen L,
                                                ADP47299 standard; protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                        M, Haak-Frendscho M,
Nocerini MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 91.9%; al Similarity 93.6%; 102; Conservative
                                                                                                                                                                                                                                                                                                  02-DEC-2003; 2003WO-US038234
                                                                                                                                                                                                                                                                                                                                                  (ABGE-) ABGENIX INC.
(LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                           02-DEC-2002; 2002US-0430724P
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-461119/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 108 AA;
                                                                                                                                                                                                                                                  WO2004050850-A2.
                                                                                                                                                                                                                           Homo sapiens
                                                                                                 09-SEP-2004
                                                                                                                                                                                                                                                                           17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                         Landes GM,
                                                                        ADP47299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                       Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
                         RESULT 4
                                 ADP47299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR23360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       원
```

```
The present sequence is the protein sequence of the light chain of human 1990 antibody 024, which specifically recognises human B cell associated antigen CD72. An scFv ADR2322 selected from an antibody phage display library was shown to specifically recognises the human CD72 receptor. The scFv was recloned in 19G expression vector CO1 using primers designed to restore complete human frameworks, thereby generating antibody 024. Such anti-CD72 immunoglobulins or their antigen-binding fragments can be used as internalising human binding molecules of the invention. These internalising human binding molecules are capable of (specifically) binding to CD72 or its antigence determinant, and preferably bind to CD72 critically) binding to CD72 or its antigence determinant, and preferably bind to casociated with cells. Upon binding to CD72 present on the surface of target cells, the binding molecules internalise. In addition to the internalising human binding molecules, the invention provides internalising human binding molecules, the invention provides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tag (toxic substance, radioactive substance, liposome and/or enzyme), nucleic acids encoding these, and compositions comprising them. The internalising human binding molecule, immunoconjugate, nucleic acid molecule or composition can be used in the diagnosis and/or treatment of a B cell associated disorder or disease, especially a B cell associated cancer and B cell associated autoimmune disorder (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMIQSPSSLSASVGDRVIITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGOGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.9%; Score 520; DB 8; Length 21
93.6%; Pred. No. 2.9e-29;
ive 4; Mismatches 1; Indels
Example 5; SEQ ID NO 52; 174pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 93.6
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

RESULT 6 ADR23358

ADR23360 standard; protein; 214 AA

(first entry)

04-NOV-2004

ADR23360;

UXXXX

61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP--TFGQGTKVEIK 107

Ź

ADR23366 standard; protein; 214

Human, CD72, B-lymphocyte, receptor; scFv, antibody; cytostatic; immunosuppressive; cancer; autoimmune disease; gene therapy.

Location/Qualifiers

Homo sapiens

Region Region

Key

1. .108 /label= V_region 109. .214 /label= C_region

27-JAN-2003; 2003WO-EP050004. 27-JAN-2003; 2003WO-EP050004

WO2004067569-A1

12-AUG-2004.

(CRUC-) CRUCELL HOLLAND BV.

Bakker ABH, Marissen WE; WPI; 2004-580978/56. N-PSDB; ADR23365

Human CD72-targeted IgG1 light chain.

(first entry)

04-NOV-2004 ADR23366;

```
ADR23366
                                                          RESULT
                                                                                                                 윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the protein sequence of the light chain of human 1951 antibody 004, which specifically recognises human B cell associated antigen CD72. An scrv ADRA3120 selected from an antibody phage display library was shown to specifically recognise the human CD72 receptor. The scrv was recloned in 19G expression vector C01 using primers designed to restore complete human frameworks, thereby generating antibody 004. Such anti-CD72 immunoglobulins or their antigen-binding fragments can be used as internalising human binding molecules of the invention. These internalising human binding molecules are capable of (specifically) associated with cells. Upon binding to CD72 present on the surface of target cells, the binding molecules internalise. In addition to the internalising human binding molecules, the invention provides internalising human binding molecules, the invention provides communicates comprising an internalising human binding molecules, immunoconjugates comprising an internalising human binding molecules, infantance, and compositions comprising them. The cag (toxic substance, radioactive substance, libosome and/or enzyme), nucleic acids encoding these, and compositions comprising them. The composition can be used in the diagnosis and/or treatment of a B cell associated disorder or disease, especially a B cell associated cancer and B cell associated autoimmune disorder (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated diseases, such as cancer or autoimmune disorders.
                                                                                                                                                     Human, CD72, B-lymphocyte; receptor; scFv; antibody; cytostatic; immunosuppressive; cancer; autoimmune disease; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 520; DB 8; Length 21
Pred. No. 2.9e-29;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; SEQ ID NO 50; 174pp; English
                                                                                                                 Human CD72-targeted IgG1 light chain.
                                                                                                                                                                                                                                                    Location/Qualifiers
ADR23358 standard; protein; 214 AA
                                                                                                                                                                                                                                                                      1. 108
/label= V_region
                                                                                                                                                                                                                                                                                                                                /label= C_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-2003; 2003WO-EP050004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-2003; 2003WO-EP050004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CRUC-) CRUCELL HOLLAND BV
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marissen WE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-580978/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADR23357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                       WO2004067569-A1
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bakker ABH,
                                                                          04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                           12-AUG-2004
                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                            Region
```

New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated diseases, such as cancer or autoimmune disorders.

Example 5; SEQ ID NO 58; 174pp; English

```
The present sequence is the protein sequence of the light chain of human 1gg1 antibody 132, which specifically recognises human B cell associated antigen CD72. An scFv ADR2332 selected from an antibody phage display library was shown to specifically recognise the human CD72 receptor. The scFv was recloned in 1gG expression vector CO1 using primers designed to restore complete human frameworks, thereby generating antibody 132. Such anti-CD72 immunoglobulins or their antigen-binding fragments can be used as internalising human binding molecules of the invention. These internalising human binding molecules are capable of (specifically) binding to CD72 or its antigenic determinant, and preferably bind to CD72 binding to CD72 present on the surface of target cells, the binding molecules internalise. In addition to the internalising human binding molecules, the invention provides internalising human binding molecules, the invention provides in the configuration of the internalising human binding an internalising human binding molecules, the invention provides in the configuration of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ఠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tag (toxic substance, radioactive substance, liposome and/or enzyme), nucleic acids encoding these, and compositions comprising them. The internalising human binding molecule, immunoconjugate, nucleic acid molecule or composition can be used in the diagnosis and/or treatment of a B cell associated disorder or disease, especially a B cell associated autoimmune disorder (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 520; DB 8; L
Pred. No. 2.9e-29;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.6%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

ï

2; Gaps

9 9

DIOMTOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS

RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109

61

ò 셤 ò

ä

ä

Gape

ñ

Length 214; Indele

Score 520; DB 8; Pred. No. 2.9e-29; 4; Mismatches 1;

91.9%; ilarity 93.6%; Conservative

Similarity

Query Match Best Local Simil Matches 102; (

ò g ò 셤

1 DIQMIQSPSSLSASVGDRVIITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109

1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS

```
New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated diseases, such as cancer or autoimmune disorders.
Human, CD72, B-lymphocyte, receptor; scFv, antibody, cytostatic; immunosuppressive, cancer; autoimmune disease; gene therapy.
                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                sxample 5; SEQ ID NO 56; 174pp; English
                                                                                                                              Human CD72-targeted IgG1 light chain.
                                                                                                                                                                                    Location/Qualifiers
1. .108
/label= V_region
109. .214
/label= C_region
                                                                               ADR23364 standard; protein; 214 AA
                                                                                                                                                                                                                                                                     27-JAN-2003; 2003WO-EP050004.
                                                                                                                                                                                                                                                                                     27-JAN-2003; 2003WO-EP050004.
                                                                                                                                                                                                                                                                                                     (CRUC-) CRUCELL HOLLAND BV.
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                    Bakker ABH, Marissen WE;
                                                                                                                                                                                                                                                                                                                                    WPI; 2004-580978/56.
                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADR23363
                                                                                                                                                                                                                                      WO2004067569-A1
                                                                                                                                                                      Ното варіеля
                                                                                                               04-NOV-2004
                                                                                                                                                                                                                                                      12-AUG-2004.
                                                                                               ADR23364;
                                       61
                                                                                                                                                                                               Region
                                                                                                                                                                                                              Region
                                                                     RESULT
         셤
                        ò
                                     유
```

```
The present sequence is the human immunoglobulin superfamily protein IGFAM-10. Its gene was isolated from a cDNA library of colon tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, anesmia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baughn MR;
                                                                                                                       Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder; cancer;
                                                                                                                                      infection; inflammation; haematopoiesis; AIDS; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guegler KJ,
Yang J;
                                                                                                                                                                                                      1. .22
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 85-86; 105pp; English.
                                                                                                                                                                                        Location/Qualifiers
            AAY96298 standard; protein; 237 AA
                                                                                                                                                                                                                                                    label= Ig_domain
                                                                                                                                                                                                                                                                                 150. .219
/label= Ig_domain
                                                                                                                                                                                                                                                                                                            193. .236 ___/label= Ig_domain
                                                                                                                                                                                                                                 23. .237
/label= IGFAM-10
                                                                                             Human IGFAM-10 immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00195853.
98US-0113635P.
99US-0128194P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT, Corley NC,
Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US027566
                                                                  16-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-387796/33.
N-PSDB; AAA27390.
                                                                                                                                                                                                                                                                                                                                                      WO200029583-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1998;
22-DEC-1998;
07-APR-1999;
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2000
                                        AAY96298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yue H,
Lu DAM,
                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                Domain
AAY96298
```

The present sequence is the protein sequence of the light chain of human antigod, 041, which specifically recognises human B cell associated antigon CD72. An SCFV ADR23330 selected from an antibody phage display library was shown to specifically recognise the human CD72 receptor. The ScFV was recloned in IgG expression vector CO1 using primers designed to restore complete human frameworks, thereby generating antibody 041. Such anti-CD72 immunoglobulins or their antigen-binding fragments can be used internalising human binding molecules are capable of (specifically) binding to CD72 or its antigenic determinant, and preferably bind to CD72 exists antigenic determinant, and preferably bind to CD72 or its antigenic determinant, and preferably bind to CD72 arguer calls, the binding molecules internalise. In addition to the internalising human binding molecules, the invention provides immunoconjugates comprising an internalising human binding an internalising human binding molecules, the invention provides

tag (toxic substance, radioactive substance, liposome and/or enzyme), nucleic acids encoding these, and compositions comprising them. The internalising human binding molecule, immunoconjugate, nucleic acid molecule or composition can be used in the diagnosis and/or treatment of a B cell associated disorder or disease, especially a B cell associated cancer and B cell associated autoimmune disorder (claimed).

Sequence 214 AA;

Thu Nov 17 14:04:39 2005

```
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Alheimer's disease, atheroscolerosis, and restenosis. The present amino acid sequence represents the light chain from a monoclonal antibody that is specific for the human phospholipase A2 (PLA2) enzyme.
rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites
                                                                                                                                                                                      9
                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                      DIOMIOSPSSLSASVGDRVIIICRASOSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; monoclonal antibody; phospholipase A2; PLA2; inflammatory disorder; degenerative disorder; joint inflammatory reaction; skin inflammatory reaction; blood vessels inflammatory reaction; Alzheimer's psoriasis; asthma; Alzheimer's disease; atherosclerosis; restenosis; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human phospholipase A2-specific monoclonal antibody light chain #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feng
                                                                                                                                                     1;
                                                                                                                                                                                                                                                                       RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP-ITFGQGTRLEIK 130
                                                                                                                                                                                                                                                      RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                     DB 3; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liang ML,
                                                                                                                                                     Indels
                                                                                                                  Score 519.5; DB 3;
Pred. No. 3.4e-29;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee YR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 18; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                      ADP47103 standard; protein; 108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haak-Frendscho M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-DEC-2003; 2003WO-US038234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-DEC-2002; 2002US-0430724P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABGE-) ABGENIX INC.
(LEXI-) LEXICON GENETICS INC.
                                                                                                                    91.88;
                                                                                                                                   93.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                   Best Local Similarity 93.6
Matches 102, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-461119/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nocerini MR;
                                                                                    Sequence 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004050850-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Landes GM,
                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                       ADP47103;
                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                     83
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jia X,
                                                                                                                                                                                                                                                                                                                                    RESULT 10
ADP47103
                                                                                                                                                                                                                                                                                                                                                                          8888888
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                    ò
```

Length 108

Score 519; DB 8; Pred. No. 1.8e-29;

91.7%;

Best Local Similarity

Query Match

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Albeimer's disease, atherosclerosis, and restenosis. The present amino acid sequence represents the light chain from a monoclonal antibody that is specific for the human phospholipase A2 (PLA2) enzyme.
                             9
                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                          1 DIOMIQSPSSLSASVGDRVIIICRASQSISRYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIOMIQSPSSLSASVGDRVIITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                             1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
 Gaps
                                                                                                                                                                                                                                                                                    Human phospholipase A2-specific monoclonal antibody light chain #13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ×
                                                                                                                                                                                                                                                                                                                                  inflammatory disorder; degenerative disorder;
johit inflammatory reaction; skin inflammatory reaction;
blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
Alzheimer's disease; atherosclerosis; restenosis; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
%
 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                         RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP--TFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 517; DB 8; Length 108;
Pred. No. 2.6e-29;
5; Mismatches 1; Indels
                                                                                        RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liang ML,
 Indels
                                                                                                                                                                                                                                                                                                                    monoclonal antibody; phospholipase A2; PLA2;
 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee YR,
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 28; 128pp; English
                                                                                                                                                                                               ż
                                                                                                                                                                                              ADP47113 standard; protein; 108
 ب
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haak-Frendscho M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2003; 2003WO-US038234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABGE-) ABGENIX INC.
(LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-2002; 2002US-0430724P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 92.7
Matches 101; Conservative
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nocerini MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-461119/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004050850-A2
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-2004.
                                                                                                                                                                                                                                                        09-SEP-2004
102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Landes GM,
                                                                                                                                                                                                                          ADP47113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jia X,
 Matches
                                                                                                                                                                  RESULT 11
                                                                                                                                                                                 ADP47113
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                               ઠ
                                                   g
                                                                                        à
                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

9

Gaps

1;

Indels

Score 515.5; DB 3; Pred. No. 6.6e-29; 4; Mismatches 3;

Query Match
Best Local Similarity 92.7%;
Matches 101; Conservative

Length 237;

23 DIQMTQSPSSLSASVGDRVTITCRAGQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 82

RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP-ITFGQGTRLEIK 130

ADP22402 standard; protein; 107 AA.

61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109

1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS

```
요
                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the human immunoglobulin superfamily protein IGFAM-1. Its gene was isolated from a cDNA library of synovial membrane tissue. It is expressed in reproductive, gastrointestinal and cardiovascular tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, ansemia, arteriosclerceis, as athma, atherosclercois, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guegler KJ, Gorgone GA, Baughn MR;
Yang J;
                                                                                                                                Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;
                                                                                                                                            infection; inflammation; haematopoiesis; AIDS; allergy
                                                                                                                                                                                                            1. .22
/label= signal_peptide
                                                                                                                                                                                                                                                                                                      /label= ig_domain
154. .176
/label= ig_signature
                                                                                                                                                                                                                                                                                                                                                                       215. .232
/label= Ig_signature
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 77-78; 105pp; English
                        AAY96289 standard; protein; 237 AA.
                                                                                                                                                                                                                                                                             Ig_domain
                                                                                                                                                                                                                                                                                                                                                          Ig_domain
                                                                                                                                                                                                                                                   IGFAM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00195853.
98US-0113635P.
99US-0128194P.
                                                                                                      Human IGFAM-1 immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US027566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Corley NC,
Lal P, Hillman JL,
                                                                                                                                                                                                                                                                                                                                                          /label= Ig
215. .232
                                                                                                                                                                                                                                                                                         .219
                                                                                                                                                                                                                                                                                                                                                 . 236
                                                                                                                                                                                                                                        .237
                                                                                                                                                                                                                                                                  .112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                   label=
                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-387796/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA27381
                                                                                                                                                                                                                                                                                                                                                                                                               WO200029583-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1998;
22-DEC-1998;
07-APR-1999;
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1999;
                                                                           16-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-2000
                                                 AAY96289;
                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lu DAM,
                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yue H,
RESULT 12
             AAY96289
```

```
human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antibacterial; antiinflammatory; antipactatic; antirhumatic; eating-disorder; immunomodulator; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonis; riff induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; bladder cancer; lung cancer; glioblastoma; stomach cancer; cancer; prostrate cancer; timmuno-mediated inflammatory disease; pancreatic cancer; prostrate cancer; immuno-mediated inflammatory disease; restenosis; paucimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a human monoclonal antibody (I) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421); and (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (S3, ADP22417) or (S4, ADP22424). Also described: (1) assaying (M1) the level of TNFa in a patient sample, comprising conteacting with (I), and detecting the level of binding between the antibody and TNFa in fragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid arthritis.
                                                                                                                 Human anti-TNFa antibody light chain variable region SEQ ID NO:308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      쫎
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O, Green L, Feng X, Klakamp
mi P, Pigott C, Liang ML, Le
Senaldi G, Qiaojuan JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 10; SEQ ID NO 308; 213pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Babcook JS, Kang JS, Foord O,
Haak-Frendscho M, Rathanaswami
Manchulencho K, Faggioni R, Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-2002; 2002US-0430729P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-2003; 2003WO-US038281.
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-480601/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004050683-A2
                                                                           09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-2004
                                   ADP22402;
```

bacteria, viruses, fungi or parasites

Sequence 237 AA;

ω

```
sxample 5; SEQ ID NO 209; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP09100300-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22842;
                                                                                                                                                                                                                                          -
                                                                                                                                                                                  Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                                                                                                                                                                                                                                                                              AAW22842
ID AAW2
                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                             ò
monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced
monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced
cc apoptosis in an animal by selecting an animal in need of treatment for
TNFa induced apoptosis by administering the human monoclonal antibody of
(1). (1) has anabolic, antiarteriosclerotic, antiarthritic,
antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
cd sorders, immunomodulator, immunosuppressive, nephrotropic,
clasorders, immunomodulator, immunosuppressive, nephrotropic,
constructive, vasotropic and antiapoptosis, nephasotropic,
constructive, vasotropic and antiapoptosis, neoplastic disease such as
cc as TNFa antagonist. The antibody (I) is useful in the preparation of
medicament for treating TNF induced apoptosis, neoplastic disease such as
concer, ovarian cancer, bidder cancer, lung cancer, glioblastoma,
cc breast cancer, endometrial cancer, kidney cancer, colon cancer,
concer, endometrial cancer, kidney cancer, colon cancer,
concer, endometrial cancer, solon cancer,
concer, endometrial cancer, simmuno-mediated inflammatory
cdiseases such as rheumatoid arthritis, glomerulonephritis,
cdiseases, graft-host reactions, septic shock, cachexia, anorexia, and
cmultiple sclerosis. The present sequence represents a human anti-TNFa
concernation of the present invention.
                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human monoclonal antibody that binds to phospholipase A2 (PLA2), useful for treating inflammatory conditions, e.g. arthritis, psoriasis, asthma, Alzheimer's disease, atherosclerosis, or restenosis.
                                                                                                                                                                                                                                                                                                                                                                                DIOMTOSPSSLSASVGDRVTITCRASOSISSYLNWYQOKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                               1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human phospholipase A2-specific monoclonal antibody light chain #14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feng X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   joint inflammatory reaction; skin inflammatory reaction;
blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
Alzheimer's disease; atherosclerosis; restenosis; light chain.
                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                   RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP--ITFGQGTRLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                            Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liang ML,
                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monoclonal antibody; phospholipase A2; PLA2; matory disorder; degenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee YR,
                                                                                                                                                                                                                                                                                                           90.5%; Score 512; DB 8; 92.7%; Pred. No. 5.7e-29;
                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP47294 standard; protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Landes GM, Haak-Frendscho M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABGE-) ABGENIX INC.
(LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-DEC-2003; 2003WO-US038234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2002; 2002US-0430724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                    Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nocerini MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-461119/43.
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                 Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004050850-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP47294;
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP47294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
The invention comprises a human monoclonal antibody that binds to phospholipase A2 (PLA2). The monoclonal antibody of the invention is useful in the preparation of a medicament for the treatment of inflammatory and degenerative disorders stemming from inflammatory reactions in the joints, skin, and blood vessels, arthritis, psoriasis, asthma, Albeimer's disease, atherosclerosis, and restenosis. The present amino acid sequence represents the light chain from a monoclonal antibody that is specific for the human phospholipase A2 (PLA2) enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIÓMTÓSPSSLSASVGDRVTITCRASÓSISSYLNWYÖÖKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a human anti-tumour antigen monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                              DIOMIQSPSSLSASVGDRVIIICRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anticancer human monoclonal antibody variable region sequences - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, tumour antigen, cancer, monoclonal, antibody, light chain, variable region, medicine, pharmacology; biochemistry, CDR;
                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human anti-tumour antigen antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 108;
                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                            Score 512; DB 8;
Pred. No. 5.8e-29;
4; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= mat_peptide
46. .56
/label= CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .22
/label=_sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variable region; medicine; pharmacc
complementarity determining region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ġ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 11; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW22842 standard; protein; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95JP-00278266.
                                                                                                                                                                                                                                                                                                                  90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95JP-00278266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .132
                                                                                                                                                                                                                                                                                                                                                                       Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-276726/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                related DNA and RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HAGI/) HAGIWARA Y.
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT75423
                                                                                                                                                                                                                                                              Sequence 108 AA;
```

```
(MAb) light chain variable region, useful in medicine, pharmacology and blochemistry. The isotype of a MAb secreted by the human/human hybridoma HT was determined to be mu and kappa. Human MAb was purified, and the antigen recognised by human MAb CIN"-IgM identified by western blotting
  8888888
```

Sequence 132 AA;

	1;	09
	Gарв	OSGVPS
	2;	ASSL
Length 132,	2; Indels	OKPGKAPKLLIYG
90.5%; Score 512; DB 2; Length 132; 92.7%; Pred No. 6 9e-29;	4; Mismatches 2; Indels 2; Gaps 1;	1 DIOMIOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
	ative	LSASVGDRV
milarity	Conserv	OIOMTOSPSS
d C	101	7
Query Match Best Local Similarity	Matches 101; Conservative 4	۸̈
		~

q ò g

Search completed: November 16, 2005, 21:51:37 Job time : 63.5147 secs

for they bear a feet to the bear of

Н

```
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
```

	; Search time 13.0239
using sw model	2005, 21:37:48
- protein search, u	November 16, 2
OM protein - p	Run on:

; Search time 13.0239 Seconds (without alignments) 805.260 Million cell updates/sec

US-10-660-357A-10 566 1 DIQMTQSPSSLSASVGDRVT.....QSYSTPPECSFGQGTKLEIK 109 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seg 8 0 0 0 Minimum I Maximum I

length: 0 length: 2000000000

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 su

summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		& Query				
S	Score	Match	Length	B	OI	Description
	511	90.3	123	7	840331	kappa
~	509	89.9	127	7	S40367	kappa
м	505	89.2	108	~	B49047	kappa
4	502	88.7	120	~	S46370	Ig kappa chain V-J
ហ	200	88.3	129	~	S40317	Ig kappa chain - h
9	491	86.7	129	н	K1HUWK	kappa
7	489	86.4	108	~	S44122	Ig kappa chain V r
8	489	86.4	108	~	S47182	Ig kappa chain - h
6	485	85.7	108	ч	K1HUHU	Ig kappa chain V-I
0	484	85.5	109	~	S31981	kappa
1	482	85.2	109	7	S31998	kappa chain -
2	482	85.2	122	N	S40314	Ig kappa chain - h
3 4	80.5	84.9	107	N	836275	lambda
	476	84.1	129	N	S52793	kappa
S	475	83.9	117	~	S24206	. Ig kappa chain V r
9	474	83.7	108	~	S19674	kappa
7	473	83.6	122	~	S40370	kappa
4	172.5	83.5	125	~	S40315	kappa
0	468	82.7	116	~	A27594	kappa
0	467	82.5	129	~	852792	карра с
-	466	82.3	107	~	S36264	lambda
2	466	82.3	107	~	836269	lambda
	466	82.3	109	7	S31979	kappa
24	465	82.2	108	~	S31977	kappa
2	465		110	~	S44118	Ig kappa chain V-J
6 4	64	82.1	106	~	33	i-teta
7	462	81.6	109	~	S31980	kappa
28	462	81.6	109	N	S31978	Ig kappa chain - h
0	462	81.6	117	7	S46371	

Ig kappa chain V-J Ig kappa chain V r		hain hain chain	19 kappa chain V-J 19 kappa chain V-J 19 kappa chain V I 19 kappa chain - h	hain hain hain
S40336 JL0139	X1000 S4033 X1HUDE S40350	\$40359 \$40352 \$36262	531595 546376 530521 532001	S46372 S52789 S34007
777	1212	0000	1000	0 0 0
124	128 108 125	129 131 107	1117 108 109	128 129 108
81.5	81.1 81.1 81.1	81.1 80.9 80.9	8 8 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	79.9 79.9
461.5	4 4 4 4 4 5 6 1 4 5 9 9 1	4 4 4 4 0 0 0 0 0	454.5 455.5 453	452 452 450.5
31	2 E E E 2 E 4 E	337	0 4 4 4 0 11 2	4 4 4 ሠ 4 7

ALIGNMENTS

```
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                CyAccession: S40331
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1999.
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:9408091; PMID:8258341
A;Recession: S40331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PID:9441351
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.3%; Score 511; DB 2; Length 123; Best Local Similarity 92.7%; Pred. No. 1.1e-35; Matches 101; Conservative 4; Mismatches 2; Indels
Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

9 1 DIOMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS Gaps ä

16 61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109 셤 ò 셤

RESULT 2

Ig kappa chain V-J-C region - human C;Species: Homo sapiens (man) C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: \$40367 R;Klbin, R.; Jaenichen, R.; Zachau, H.G. Bur. J. Immunol. 23, 3248-3271, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: \$40312; MUID:94080891; PMID:8258341

A; Status: preliminary; translation not shown A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-127 < KLBA A; Residues: 1-127 < KLBA A; Cross-references: EMBL: X72477 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heteroterramer; immunoglobulin F; 33-107/ Domain: immunoglobulin homology < IMM>

89.9%; Score 509; DB 2; Length 127;

Query Match

N

```
C;Accession: A01883
R;Klobeck, H.G.; Combriato, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A;Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell A;Reference number: A93534; MUD:85014148; PMID:6091049
A;Accession: A01883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Cross-references: GDB:136264
A.Map position: 2p12-2p12
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp and isulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fil-22/Domain: signal sequence #status predicted <SIG>Fil-22/Domain: signal sequence #status predicted <MAT>Figl-129/Product: 1g kappa chain V-I region (Walker) #status predicted <MAT>Figl-45/Region: framework Figl-45/Region: immunoglobulin homology <INM>
                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Species: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Species: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 DIQMTQSPSSLSTSLGDRVTITCRASQSIGTYLNWYQQKPGKAPKFLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                 C,Accession: S40317
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
A:Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:9441323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GapB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                  71 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSFSNPPEYTFGQGTKLEI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.3%; Score 500; DB 2; Length 129; 89.0%; Pred. No. 9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72427; NID:g441322; PIDN:CAA51095.1;
A;Cross-references: EMBL:X72427; NID:g441322; PIDN:CAA51095.1;
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/bomain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-129 <KLO.
A;Cross.references: UNIPROT:P04431
A;Note: the sequence was determined from the differentiated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 491; DB 1;
Pred. No. Se-34;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain precursor V-I region (Walker) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:111-119/Region: complementarity-determining 3
F:120-129/Region: framework 4
F:45-110/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;46-56/Region: complementarity-determining 1
F;57-71/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;72-78/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translation not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.7%;
ilarity 90.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 89.0
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;79-110/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                   Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: GDB: IGKV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig Rappa.chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cipate: 194047
Cipate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
S46370
Ig Aappa chain V-J region (T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: $46310; S3864
R;Bensimon, C; Chastagner, P; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea A;Reference number: $46369; MUID:94313975; PMID:8039491
A;Accession: $46370
A;Molecule type: mRNA
A;Residues: 1-120 <a href="https://docs.org/">https://docs.org/</a>
A;Cross-references: EMBL: Z27171; NID:9415957; PIDN:CAA81695.1; PID:9415958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                               DIOMTOSPSSLSASVGDRVTITCRASQSISNYLNWYQRKPGKAPKILIYAASSLQSGVPS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIQMTQSPSSLSASVGDRVT1TCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
7
                                                                                                                                                                                                                                                                                                        RFSGSGSGTDFTLTISSLOPEDFATYYCQOSYSTP--LTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                     RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGOGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 88.7%; Score 502; DB 2; Length 12
Best Local Similarity 88.9%; Pred. No. 5.7e-35;
Matches 96; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 505; DB 2; Length 10
Pred. No. 2.9e-35;
4; Mismatches 3; Indels
                                                                     Indels
1.66-35;
                                                              5; Mismatches
                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.2%;
                           91.78;
                               Best Local Similarity 91.7
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                    78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 8
                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                 ò
```

9 81 ä

m

8 ઠ 셤

ઠ

us-10-660-357a-10.rpr

```
Algoresion: A01868
A; Molecule type: protein
A; Cross-references: UNIPROT: P01600
A; Note: the C region of this chain has the Inv (3) marker
B; Steiner, V.; Chang, J.Y.
B; Steiner, V.; Chang, J.Y.
A; Title: Chemical modification of the carboxyl groups of protein substrates enhances then A; Reference number: 802572; MUD: 88005152; PMID: 3115831
A; Contents: annotation
C; Comment: This is a Bence Jones protein.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 2p12-2p12

C,Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp

hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into lan

C,Superfamily: immunoglobulin V region; immunoglobulin homology

C,Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

F;23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Species: Homo sapiens (man)
C'Date: Ob-dan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C'Accession: 831981
R;Portclano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
R;Portclano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
R;Portclano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
R;Portclano, S.M.; Rapoport, B.
R;Portcription: Lack of promiscuity in autoantigen-specific H and L chain combinations as A;Reference number: 831977
                                                                                                                                                                                                                                                                                                                                            immunoglobulin L-chain of subga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIOMIQSPSSLSASVGDRVIIICRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A01868; S02574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIOMIOSPSSLSASVGDRVIITCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: EMBL:215077; NID:g38493; PIDN:CAA78786.1; PID:g38494
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLOPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indele
                                                                                                                                                                                                                                               Riwatanabe, S.; Hilschmann, N. M. Phype-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
A; Title: The primary structure of a monoclonal kappa-type A; Reference number: A01868; MUID:11032830; PMID:4097974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.3e-33;
8; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.5%; Score 484; DB 2;
86.2%; Pred. No. 1.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 485; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                              Ig kappa chain V-I region (Hau) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.2%;
Matches 95; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S31981
Ig kappa chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:136264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S31981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Gene: GDB: IGKV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain - human

[1] kappa chain - human

[2] kappa chain - human

[2] kappa chain - human

[3] kappa chain - human

[3] kappa chain - human

[4] kappa chain - human

[5] kaceissions (47182

[6] kaceissions (47182

[7] kappa chain and analysis of IgM anti-thyroglobulin autoantibodies from patien

[7] kappa chain ary

[8] kappa chain ary

[8] kappa chain and analysis of IgM anti-thyroglobulin autoantibodies from patien

[8] kappa chain ary

                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region - human (5.5pecies: Homo sapiens (man) (7.5pecies: Homo sapiens (man) (7.5pecies: Homo sapiens (man) (7.5pecies: Homo sapiens (man) (7.5pecies: Homo sapiens) (7.5pecies: Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVIITCRASQSISSYLNWYQQKLGKAPKLLIYSASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
9
                                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAA83265.1; PID:g940533 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology cIMM> P;16-90/Domain: immunoglobulin homology cIMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP--ITSGQGTRLEIK 107
                                                                                                                                                                                                                    RFSGSGSGTDFTLTISSLQPEDSATYYCQQSYST--LITFGQGTRLEIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFSGSGSGTDFTLT1SSLQPEDFAIYYCQQSYSTP--WTFGQGTKVBIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                      RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 489; DB 2; Length Luc
Pred. No. 6.2e-34;
Fred. No. 5.2e-34; Sredels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 489; DB 2;
Pred. No. 6.2e-34;
7; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 86.4%;
1 Similarity 88.1%;
96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 96
                                                                              23
                                                                                                                                                                 61
                                                                                                                                                                                                                                                         83
```

g

ઠ 요

ð

മ്

ò 셤

8

Thu Nov 17

```
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.3%;
Matches 93; Conservative E
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.2'
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-117 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: S52793
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-129 <ROC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                RESULT 11
S31998
Ig Akapa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S31998
R;Portcolano, S; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
Submitted to the EMBL Data Library, June 1992
A;Bescription: Lack of promisculty in autoantigen-specific H and L chain combinations as A;Reference number: S31979
A;Reference number: S31998
A;Reference number: B31998
A;Reterence number: BABL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
S40114
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840314
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
A;Accession: S40314
A;Accession: S40314
A;Accession: S40314
A;Residues: 1-122 cKLE>
A;Cross-references: EMBL:772424
C;Staperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMTOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
  RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                        RFSGSGSGTDFTLTISSLQPEDYATYYCQQSYSTP--FTFGQGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFSGSGSGTDFTLIISSLQPEDFGTYYCQQTHTTPP--TFGQGTKVEIK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 482; DB 2; Length 10
Pred. No. 2.4e-33;
6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 95; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 94; Conserv
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             836275
  à
                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
```

```
C;Accession: S36275
R;Griffitha, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1939
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:767990
A;Recession: S36275
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region - human (fragment)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibate: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
CiAccession: 582793
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, Submitted to the EMBL Data Library, March 1995
A;Bescription: Light chain V region gene usage restriction and peculiarities in myeloma-A;Reference number: 552789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V region (Vx Ol2 and Vx O2) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Es-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: S24206; S24206; S. Thiebe, R.; Mitzel, S.; Zachau, H.G.
R;Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Bur. J Immunol. 21, 1821-1827, 1991
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated O reg1
A;Reference number: S24205; MUID:91330953; PMID:1907917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMIQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DIQMIQSPSSLSASVGDRVTITCRASQNISYLNWYQQKPGKAPKLLMYAASSLQSGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X85997; NID:g758600; PIDN:CAA59989.1; PID:g758601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:218827; NID:g33416; PIDN:CAA79279.1; PID:g939909
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٠.
م
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 RFVGSGSGTDFTLTISSLQPEDFATYYCQQTXSAP--LTFGGGTKVEIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLBIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDVAVYYCQQYYSTP---TFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 476; DB 2; Length 129;
Pred. No. 8.8e-33;
8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;38-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.9%; Score 480.5; DB 2;
87.2%; Pred. No. 3.1e-33;
ive 4; Mismatches 7;
```

```
A,Cross-references: EMBL:X59315; NID:g33247; PIDN:CAA42002.1; PID:g33248
A,GERDETICE: G1
A,Accession: S24209
A,Anolecula type: DNA
A,Rocession: S24209
A,Genetics: G2
C,Genetics: G2
A,Genetics: G2
A,Anap position: 2
A,Introns: 19/1
C,Genetics: G2
A,Anap position: 2
A,Introns: 19/1
C,Genetics: G2
A,Rocession: S4
A,Introns: 19/1
C,Genetics: G2
A,Rocession: S4
A,Introns: 19/1
C,Superfamily: immunoglobulin homology <IRM+>
C,Genetics: G2
A,Introns: 19/1
C,Superfamily: immunoglobulin homology <IRM+>
C,Genetics: G2
A,Introns: 19/1
C,Superfamily: immunoglobulin homology <IRM+>
C,Genetics: G2
A,Introns: S4
A,Introns: S4
A,Introns: S4
A,Introns: S6
A,
```

Search completed: November 16, 2005, 22:04:07 Job time : 14.0239 secs

Constitution of the state of th

Н

```
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
  240
1108
1108
11108
1111
1108
1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 99; Consern
76.3
76.2
76.2
76.2
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.1
775.
NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UL77;
                                                                                                                                                                                                                                                                    096SA9 ;
                                                                                                                                                                                                                                                      Q96SA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
Q9UL77
ID Q9UL
AC Q9UL
                                                                                                                                                                                                                               RESULT 1
 296SA9
                                                                                                                                                                                                                                                        윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapien sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapien
sapien
                                                                              ; Search time 61.1121 Seconds (without alignments) 913.348 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                          566
1 DIOMTQSPSSLSASVGDRVT.....QSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo
homo
homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homo
homo
homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGRW1
QGGRW2
QGGRW3
Q7234
Q7234
Q7234
Q6pih7
Q9u170
P01652
P01612
P01612
P01612
P01612
P01612
P01612
P01612
P01612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01594 | P04430 | P01611 | P01598 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0968a9
09ul77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P04431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P01593
Q652C8
Q72473
Q6pih4
P01603
Q6gmx9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9u181
       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0968A9
090L77
KVIH HUMAN
KVIH HUMAN
Q9ULBI
06GWWI
06GWX8
Q05WLRA
06GWX8
Q01L31
C6GWX8
Q01L37
KVIN HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OGPIH4
KV1K HUMAN
QGGMX9
KV1P_HUMAN
                                                                                2005, 21:36:13
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                   UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                               US-10-660-357A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             November 16,
                      Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                Minimum DB seq
Maximum DB seq
                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460
459
450
449.5
449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                        OM protein -
                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
No.
```

```
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
mus musculu
homo sapien
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE-98375893; PubMed=9712075;

KA Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;

Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;

The carditie: human anti-N-acetylglucosamine/anti-myosin antibody V region genes;

Thibody V region genes;

T. Immunol. 161:2020-2031(1998).

R. J. Immunol. 161:2020-2031(1998).

R. J. Immunol. 161:2020-2031(1998).

R. SHR; B49047;

PIR; 91840;

PIR; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variable region (Fragment).

Homo sapiens (Human).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q652C9
P011596
P0115996
P011509
P01609
P01602
P01602
P01602
P01603
P01646
P01646
P01646
P01646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.9%; Score 497.5; DB 2; Length 107; llarity 90.8%; Pred. No. 8.2e-42; Conservative 4; Mismatches 3; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 107
107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
Q652C9
KV1D HUMAN
KV1C HUMAN
KV1C HUMAN
KV1X HUMAN
Q6PITS
KV1L HUMAN
KV1J HUMAN
Q96PF
KV5M MOUSE
KV5M MOUSE
KV5M MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
```

```
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV1H_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT TARKER BEAR SET THE SET TH
         STITILITY ON SERVICE SOLUTION OF SERVICE SOLUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIOMTOSPSSLSASVGDRVTITCRASOSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJNE-8501418; PubMed-6091049;
Klobeck H.G., Combriato G., Zachau H.G.;
Immunoglobulin genes of the Kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST--SWTFGEGTKVEIK 107
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 108;
4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.6%; Score 496; DB 2;
89.9%; Pred. No. 1.2e-41;
ive 5; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
PIR; B49047; B49047.
HSSP, P01607; IBWW.
InterPro; IPR007710; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
18 Aappa chain V-I region Walker precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X00965; CAA25477.1, ALT_TERM.
PIR, A01883; KIHUWK.
HSSP, P01607; 1BWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108
                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Young D.C.;
                                                                                                                        (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KV1W HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P04431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KV1W HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLMWYQQKPGKAPKLLIYAASSLQSGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin I
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                     Ig kappa chain V-I region Walker. Framework-1. Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; PF00047; ig; 1. --
SWART; SWOAG6; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
3D-structure; Bence-Jones protein; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 491; DB 1; Length 129; 90.8%; Pred. No. 4.5e-41; ive 3; Mismatches 5; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Framework-1.
Complementarity-determining-1.
Framework-2.
                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-2. Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14069 MW; F941FA07D4AFC2F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
8 kappa chain V-I region Hau.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006555; P:immune response; NAS. InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1.
SWART; SMO0406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Framework-4.
                                                                                                                                                                                                                                                                                                                                                    Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 1F6L; X-ray; L=1-108.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; P:antigen binding; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=71032830; PubMed=4097974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.8
nes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             !mmunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A01868; K1HUHU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subgroups.";
```

```
Mammalia; Euther:
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                           ISSUE=Spleen;
                                                                                                                                                                                                                                                                 and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGGMX0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6GMX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCOOR BETTER
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                9
                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIOMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLMWYQQKPGKAPNLLIYAASSLQSGVPS
                                                                                                                           1 DIOMIOSPSSLSASVGDRVIITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLOSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
                                                                                             ;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLQPEDPATYYCROSYSTPPECSFGGGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITP--TSFGQGTRVEIK 107
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; MEDINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wux X. Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 107;
                                                                       85.7%; Score 485; DB 1; Length 108;
larity 87.2%; Pred. No. 1.5e-40;
Conservative 8; Mismatches 4; Indels
        Complementarity-determining-3.
Framework-4.
                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 84.0%; Score 475.5; DB 2; Length Local Similarity 86.2%; Pred. No. 1.3e-39; Length es 94; Conservative 5; Mismatches 7; Indels
88 Framework-3.
97 Complementarity-determinir
107 Framework-4.
88 By similarity.
11671 MW; 08D3A6160D8D0618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 107
107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035033, AAD56269.1; -.
HSSP; P01607; 1BWW.
InterPro; IPR007110; Ig-like.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypochetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
 57
89
98 1
23
108 1
                                                                                  Local Similarity
ses 95; Conserv
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
NON TER
SEQUENCE
            DOMAIN
DOMAIN
DISULFID
NON TER
SEQÜENCE
                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGGMW1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6GMW1
                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC DOT DOT DOT OOS HHOOS
                                                                                                                                                                                                                        09UL81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
 833333
                                                                                                                                   g
                                                                                                                                                         ઠે
                                                                                                                                                                                                                                   g
```

```
A NEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Bitchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfeard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 IQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPSR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 IQMTQSPSSLSASVGDRVTITCRASQCISNDLGWYQQKPGKAPKLLIYAASSLQSGVPSR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 FSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.6%; Score 473; DB 2; Length 236;
88.0%; Pred. No. 5.6e-39;
ive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Straubberg R.;
Straubberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073791, AAH73791.1;
InterPro; IPR007310; Ig-1ike.
InterPro; IPR003599; Ig_-C1.
InterPro; IPR003596; Ig_-C1.
InterPro; IPR003596; Ig_-V.
Pfam; PF07654; C1-8et; I.
Pfam; PF00047; Ig_-2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
```

```
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bask S.A., McKernan R.J., Malek J.A., Gunarane P.H.,
A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A. Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Moses S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMIQSPSSLSASVGDRVIIICRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Skeletal Muscle;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSFP--FTFGFGTKVDIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.5%; Score 467; DB 2; Length 236; 84.4%; Pred. No. 2.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073764; AAH73764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, BC073/04; con. 19.
InterPro; IPR001599; Ig.1ke.
InterPro; IPR001597; Ig.cl.
InterPro; IPR001597; Ig.cl.
InterPro; IPR001506; Ig.MtC.
InterPro; IPR001596; Ig.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.4
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF07654, C1.8et; 1. Pfam; PF07654, C1.8et; 2. SmART; SM00407; 1G; 2. SmART; SM00407; 1Gc1; 1. SMART; SM00406; 1Gv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissum=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7Z3Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7Z3Y4
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                          Attaubherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Straubherg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max G.I., Haich F.,

A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B placton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Eromstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Frange C.,

R Aha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaue S., Sanchez A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,

Jones S.J., Marra M.A.,

""Green E.D., Schnerch A., Schner J.E.,

""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                           TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 471; DB 2; Length 23. Pred. No. 8.98-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.2%; Scor.
84.4%; Pred. No. b...
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: BC073775; AA473775...
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003006; IG.
InterPro; IPR003006; IG.
InterPro; IPR003056; IG.
InterPro; IPR003506; IG.
InterPro; IPR003506; IG.
InterPro; IPR0047; IG.
InterPro; IPR0047; IG.
InterPro; IPR00407; IG.
InterPro; IPR00407; IG.
InterPro; IPR00407; IG.
InterPro; IPR00406; IG.
INTERPPRO; IPR00406; IG.
INTERPPRO; IRR00406; IG.
INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last seques-JUL-2004 (TrEMBLrel. 27, Last annown Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 84.4
les 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGGMX8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O6GMX8
```

RESULT 8
QGGMX8
DGGMX9
AC QGGMQ
DT 05-JI
DT 05-JI
DT 05-JI
DE HYPOTO
OC HOMO
OC MAMME
OX NCBI
RP 5EQ1
RP 5EQ1
RP 5EQ1
RP 5EQ1

g ò

9 82

Gaps

7

6; Indels

S

```
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6PIH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                     PALE SERVICE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Latchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Muhing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Carimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DIOMIQSPSSLSASVGDIVIIICRASQDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 169:56-59(1970).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kohler H., Shimizu A., Paul C., Putnam F.W.; "Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC005332; AAH05332.1; -. HSSP; P01834; 1HEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 procein.
236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 465; DB 2;
Pred. No. 3.5e-38;
4; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
K Appa chain V-I region OU.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=70201507; PubMed=5447531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-8et; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.2%;
86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Skeletal Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A01872; K1HUOU.
HSSP; P01607; 1BWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macroglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Simple 94; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVIN HUMAN
AC 21-006-1986
DT 21-JUL-1986
DT 21-JUL-1986
DT 95-JUL-2004
DE 19 kappa cha:
GS Homo sapiens
OC PARAYOCE;
MON CEL TAXID=9
RN (1)
RN (1)
RN KNDEL TAXID=9
RN (1)
RP KN KNDLINE=7020
RN KN KNDLINE=7020
RN KN KNDLINE=7020
RN KN KNOHET H.;
RN KNDLINE=7020
RN KN KNOHET H.;
RN KNDLINE=7020
RN CONHET H.;
RN KNOHET H.;
RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                 $\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
TISSUE=LUNG:

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A trausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

A tacchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A tacchul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,

Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley N.A., McEwran K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., McEwan P.J., McEwran K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrayminski M.I., Skalska U., Smailus D.E., Schnerch A., Scheln J.E.,

A Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۲,
ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGGTBFTFTISSLZFZBFATYYCZZSYSSP--TTFGZGTRLZIK 107
                                                                                                                                                                                                                                                                                                                      Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.4%; Score 461; DB 1; Length 108; 75.2%; Pred. No. 3.6e-38; ive 18; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8283D4A24105827E CRC64;
                                                                                                                          PEam, PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
DroSITE; PS50815; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G6PIH7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                      Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Framework-4
GO, GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 75.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    49
56
88
97
107
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
```

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases

```
KV1M HUMAN
P01605;
                                                                                                                      KV1E HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                              RESULT 13
KVIE HUMAN
                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIOMIOSPSSLSASVGDRVIITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo Jeanning (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGTDFTLTISSLQPEDVATYXC-QKYNSAPR-TFGPGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                          InterPro; IPR00110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR00409; IG.
InterPro; IPR00409; IG.
InterPro; IPR00406; IG.
InterPro; IPR00406; IG.
InterPro; IRR; InterPro; IPR03TE; InterPro; IRR; In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.3%; Score 460; DB 2; Length 10
85.3%; Pred. No. 4.5e-38;
ive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 461; DB 2;
Pred. No. 8.8e-38;
8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ciin. Immunol. Immunopathol. 87:184-192 (1998).
EMBL; AF035044; AAD56280.1; -.
PIR; PH0863; PH0863.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
INTERFY: SM0466; IG-like.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                  EMBL, BC034141; AAH34141.1; -
HSSP; P01607; 1AR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.4%;
83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85...
Best Local Similarity
Local Similarity
Local 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.5
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
OQULT)
AC QQULT)
AC QQULT)
DT 01-MA
DT 01-MA
DT 01-OC
DE MYOSI
RA NUX.
RA WUX.
RA WUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE. When the sequence of the variable domains of two human IgM "Complete amino acid sequence of the variable domains of two human IgM "Complete amino acid sequence of the variable domains of two human IgM "Complete".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=72053133; PubMed=5124396;
Milstein C.P., Deverson E.V.;
"The amino acid sequence of a human kappa light chain.";
"In a mino 3. 123:945-958(1971).
"In MISCELLANEOUS: The C region of this chain has the INV (3) marker.
PIR; A01865; KHHUDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISGLLPEDFATYYCQQSYTTP--YTFGPGTKVEM 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-2.
Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.1%; Score 459; DB 1; Length 10
80.6%; Pred. No. 5.6e-38;
ive 12; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11661 MW; BDD6E350017F1E51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEam; PF00047; ig; 1. SMART; SM00406; IGy; 1. DROSITE; PS50335; IG LIKE; 1. Droctin sequencing; Immunoglobulin V region. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-I region Lay.
Homo sapiens (Human).
                                  P01597;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 kappa chain V-1 region DEE.
Homo sapiens (Human).
108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; PO1607; IBWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:000855; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; Ig_v.
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 80.6 Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
35
50
57
89
98
108
108
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYIM HOWAN

ID KVIM H

KYIM H

E 21-JUL-

DT 21-JUL-

DT 21-JUL-

DE 19-JUL-

DE 19-JUL-

DE 19-JUL-

DE 00-JUL-

E 00-JUL-
```

```
용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";

Scand. J. Immunol. 5:677-684(1976).

Cand. J. Immunol. 5:677-684(1976).

Cand. J. Immunol. 5:677-684(1976).

T. Imm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMIQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eulitz M., Linke R.P.;
"Primary structure of the variable part of an amyloidogenic Bence-Jones Protein (Mev). An unusual insertion in the third hypervariable region of a human kappa-immunoglobulin light chain.";
Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
-!- MISCELLANEOUS: Another form that lacked residues 1-3 was also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I- MISCELLANEOUS: This chain was isolated from a myeloma protein. PIR, A01879; KIHUM.
HSSP, PRO1562; IMTL.
GO; GO:000552; IMTL.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPR00110; Ig-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11834 MW; 739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; TGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 450; DB 1;
Pred. No. 4.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region Mev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=83081018; PubMed=6816713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.5%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003596;
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
35
50
50
89
98
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV1T_HUMAN
ID KV1T_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
             SO STATE THE TELEFORM SO SENSE SO SENSE SENSE SO SENSE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

```
1 DVQMTQSPSSLSASVGDRVIITCRASQSSVDYLNWYQQKPGKAPKLLIFDTSNLQSGVPS 60
                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                     Length 109;
                                                             Framework-1.
Complementarity-determining-1.
Framework-2.
                                                                                                           Complementarity-determining-2.
                                                                                                                                         Complementarity-determining-3. Framework-4.
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                        11870 MW; B6ABF4515D55F5A0 CRC64;
                                                                                                                                                                                                                                     Score 449.5; DB 1;
Pred. No. 5e-37;
9; Mismatches 11;
                               protein sequencing
                                                                                                                                                                           By similarity.
                                                                                                                              Framework-3.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Bence-Jones protein; Direct p
                                                                                                                                                                                                                                      79.4%;
                                                                                                                                                                                                                       Query Match
Best Local Similarity 80...
Best Local 88; Conservative
                                                [mmunoglobulin V region
                                                                                                                                                                                     NON TER
SEQUENCE
                                                                                                                                                                           DISULFID
                                                           DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                            DOMAIN
```

Search completed: November 16, 2005, 22:01:51 Job time: 62.1121 secs

Control of the control

Sequence:

6

ĕ

Database

Result No.

```
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                            Sequence
Sequence
Sequence
Sequence
                              Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                          Sequence 2.7.

Batent No. 6696245

GENERAL INFORMATION:

APPLICANT: Winter, Greg

TITLE OF INVENTION:

FILE REFERENCE: 3789/72916

CURRENT APPLICATION WHERE: US/09/192,854

CURRENT APPLICATION WHERE: 09/066,729

EARLIER FILING DATE: 1998-11-17

EARLIER FILING DATE: 1997-11-21

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPN--TFGQGTKVEIK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 511; DB 4; L
Pred. No. 2.4e-39;
4; Mismatches 2;
               US-09-240-274-31
US-09-240-274-31
US-09-240-274-41
US-09-240-274-156
US-09-240-274-176
US-09-240-274-176
US-09-240-274-181
US-09-240-274-181
US-09-240-274-181
US-09-240-274-181
US-09-240-274-181
US-08-51-251-43
US-08-51-251-43
US-08-51-21-43
US-08-51-21-43
US-08-51-21-43
US-08-378-939-14
US-09-470-274-38
US-09-240-274-38
                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/09240274; Patent No. 6255455; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 101; Conservative
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 2
US-09-240-274-32
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-192-854-2
                                                                                                                                                                                                                                        JS-09-192-854-2
 496.5
496.5
496.5
495.5
495.5
491.5
491.5
491.5
491.5
491.5
491.5
491.5
491.5
491.5
491.5
491.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Search time 18.534 Seconds
(without alignments)
439.017 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28,
43,
28,
105,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104,
158,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9,0
                                                                                                                  566
1 DIQMTQSPSSLSASVGDRVT.....QSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                       Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

//cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

//cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

//cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

//cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

//cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-192-854-2
US-09-240-274-32
US-09-240-274-33
US-09-340-274-43
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-490-153-14
US-09-025-769B-28
US-09-025-769B-28
US-09-490-153-43
US-09-490-153-43
US-09-490-153-43
US-09-490-153-43
US-09-490-153-105
US-09-490-153-105
US-08-899-575-105
US-08-899-575-104
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                              513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                  November 16, 2005, 21:41:29
                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                protein search, using sw model
                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                    length: 0
length: 2000000000
                                                                                                         US-10-660-357A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4499
4498
4498
4498
4498
7698
7698
7698
                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                               protein -
```

ä

Gaps

9

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,057
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POOC, BAIAN W
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0133-
TELECOMMUNICATION INFORMATION:
MEDIATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

89.2%; Score 505; DB 2;
Best Local Similarity 91.7%; Pred. No. 3.6e-39;
Matches 100; Conservative 4; Mismatches 3.
  IITLE OF INVENTION: In Diagnosis and Therapy
                       NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 727-3670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAN: (206) 727-367
TELEPAX: (206) 727-3601
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-379-057-29
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                          STREET: 3005 Fi
CITY: Seattle
STATE: Washingt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1251 A. CITY: New York
                                                                                                                                                                                ZIP: 98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-025-769B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: No COUNTRY:
                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Пр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal Antibodies Specific For Different Epitopes of Human gp39 and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh.(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
TITLE REPERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: 00/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER PILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER PILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PALENT VET. 2.0
SEQ ID NO 43
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                     2 ELTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 QMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPSRF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 OMTOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 108;
                                                                                                                                                                                                        DB 3; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                    63 SGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGGGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                             62 SGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP-YTFGQGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 SGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                   89.3%; Score 505.5; DB 3; ilarity 92.5%; Pred. No. 3.2e-39; Conservative 5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.3%; Score 505.5; DB 3
92.5%; Pred. No. 3.2e-39;
iive 5; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-43
                                                                                                                             ; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/08379057
Patent No. 5876950
GENERAL INFORMATION:
APPLICANT: Siadak, Anthony W.
APPLICANT: Hollenbaugh, Diane L.
APPLICANT: Gilliand, Lisa K.
APPLICANT: Gordon, Marcia L.
APPLICANT: Bajorath, Jurgen
APPLICANT: Anuffo, Alajandro A.
APPLICANT: Aruffo, Alajandro A.
TITLE OF INVENTION: Monoclonal Anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 43, Application US/09240274; Patent No. 6255455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.5°
SOFTWARE: Patentin Ver. 2.0
                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-379-057-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-240-274-43
                                            LENGTH: 108
                         SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

ઠે

```
1 DIGMTÓSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                       Gарв
                                                       5
                                                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP--LTFGGGTKVEIK 107
Length 108;
                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
```

9

```
JS-09-490-153-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.

STATE: D.C.

COUNTRY: USA

ZIP: 20066

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTP--LTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1666 K Street, N.W., Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: BP 95 11 3021.0
FILING DATE: 19-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         4.46-39
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 89.0%; Score 504; DB Best Local Similarity 91.7%; Pred. No. 4.4e Matches 100; Conservative 3; Mismatches
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTONNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ ID NO: 11 TELECOMUNICATION SEG ID NO: 14:
SUGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 912-2020
                                                                                                                                                                                                                                                                               LENGTH: 108 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear; MOLECULE TYPE: protein US-09-025-7698-14
                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-490-070A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                   1 DIOMTOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                    2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTP--LTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RPSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30 (EPO)
                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT Knappik, Achim
Pack, Peter
Ilaq, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: FlOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACEMENTE Release #1.0, Versi

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FRED-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-RGG-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                Query Match

89.0%; Score 504; DB 4;
Best Local Similarity 91.7%; Pred. No. 4.4e-39;
Matches 100; Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHRRACTERISTICS:
SEQUENCE CHRRACTERISTICS:
ENGTH: 108 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: probology: innear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-153-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
| INPORMATION FOR SEQ ID NO: 14:
| SEQUENCE CHARACTER.STICS:
| LENGTH: 108 amino acids
| TYPE: amino acid
| STRANDEDNESS: <Unknown>
| TOPOLOGY: linear
| MOLECULE TYPE: protein
| SEQUENCE DESCRIPTION: SEQ ID NO: 14:
| US-09-490-070A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: James F. Haley, Jr., REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09490153
Parent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
```

61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTP--LTFGGGTKVEIK 107

Query Match

```
Sequence 167, Application US/09240274

Sequence 167, Application US/09240274

Patent No. 625455

GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF

TITLE OF INVENTION: USBER: US/09/240,274

CURRENT PILLING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER APPLICATION NUMBER: 60/081,550

EARLIER PILLING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 167

LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.6%; Score 501.5; DB 3; Length 108; 91.6%; Pred. No. 7.5e-39; live 5; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us-09-025-769B-28

Sequence 28, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Raappix, Achim
APPLICANT: 1lag, Vic
APPLICANT: 1lag, Vic
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Pluckhun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEBE: James F. Haley, Jr., Esg. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
COUNTRY: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 SGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP-YTFGQGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: anti-Rh(D) antibody clone SH34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 98; Conserv
                                                                                                  JS-09-240-274-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-240-274-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIQMIQSPSSLSASVGDRVIITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                               1 DIOMTOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIOMIOSPSSLSASVGDRVIITCRASOSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 18-4-J998

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FBE-1998

APPLICATION NUMBER: E9 51 1 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTDFTLFISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTP--LTFGGGTKVEIK 107
89.0%; Score 504; DB 4; Length 108; 91.7%; Pred. No. 4.4e-39; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.0%; Score 504; DB 4; Length 10 Best Local Similarity 91.7%; Pred. No. 4.4e-39; Matches 100; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCES: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794 REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
IYPE: amino acids
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Knappik, Achim
                         Best Local Similarity 91.7
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-490-324-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-490-324-14
                                                                                                                                             g
                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
US-09-490-070A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                       셤
                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPSSLSASVGDRVIITCRASQGISSYLAWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 109;
                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: James F. Haley, Jr., Bsq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Pack, Deter
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plucekhun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Janes F. Haley, Jr., Esq.
REGISTATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
NAME: James F. Haley, Jr., Esq.
RECISTATION NUMBER: 27,794
REFERENCE DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INPORMATION:
TELEFAN: (212)596-9000
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS: LENGTH: 109 amino acids TYPE: amino acid modulogy: linear
                                                                                                                                                                                                                                                                                                        88.3%;
                                                                                                                                                                                                                                                                                                    Query Match 88.3
Best Local Similarity 89.9
Matches 98; Conservative
                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                              US-09-025-769B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-025-769B-43
                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
1 DIQMIQSPSSLSASVGDRVIITCRASQGISSYLAWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                  1 DIOMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floor disk

COMPUTER: IBW PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, EEG.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Colin G. Sandercock, Egg. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RESGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGOGTKLEIK 109
                                                                                                                                                                                                    61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                 88.3%; Score 500; DB 4; Length 109; ilarity 89.9%; Pred. No. 1e-38; Conservative 5; Mismatches 4; Indels
DB 3; Length 109;
                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Knappik, Achim
Pack, Peter
Ilag, vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
Score 500; DB 3;
Pred. No. 1e-38;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                     US-09-490-070A-28; Sequence 28, Application US/09490070A; Sequence 28, Application US/09490070A; Patent No. 6696248; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 912-2020 INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
Query Match
Best Local Similarity 89.9%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 98; Conserv
```

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIOMIQSPSSLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIOMIOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                           Ge, Lining
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esg. c/o Heller Ehrman
Minte & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHYTTPP--TFGQGTKVEIK 107
61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHYTTPP--TFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.3%; Score 500; DB 4; Length 109; 89.9%; Pred. No. 1e-38; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/490,070A

PRIOR APPLICATION NUMBER: US/09/490,070A

PRIOR APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
NAME: COLIN G. SANGETCOCK, ESQ.

REFERENCE/DOCKET NUMBER: 37629-0005

TELEPHONE: (202) 912-2020

TELEPHONE: (202) 912-2020

TELEPHONE: SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; sequence description: SEQ ID NO: 43: US-09-490-070A-43
                                                                                                   Sequence 43, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/09490153
Patent No. 6706494
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.3
Best Local Similarity 89.9
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                            RESULT 13
US-09-490-070A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-490-153-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMIOSPSSLSASVGDRVIITCRASQGISSYLAWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ## Sequence 43, Application US/09490153

## Pacent No. 6766484

## Pacent Pa
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: New YOFK
COUNTER: New YOFK
COMPUTER: New YOFK
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Relase #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
REGISTARTION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
%
                                                                                                                                                                                                                       ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQHYTTPP--TFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.3%; Score 500; DB 4; Length 109; 89.9%; Pred. No. 1e-38; tive 5; Mismatches 4; Indels
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: proteln
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
15-09-490-153-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212)596-9000
TELEPRA: (212)596-9090
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 109 amino acide
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 89.94
Matches 98, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
```

Search completed: November 16, 2005, 22:07:18 Job time : 18.534 secs

Control of the second

US-09-192-854-2 US-09-968-561A-2

Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 100, App Sequence 124, Appl Sequence 32, Appl Sequence 221, Appl Sequence 221, Appl Sequence 128, Appl Sequence 15, Appl Sequence 15, Appl Sequence 16, Appl

Sequence 5, Appli Sequence 8, Appli Sequence 8, Appli Sequence 4, Appli Sequence 7, Appli Sequence 105, Appli Sequence 155, App

US-09-668-744A-2 US-09-668-561A-2 US-010-744-774-1 US-11-115-682-2 US-10-726-332-22 US-10-726-332-22 US-10-916-840-100 US-11-031-485-124 US-09-848-798-43 US-09-848-798-43 US-10-726-332-221 US-10-726-332-221 US-10-726-332-221 US-10-726-332-221 US-10-726-332-221 US-10-726-332-128 US-10-738-353-103 US-10-938-353-103 US-10-938-349-4 US-10-105-687-4 US-10-106-986-105 US-10-106-986-105

Sequence Sequence Sequence Sequence

Sequence

```
US-10-330-613-10
                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
  ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        App
App
Appl
Appl
                                                                                            November 16, 2005, 22:02:09; Search time 66.9228 Seconds (without alignments) 681.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, A
Sequence 214,
Sequence 64, A
Sequence 28, A
Sequence 28, A
Sequence 29,
Sequence 29, A
Sequence 28, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                    US-10-660-357A-10
566
1 DIQMIQSPSSLSASVGDRVI......QSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                PUDITIONER APPLICATIONS AND TO THE COME TO THE COME OF THE COME OF
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-330-613-10
US-10-330-530-10
US-10-660-357-10
US-10-726-332-214
US-10-726-332-18
US-10-726-332-28
US-10-726-332-28
US-10-726-332-29
US-10-726-332-209
US-10-72-155-308
US-10-72-155-308
US-10-72-155-308
US-10-72-155-308
US-10-72-155-308
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     1867879 segs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    protein search, using sw model
                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
117
117
117
117
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0
100.0
100.0
91.9
91.7
91.3
91.3
90.5
90.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111:
112:
113:
114:
116:
119:
119:
120:
                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5566
5566
550
550
551
551
551
551
551
551
551
                                                                                                                                                     Title:
Perfect score:
                                                                       ı
                                                                     OM protein
                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2643978611
                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š.
```

Haak-Frendscho

```
US-10-805-177-64
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
Sequence 10, Application US/10330530
| Publication No. US20030152514A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
| FILE REPERENCE: ABGENIX. 031A
| CURRENT APPLICATION UNMER: US/10/330,530
| FILE REPERIOR: 2002-12-26
| PRIOR PAPLICATION NUMBER: US/10/330,530
| PRIOR PELING DATE: 2001-12-18
| NUMBER OF SEQ ID NOS: 40
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 566; DB 16; Length 109; 100.0%; Pred. No. 2.4e-38; cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-660-357-10

Sequence 10, Application US/10660357

Publication No. US20040115205A1

Publication No. US20040115205A1

APPLICANT: Bar-Eli, Menashe

APPLICANT: Green, Larry L.

TILLE OF INVENTION: ANTIGEN

TITLE OF INVENTION: ANTIGEN

FILE REFERENCE: ABGENIX.030.790

CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT FILING DATE: 2003-09-10

PRIOR FILING DATE: 2002-12-26

NUMBER OF SEQ ID NOS: 40

SEQ ID NO: 40

BENGTHARE: PateSEQ for Windows Version 4.0

LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 566; DB 14;
100.0%; Pred. No. 2.4e-38;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 214, Application US/10726332; Publication No. US20050058649A1
GENERAL INFORMATION: APPLICANT: GPPLICANT: Gregory M. Landes
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-726-332-214
                                                                                                                                                                                                                                                                                                                                                                            US-10-330-530-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-660-357-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
PAPLICANT: Landes, Gregory M.
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Beazabe, Binyam
APPLICANT: Foltz, Jan
APPLICANT: Foltz, Jan
APPLICANT: Greffers, Michael
APPLICANT: Greffers, Michael
APPLICANT: Starling, Gary
APPLICANT: Starling, Gary
APPLICANT: Khramtsov, Nikolia
APPLICANT: Michael
APPLICANT: Michael
APPLICANT: Michael
APPLICANT: Nikolia
APPLICANT: Nik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVIITCRASQSISSYLNWYQQKRGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIOMTOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLQPEDFATYYCROSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPP--TFGQGTKVEIK 107
                                    APPLICANT: Meina Lidang
APPLICANT: Xiao Feng
APPLICANT: Xiao Coni Jia
APPLICANT: Xiao-Chi Jia
APPLICANT: Mark R. Nocerini
TITLE OF INVENTION: ANTHEODIES DIRECTED TO PHOSPHOLIPASE A2
TITLE OF INVENTION: ANTHEODIES THEREOF
FILE REPERENCE: ABGENIX.072A
CURRENT APPLICATION NUMBER: US/10/726,332
CURRENT APPLICATION NUMBER: n/a
FRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 222
SOFTWARE: FARSEOF FOR Windows Version 4.0
SEQ ID NOS: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.9%; Score 520; DB 17; Length 108; Best Local Similarity 93.6%; Pred. No. 1.2e-34; Matches 102; Conservative 4; Mismatches 1; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.9%; Score 520; DB 17; Length 108; 93.6%; Pred. No. 1.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 64, Application US/10805177; Publication No. US20050084449A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 93.63
Matches 102; Conservative
Yen-Wah R. Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-726-332-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo Sapiens
US-10-805-177-64
```

```
Query Match 91.3%;
Best Local Similarity 92.7%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: John S. Babcook
APPLICANT: Jaspal S. Kang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orit Foord
Larry Green
Xiao Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-727-155-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-726-332-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                 පු
                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
  61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7

US-10-726-332-28

Sequence 28, Application US/10726332

Sequence 28, Application US/10726332

Sublication No. US20050058649A1

GENERAL INFORMATION:

APPLICANT: Gray Haak-Frendscho

APPLICANT: Ling Chen

APPLICANT: Mary Haak-Frendscho

APPLICANT: Mary Haak-Frendscho

APPLICANT: Mary Haak-Frendscho

APPLICANT: Mary Haak-Frendscho

APPLICANT: Maro Feng

APPLICANT: Mao Feng

APPLICANT: Mack R. Nocenini

TITLE OF INVENTION: AND USES THEREOF

TITLE OF INVENTION: AND USES THEREOF

CURRENT APPLICATION NUMBER: u/a

CURRENT FILING DATE: 2003-12-02

PRIOR FILING DATE: 2003-12-02

PRIOR FILING DATE: 2003-12-02

NUMBER OF SEQ ID NOS: 222

NUMBER OF SEQ ID NOS: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.7%; Score 519; DB 17; Length 108; Best Local Similarity 93.6%; Pred. No. 1.5e-34; Matches 102; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                            APPLICANT: Yen-Wah R. Lee
APPLICANT: Meina Liang
APPLICANT: Xiao Feng
APPLICANT: Xiao-Chi Jia
APPLICANT: Mark R. Nocerini
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: ABGENIX.072A
CURRENT APPLICATION NUMBER: US/10/726,332
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: n/a
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 222
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                          US-10-726-332-18
. Sequence 18, Application US/10726332
. Publication No. US20050058649A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                 APPLICANT: Gregory M. Landes
APPLICANT: Mary Haak-Frendscho
APPLICANT: Ling Chen
APPLICANT: Yen-Wah R. Lee
APPLICANT: Xiao Peng
APPLICANT: Xiao Peng
APPLICANT: Xiao-Chi Jia
APPLICANT: Mark R. Nocerini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 18
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-726-332-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-10-726-332-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 28
LENGTH: 108
                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPSSLSASVGDRVIITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                       Gaps
                                                     .;
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
7
                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP--ITFGQGTRLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.5%; Score 512; DB 17; Length 107; Best Local Similarity 92.7%; Pred. No. 5.3e-34; Matches 101; Conservative 4; Mismatches 2; Indels 3
  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Raffealla Faggioni
APPLICANT: Raffealla Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Giorgio Senaldi
APPLICANT: Giorgio Senaldi
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: FACTOR AND USES THEREOF
FILE REFREENTS.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FactSEQ for Windows Version 4.0
SEQ ID NO 308
LENGTH: 107
                                                  IndelB
Score 517; DB 17;
Pred. No. 2.1e-34;
5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scott Kläkamp
Mary Haak-Frendscho
Palaniswami Rathanaswami
Craig Pigott
Meina Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 209, Application US/10726332 Publication No. US20050058649A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        US-10-727-155-308
; Sequence 308, Application US/10727155
; Publication No. US20050049402A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gregory M. Landes
APPLICANT: Mary Haak-Frendscho
APPLICANT: Ling Chen
APPLICANT: Yen-Wah R. Lee
APPLICANT: Meina Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rozanne Lee
Kathy Manchulencho
```

```
RESULT 12
US-10-409-814A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-409-814A-4
                                                                                                                                                                                                                                                    LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 108
                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIOMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 DIQMTQSPSSLSASVGDRVTFTCRASQNITNYLMWYQQKPGKAPKLLIYAASSLPRGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RESGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xiao-Chi Jia
APPLICANT: Mark R. Nocerini
TILLE OF INVENTION: ANTHEODIES DIRECTED TO PHOSPHOLIPASE A2
TILLE OF INVENTION: ANTHEODIES THEREOF
TITLE OF INVENTION: AND USES THEREOF
GURRENT APPLICATION NUMBER: US/10/726,332
CURRENT FILLING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: n/a
PRIOR APPLICATION NUMBER: n/a
NUMBER OF SEQ ID NOS: 222
SOFTWARE: FARLSEQ for Windows Version 4.0
SEQ ID NO 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.5%; Score 512; DB 20; Length 238; 89.0%; Pred. No. 1.1e-33; ive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                     Length 108;
                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                   90.5%; Score 512; DB 17;
92.7%; Pred. No. 5.4e-34;
tive 4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 28, Application US/11011485
; Sequence 28, Application US/11011485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MACCAM
; FILE REFERENCE: ABX-PF6
; CURRENT RPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PALENTIN Ver. 3.3
; SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 67, Application US/09791153A; Publication No. US20030103978A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 89.07
                                                                                                                                                                                                                                                                                                                                                                                             Matches 101; Conservative
                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-10-726-332-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-791-153A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-031-485-28
                                                                                                                                                                                                                                                  LENGTH: 108
                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

APPLICANT: Deshpande, Rajendra

```
APPLICANT: BOYLE, William APPLICANT: SUllivan, John TILLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN FILLE REPERENCE: A-6.33A CURRENT APPLICATION NUMBER: US/09/791,153A CURRENT APPLICATION NUMBER: US/09/791,153A PRIOR RILING DATE: 2001-07-17 PRIOR RPPLICATION NUMBER: 09/511,139 PRIOR FILING DATE: 2000-02-23 NUMBER OF SEQ ID NOS: 154 SOFTWARE: Patentin version 3.0 SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMIQSPSSLSASVGDRVIITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMIQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10409814A
Publication No. US2004020295A1
GENERAL INFORMATION
APPLICANT: de Wildt, Rudolf
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND SCREENING METHODS
FILE REPERENCE: 9039/2032
CURRENT APPLICATION NUMBER: US/10/409,814A
CURRENT FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPN--TFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLOPEDFATYYCROSYSTPPECSFGOGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP--WTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.3%; Score 511; DB 16; Length 108; Best Local Similarity 92.7%; Pred. No. 6.4e-34; Matches 101; Conservative 4; Mismatches 2; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 511; DB 10; Length 107;
Pred. No. 6.4e-34;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-805-177-20
; Sequence 20, Application US/10805177
; Sequence 20, Application No. US20050084449A1
; GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
APPLICANT: Foltz, Ian
; APPLICANT: Test, Kam Fai
; APPLICANT: Jeffers, Michael
; APPLICANT: Mesri, Mehdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-791-153A-67
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/0968561A
Patent No. US20020164642A1
GENERAL INFORMATION:
APPLICANT: Tomlinson
APPLICANT: Winter, Gregory
ITILE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
APPLICANT: Mezes, Peter
APPLICANT: Mezes, Peter
APPLICANT: Khramtsov, Nikolia
TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
TITLE OF INVENTION: DOMAIN AND MUCIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
FILE REPERENCE: ABXCUR.006A
CURRENT APPLICATION NUMBER: US/10/805,177
CURRENT FILING DATE: 2004-03-19
PRIOR PLILING DATE: 2004-03-19
PRIOR PLILING DATE: 2003-03-19
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQLTQSPSSLSASVGDRVTITCRASQSIYSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIOMIOSPSSISASVGDRVIIITCRASOSISNYLNWYQOKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09192854
; Patent No. US20020068276A1
; GeneRAL INPORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPN--TFGQGTKVEIK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDPATYYCQQSYSTPP--TFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 511; DB 17; Length 108;
Pred. No. 6.4e-34;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 511; DB 9;
Pred. No. 1.4e-33;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.3%;
Best Local Similarity 91.7%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.7
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo Sapiens
US-10-805-177-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-968-561A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-192-854-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-192-854-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYGASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPN--TFGQGTKVEIK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCRQSYSTPPECSFGQGTKLEIK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 511; DB 9; L
Pred. No. 1.4e-33;
4; Mismatches 2;
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9722131.1
FRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
FRIOR PILING DATE: 1997-11-13
FRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1998-10-20
PRIOR PILING DATE: 1998-10-20
PRIOR PILING DATE: 2000-02-24
NUMBER: OF SEQ ID NOS: 350
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 240
TYPE: PATENTING DATE: 1998-10-20
PRIOR FILING DATE: 2000-02-24
NUMBER: OF SEQ ID NOS: 350
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 16, 2005, 23:05:40 Job time : 66.9228 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.3%;
Best Local Similarity 92.7%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-968-561A-2
```

771.310102.192 /2016 (23770)

```
November 16, 2005, 21:35:48; Search time 61.3676 Seconds (without alignments) 674.351 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                    protein search, using sw model
                                                                                                    OM protein -
                                                                                                                                                       Run on:
```

555 1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPLTFGGGTKVEIK 107 2105692 Total number of hits satisfying chosen parameters: 2105692 segs, 386760381 residues Gapop 10.0 , Gapext 0.5 US-10-660-357A-14 **BLOSUM62** Perfect score: Scoring table: Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 seq Minimum DB : Maximum DB :

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* Geneseq 16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp20048;* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Anti-huma Anti-huma Anti-huma Human mAb Anti-huma Anti-huma Murine-ex Human ant Anti-huma Human ant Adc99785 Anti-huma Anti-huma Human mAb Murine-ex Anti-MUC Human Human Human Human Human Human Human Human Description Add05389 / Adf09827 / Adk18843 / Adk18861 / Adk18594 / Adk18594 / Adk18599 / Adk18809 / Adk18800 / Adk1800 / Adk18800 / A Add 25406 F Add 25406 F Add 25906 F Add 2399 F Add 2314 F Add 2312 F Add 2212 F Add 2212 F Add 2590 F Add 18839 F Add 18839 F Add 18839 F Add 18839 F Add 25318 F Add 22318 F Add 22318 F Add 22318 F Add 2590 F Adp22106 Adp03917 SUMMARIES ADK18594 ADK18809 ADP03911 ADL25406 ADP22399 ADP22314 ADK18839 ADK18805 ADP22106 ADP22220 ADP22126 ADP03917 ADP22102 ADF09827 ADK18843 ADP22367 ADP22302 ADL25398 ADP22098 ADC99785 ADK18861 Length DB 107 Query Match 100.0 100.0 100.0 100.0 0.001 Score Š. Result

ant ant ant

ant ant

244444444444	Adk18916 Anti-huma Adk18892 Anti-huma Adk18612 Anti-huma Adk18602 Anti-huma Adk18810 Anti-huma
ADP03918 ADS84418 ADS84418 ADS84476 ADP221350 ADP22134 ADP22134 ADP22138 ADP22138 ADP22138 ADP2346 ADP05393 ADF09831	ADK18916 ADK18892 ADK18612 ADK18602 ADK18810
1100 1100 1100 1100 1100 1100 1100 110	7 7 7 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
000000000000000000000000000000000000000	67.59 67.59 67.59 6.83.79
\(\alpha	541 541 541 541
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 4 1 4 6 4 6

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 14. ADC99785 standard; protein; 107 AA (first entry) lung cancer; human 01-JAN-2004 ADC99785; ADC9978

26-DEC-2002; 2002WO-US041581. WO2003057838-A2 Homo sapiens 17-JUL-2003

28-DEC-2001; 2001US-0346299P WPI; 2003-587113/55. (ABGE-) ABGENIX INC Gudas J;

N-PSDB; ADC99787

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

claim 3, SEQ ID NO 14; 78pp; English

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WCOSH. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUCIS on the pancreatic or condition associated with the articularly cervical pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUCIS monoclonal antibody

ant

Adp22220 | Adp22126 |

N

SXS

8 S

```
100.08; FL
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
              Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-598367/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADF09829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                            107;
                                                                                                                                                                                                                                                                                                                           12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-2003
                                                                                                                                                                                                                                                                                         ADF09827;
                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gudas J;
              Local
                Best Loca
Matches
                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                  ð
                                                                                              g
                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a menoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                                                                       DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-MUC18 antibody light chain variable region protein, SEQ ID No 14.
                                                                                                                                                    1 DIOMIOSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccin
antigen; tumour metastasis; melanoma; metastatic; human; light chain.
                                                                                                                  Gaps
                                                                                                                  o;
                                                                                                                                                                                                                                         RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                              Length 107;
                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                  Indels
                                                                              Score 555; DB 7; 1
Pred. No. 9.2e-35;
Mismatches 0;
              light chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 14; 87pp; English.
                                                                                                                                                                                                                                                                                                                                          ADD05389 standard; protein; 107 AA
                                                                                                                .
                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2001; 2001US-0346460P.
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein of the invention.
                                                                                                                Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-577496/54.
                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metastatic tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADD05391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003057006-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 107
                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gudas J,
                                                                                                                                                                                    н
                                                                                                                                                                                                                                                                                                                                                                           ADD05389;
                                                                              Query Match
                                                                                                  Best Local
```

100.0%; Score 555; DB 7; Length 107;

Query Match

```
ô
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanome or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting or inhibiting tumour metastasis. The method is useful for inhibiting or inhibiting or inhibiting action in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                                                                                      9
                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; light chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                    ö
                                                                                                                                                                                                                                                RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                         RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGTEFILTISSLQPEDFATYYCLQHNSYPLIFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human anti-MUC18 monoclonal antibody light chain #4.
Pred. No. 9.2e-35; 
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 555; DB 7;
100.0%; Pred. No. 9.2e-35;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 14; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF09827 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2002; 2002WO-US041580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK18594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, .such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 107;
                                                                                                                                                                                                                                                    antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-human PDGF-D antibody protein related sequence #87.
                                                                                                                                                                                                           Anti-human PDGF-D antibody protein related sequence #69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 555; DB 7;
100.0%; Pred. No. 9.2e-35;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 267; 255pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK18861 standard; protein; 107 AA
                                                                              ADK18843 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-2003; 2003WO-US000398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JAN-2002; 2002US-00041860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                       WO2003057857-A2
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-2004
                                                                                                                                                                 06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                              17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK18861
                                                                                                                          ADK18843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
ADK18861
ID ADK1.
XX
AC ADK1.
XX
DT 06-M
XX
                                                        ADKING BRANCH BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

```
The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; immunomodulator; cytostatic; gene therapy
antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                       Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human PDGF-D antibody light chain protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 555; DB 7;
Pred. No. 9.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                       Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Scc...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 285; 255pp; English
                                                                                                                                                                                                                                                                                                                                                                                       Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK18594 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                          ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                       06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                           07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                                                                                                                                          Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                  (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 107 AA;
                                                                                                           WO2003057857-A2
                                                                                                                                                                                                                                                                                                                                                                                    Corvalan JRF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                       Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-2003
```

ô

Gaps

ö

9 9

```
monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; light chain variable domain.
               The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188. O 99 arising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCBF4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                  Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ
                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 555; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 9.2e-35;
Matches 107; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RESGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP03911 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-2002; 2002WO-US038550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Handa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-523295/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foltz I,
                                                                                                                                                                                                                                                   Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003048328-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gudas J,
    셤
                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                  The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0 99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                           Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weber R;
                                                                                                                                             factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESGSGSTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                           Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-human PDGF-D antibody protein related sequence #35
                                         Feng X, Yang X, Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 555; DB 7;
100.0%; Pred. No. 9.2e-35;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen F,
                                                                                                                                                                                                                             Disclosure; SEQ ID NO 18; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK18809 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2002; 2002US-00041860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 100.
107; Conservative
                                       Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jia X,
                                                                                                   WPI; 2003-587119/55.
(ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003057857-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corvalan JRF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bezabeh B;
                                                            Bezabeh B;
```

-Н

8

g

61 61

8

ADK18809

RESULT 7

Query Match Best Local S

Matches

```
The invention relates to a novel isolated monoclonal antibody (Mab) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention anhydrates cyrostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal
                                                                                                                                                                                                                                  New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ ID NO 51; 89pp; English
```

New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

WPI; 2003-587119/55.

Disclosure; SEQ ID NO 233; 255pp; English

S

ö

မ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described: (1) a method of freating nephritis; (2) a method of treating nephritis; (3) a method of treating mesangial cell proliferation; and (4) a method of treating mesangial proliferative glomerulonephritis. The antibody has nephrotropic, antinflammatory, dermatological, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds PDGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human
tumour or breast cancer, possibly via gene therapy. The current sequence is that of a muriane-expressed anti-human CA IX monoclonal antibody VL (light chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a
                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monoclonal antibody (mAb) variable region sequence, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antidiabetic; gene therapy; human; monoclonal antibody; mAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of an antibody or its binding fragment that binds platelet derived 
*th factor-DD (PDGF-DD) for preparing a medicament for treating
                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lichenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human mAb 1.17 light chain variable region protein SEQ ID NO:16.
                                                                                                                                                                              ..
0
                                                                                                                                           Length 107;
                                                                                                                                                                                                                                                                                    RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larochelle WJ,
                                                                                                                                                                                ;
                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 9.2e-35;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 16; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keyt B,
                                                                                                                                                                                                                                                                                                                                                                                                             ADL25406 standard; protein; 107 AA
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floege J, Gazit-Bornstein G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-2003; 2003WO-US029414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-2002; 2002US-0411137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                          strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABGENIX INC.
CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-269881/25.
                                                                        transgenic mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADL25405
                                                                                                           Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004024098-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nephritis.
                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL25406;
                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABGE-)
(CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UBe
                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
ADL25406
                                                                                                                                                                                                                                                                                                                                                                                                               88888888
                                                                                                                                                                                                                                             원
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                 8
```

```
The present invention describes a human monoclonal antibody (I) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises: (a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined 5 amino acid sequence (SI, ADP22417) or (S2, ADP22421), and (b) a light chain CDR1 having the two fully defined 11 amino acid esquence (S3, ADP22418) or (S4, ADP22424). Also described: (I) assaying (MI) the level of TNFa in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and TNFa in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ovarian cancer;
                                                                                                                                                                          New recombinant human monoclonal antibody that specifically binds to
Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis; restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antibacterial; antihfalmmatory; antipsoriatic; antirheumatic; eating-disorder; immunoauppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonist; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian calladder cancer; kidney cancer; colon cancer; prostrate cancer; prostrate cancer; prostrate cancer; prostrate cancer; immuno-mediated inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human anti-TNFa antibody light chain variable region SEQ ID NO:305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В,
                                                                                                               ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                    RFSGSGGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                         Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klakamp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babcook JS, Kang JS, Foord O, Green L, Feng X, Klaka
Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML,
Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               septic shock; cachexia; anorexia; multiple sclerosis.
                                                                         Score 555; DB 8;
Pred. No. 9.2e-35;
                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; SEQ ID NO 305; 213pp; English.
the present invention.
                                                                                                                                                                                                                                                                                                                                                                   ADP22399 standard; protein; 107 AA
                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-2003; 2003WO-US038281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-2002; 2002US-0430729P
                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-2004 (first entry)
                                                                     Query Match
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-480601/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC.
exemplification of
                                      Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004050683-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis
                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                          ADP22399;
                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                       셤
                                                                                                                                                                                                                               ò
```

ဖ

```
The Bamples; (2.) a composition compitating the animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (1); and (4) inhibiting (M3) TNPa induced apoptosis in an animal by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (1); and (4) inhibiting (M3) TNPa induced apoptosis by administering the human monoclonal antibody of (1); and interest in an animal by selecting an animal in need of treatment for TNPa induced apoptosis, nephrotropic, antiarterioscalerotic, antiarthritic, antiarterioscalerotic, antiarthritic, antiarterioscalerotic, antiarthritic, antiarterioscalerotic, antiarthritic, antiarteriorotic antiarthritic, reuroprotective, vasotropic and antiapoptosis, nephratropic and antiapoptosis, neoplastic disease such as TNPa antagonist. The antibody (1) is useful in the preparation of medicament for treating TNP induced apoptosis, neoplastic disease such as breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, bladder cancer, only attritis, glomerulonephritis, atherosclerosis, psoriasis, restenciosis, antionmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antibactrial; antiinclamatory; antibocatatic; antiinclamator; eating-disorder; immunomodulator; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonist; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; bladder cancer; lung cancer; glioblastoma; stomach cancer; endometrial cancer; plond astoma; stomach cancer; prostrate cancer; immuno-mediated inflammatory disease; rheumatold arthritis; glomerulonephritis; atherosclerosis; psoriasis; restenosis; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; anorexia; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRIYAASSLQSGVPS 60
  sample; (2) a composition comprising the antibody or its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human anti-TNFa antibody light chain variable region SEQ ID NO:220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 555; DB 8; Length 107; 100.0%; Pred. No. 9.2e-35; ive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLIISSLQPEDFATYYCLQHNSYPLIFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP22314 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-2002; 2002US-0430729P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2003; 2003WO-US038281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004050683-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP22314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
ADP22314
ID ADP22
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
```

```
The present invention describes a human monoclonal antibody (1) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined and acid sequence (S1, ADP22417) or (S2, ADP22421);

c two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);

c the sign and the lavel of TNFa in a patient sample, comprising contacting with (I), and detecting the lavel of binding between the antibody and TNFa in the sample; (2) a composition comprising the antibody or its functional fragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human concolonal antibody of (I); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced apoptosis by administering cartivities, anticreparation of antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eatingmatory as TNFa antibody (I); and antippoptotic activities, and can be used as TNFa antibacterial and antippoptosis, neoplastic disease such as rheumatoid architis, glomerulonephritis, and antipposis, paorians cancer, induced apoptosis, neoplastic diseases such as rheumatoid arthritis, glomerulonephritis, and antippositions and antippositi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                              Tumor Necrosis Factor-alpha, useful for treating neoplastic disease sucl
as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                         New recombinant human monoclonal antibody that specifically binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human anti-TNFa antibody light chain variable region SEQ ID NO:273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human, monoclonal antibody, tumour necrosis factor-alpha, TNFa, anti-TNFa antibody, anabolic, antiarteriosclerotic, antiarthritic, antibacterial; antiinflammatory, antipsoriatic, antirheumatic;
                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
Green L, Feng X, Klakamp S;
                       Liang ML, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 555; DB 8; Length 107;
; Pred. No. 9.2e-35;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                       c C, Liang Mu
Qiaojuan JS;
               Rathanaswami P, Pigott
Faggioni R, Senaldi G, (
                                                                                                                                                                                                                                                                                                     Example 10; SEQ ID NO 220; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
Babcook JS, Kang JS, Foord O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP22367 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 107; Conservative
                                                                                                 WPI; 2004-480601/45.
                                                                                                                       N-PSDB; ADP22313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 107 AA;
                                               Manchulencho K,
                       Haak-Frendscho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP22367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP22367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

neuroprotective; vasotropic, antiapopotic; TNPa antagonist; TNP induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; bladder cancer; lung cancer; glioblastoma; stomach cancer; endometrial cancer; kidney cancer; colon cancer; parcreatic cancer; prostrate cancer; immuno-mediated inflammatory disease; theumatorial arthritis; glomerulonephitis; atheroseclerosis; psoriasis; restenosis; autoimmune disease; crohn's disease; graft-host reaction; septic shock; cachexia, anorexia; multiple sclerosis. eating-disorder; immunomodulator; immunosuppressive; nephrotropic; 02-DEC-2003; 2003WO-US038281. 02-DEC-2002; 2002US-0430729P WPI; 2004-480601/45. (ABGE-) ABGENIX INC. WO2004050683-A2 Homo sapiens. 17-JUN-2004.

Α, Klakamp S; g ML, Lee F Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakar Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS; New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid

Example 10; SEQ ID NO 273; 213pp; English.

The present live interaction describes a numan monocloust and the present live interactions and monocloust and the present live interactions and monocloust and the present live interactions and monocloust and the following the two fully defined 1 amino acid sequence (81, ADP2241); and (b) a light chain CDR1 having the two fully defined 11 amino acid cand (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (83, ADP22418) or (84, ADP22424). Also described: (1) assaying (MI) the level of TYRE in a patient sample, comparising contacting with (1), and detecting the level of binding between the antibody and TYRE in the sample; (2) a composition comprising the antibody or its functional fragment and a carrier; (3) treating (M2) an animal suffering the human composition comprising the antibody or (1), and detecting the level of treatment for the disease by administering the human monoclonal antibody of (1); and (4) inhibiting (M3) TYRE induced apoptosis by administering the human monoclonal antibody of (1). (1) has anabolic, antiarteriosclerotic, antiarthritic, antibody of (1). (1) has anabolic, antiarteriosclerotic, antiarthritic, antibody of disease such as TYRE antagonist. The antibody (1) is useful in the preparation of medicament for treating TYRE induced apoptosis, neoplastic disease such as a TYRE antagonist. The antibody (1) is useful in the preparation of medicament for treating TYRE induced apoptosis, neoplastic disease such as theumatoid arthritis, glomerulonephritis, atthemetic cancer, ovarian cancer, bladder cancer, colon cancer, colon cancer, colon cancer, cancer, breast cancer, cancer, such as theumatoid arthritis, glomerulonephritis, and disease such as theumatoid arthritis, glomerulonephritis, and disease, graft-host reactions, septic shock, cachexia, anorexia, and cantibody light chain variable region, which is used in the expension of the present invention. present invention describes a human monoclonal antibody (I) that

Sequence 107 AA;

ö Gaps ; 0 Query Match 100.0%; Score 555; DB 8; Length 107; Best Local Similarity 100.0%; Pred. No. 9.2e-35; Matches 107; Conservative 0; Mismatches 0; Indels 0

human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antibacterial; antibacterial; antibacterial; antibacterial; antibacterial; antibacterial; antibacteriosclesio; nephrotropic; neuroprotective; immunoamodulator; immunosuppressive; nephrotropic; TNF antagonist; ander cancer; blung cancer; globlastoma; stomach cancer; ovarian cancer; prostrate cancer; immuno-mediated inflammatory disease; prostrate cancer; immuno-mediated inflammatory disease; prostratic cancer; immuno-mediated inflammatory disease; restenosis; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; anorexia; multiple sclerosis. Human anti-TNFa antibody light chain variable region SEQ ID NO:208 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107 61 RPSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107 ADP22302 standard; protein; 107 AA (first entry) 09-SEP-2004 ADP22302; ADP22302 셤 셤 ð

Homo sapiens.

WO2004050683-A2

17-JUN-2004

02-DEC-2003; 2003WO-US038281.

02-DEC-2002; 2002US-0430729P.

(ABGE-) ABGENIX INC.

Klakamp S; Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakam Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS; Babcook JS, Kang Haak-Frendscho M,

WPI; 2004-480601/45. N-PSDB; ADP22301.

New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid arthritis.

Example 10; SEQ ID NO 208; 213pp; English.

The present invention describes a human monoclonal antibody (I) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises: (a) a heavy chain complementarity determining region I (CDRI) having the two fully defined 5 amino acid sequence (SI, ADP22417) or (S2, ADP22421); and (b) a light chain CDRI having the two fully defined 11 amino acid sequence (SI, ADP22418) or (S4, ADP22424). Also described: (I) assaying (MI) the level of TNPa in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and TNPa in the sample; (2) a composition comprising the antibody and TNPa in coplastic, or an immuno-mediated inflammatory disease by selecting an enoplastic, or an immuno-mediated inflammatory disease by selecting an enoplastic, or an immuno-mediated inflammatory disease by selecting an enoplastic or an immuno-mediated inflammatory disease by selecting an enoplastic antianal by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) TNPR induced apoptosis by administering the human monoclonal antibody of (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,

ω

```
disorders, immunomodulator, immunosuppressive, nephrotropic, neuroprotective, vasotropic and antiapoptotic activities, and can be used as a TWB antagoomist. The antiabody (1) is useful in the preparation of medicament for treating TWP induced apoptosis, neoplastic disease such as breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, pancreatic cancer, andometrial cancer, kidney cancer, colon cancer, pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory diseases such as rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, canchexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human anti-TNFa antibody light chain variable region SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Score 555; DB 8;
Pred. No. 9.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP22098 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADP22098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP22098
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

```
human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antibacterial; antiinflammatory; antiportatic; antiarthmatic; eating-disorder; immunomodulator; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonist; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; bladder cancer; ung cancer; glioblastoma; stomach cancer; endometrial cancer; timmuno-mediated inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis; restenosis; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; anorexia; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
PART OF STATE OF STAT
```

```
Feng X, Klakamp
                                                                                                                                                                                                                         Liang ML,
                                                                                                                                                                                                                     Haak-Frendscho M, Rathanaswami P, Pigott
Manchulencho K, Faggioni R, Senaldi G, C
                                                                                                                                                                                                    Green L,
                                                                                                                                                                                                    Foord O,
                                                                              02-DEC-2003; 2003WO-US038281.
                                                                                                                    02-DEC-2002; 2002US-0430729P.
                                                                                                                                                                                                    Babcook JS, Kang JS,
Haak-Frendscho M, Rati
                                                                                                                                                            (ABGE-) ABGENIX INC.
WO2004050683-A2.
                                      17-JUN-2004.
```

New recombinant human monoclonal antibody that specifically binds to

2004-480601/45.

N-PSDB; ADP22097.

Qiaojuan JS;

The present invention describes a human monoclonal antibody (I) that specifically binds to tumour necrosis factor-alpha (TNPa) and comprises:

(a) a heavy chain complementarity determining region I (CDRI) having the two fully defined 5 amino acid sequence (SI, ADP22417) or (S2, ADP22421);

c two fully defined 5 amino acid sequence (SI, ADP22417) or (S2, ADP22421);

and (b) a light chain CDRI having the two fully defined 11 amino acid sequence (S3, ADP22418) or (S2, ADP224218) or (S2, ADP24 human, monoclonal antibody; tumour necrosis factor-alpha; TNFa; antibody; anabolic; antiarteriosclarcic; antiarthritic; antibacterial; antiinflammatory; antipocriatic; antirheumatic; eating-disorder; immunomodulator; immunosuppressive, nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonist; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; bladder cancer; lung cancer; globlastoma; stomach cancer; ovarian cancer; prostrate cancer; mumon-mediated inflammatory disease; rheumatorial cancer; immuno-mediated inflammatory disease; psortasis; restenosis; autoimmune disease; Crohn's disease; graft-host reaction; 9 9 Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid 1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS diseases such as rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the exemplification of the present invention. **Gaps** Human anti-TNFa antibody light chain variable region SEQ ID NO:28 ö 61 RFSGSGSGTEFTLIISSLQPEDFATYYCLQHNNYPLTFGGGTKVEIK 107 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107 99.5%; Score 552; DB 8; Length 107; 99.1%; Pred. No. 1.6e-34; ive 1; Mismatches 0; Indels Example 10; SEQ ID NO 4; 213pp; English. ADP22122 standard; protein; 107 AA 09-SEP-2004 (first entry) Conservative Local Similarity Sequence 107 AA; Matches 106; arthritis. ADP22122; Query Match RESULT 15 ADP22122 ###X#XDDDDDDDDDDDDDDDDDDDDDXX 엄 ð g à

```
septic shock; cachexia; anorexia; multiple sclerosis.
```

Homo sapiens.

WO2004050683-A2

17-JUN-2004

02-DEC-2003; 2003WO-US038281.

02-DEC-2002; 2002US-0430729P.

(ABGE-) ABGENIX INC

Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S; Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;

WPI; 2004-480601/45. N-PSDB; ADP22121.

New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid

3xample 10; SEQ ID NO 28; 213pp; English.

The present invention describes a human monoclonal antibody (I) that

C specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region I (CDR1) having the

two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);

CC and (b) a light chain CDR1 having the two fully defined 11 amino acid

sequence (S1, ADP22418) or (S4, ADP22424). Also described: (I) assaying

(M1) the level of TNFa in a patient sample, comprising contacting with

(I), and detecting the level of binding between the antibody and TNFa in

the sample; (I) a composition comprising the antibody or its functional

(Eragment and a carrier; (3) are composition comprising the human

CC neoplastic, or an immuno-mediated inflammatory disease by selecting an

animal in need of treatment for the disease by administering the human

monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced

apoptosis in an animal by selecting an animal in need of treatment for

CTNFa induced apoptosis by administering the human monoclonal antibody of

CTNFa induced apoptosis by administering the human monoclonal antibody of

apoptosis in an animal by selecting an animal in need of treatment for

CTNFa induced apoptosis by administering the human monoclonal antibody of

apoptosis in an animal by selecting an animal in need of treatment for

CTNFa induced apoptosis by administering the human monoclonal antibody of

(1). (1) has anabolic, antiartering the human monoclonal antibody

confers, inmunomodulator, immunosuppressive, nephrotropic,

antibacterial, antinflammatory, antipsoriatic, antirtheumatic, antimocolonal antibody

confers, inmunomodulator, immunosuppressive, nephrotropic

as a TNFa antagonist. The antibody (I) is useful in the preparation of

conference oversian cancer, bander cancer, or immuno-mediated inflammatory

conference of the present sequence representes a human anti-TNFa

antibody light chain variable region, which is used in the

conference of the present invention.

Sequence 107 AA;

99.5%; Score 552; DB 8; Length 107; 99.1%; Pred. No. 1.6e-34; ive 1; Mismatches 0; Indels 0; Gaps Query Match Best Local Similarity 99.1' Matches 106; Conservative

8 g ò

RFSGSGSGTEFTLTISSLQPEDPATYYCLQHNSYPLTFGGGTKVEIK 107 61

61

completed: November 16, 2005, 21:51:38 le : 62.3676 secs Search co Job time

THIS PAGE DI ANK (CEPTO)

•:'

```
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 340313
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-J region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-125 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-123 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-J
Ig kappa chain V-I
Ig kappa chain V-I
Ig lambda chain V-I
Ig lambda chain V-I
Ig lambda chain V-I
Ig kappa chain V-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kappa chain V-J
kappa chain V-J
kappa chain V-I
                                                                        November 16, 2005, 21:37:48 ; Search time 12.7849 Seconds (without alignments) 805.260 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                      Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  protein search, using sw model
                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    840335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               868898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B49047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S19674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S40331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340317
                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                               US-10-660-357A-14
555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %
Query
Match Length DB
           Copyright
                                                                                                                                                                                                                                                                                                                                                                          PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing:
                                                                                                                                                                                                                                                                                seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                             Minimum DB Maximum DB
                                                  OM protein
                                                                                                                                                           Sequence:
                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
```

```
Ig kappa chain V r
Ig kappa chain V-J
Ig kappa chain V-I
Ig kappa chain V r
                                                                                                                                                                                                                                                                                                                               Species: Homo sapiens (man)
| Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                           C,Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: 540353
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X72463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translation not shown
                                                                                                                     $30521
$47183
C21056
$11240
A49134
KIHUHU
$38646
                                       $40318
$46371
$36275
K1HUWS
$40350
$46372
               S46376
K1HUBN
                                                                                                                                                                                                                                                                                                                 kappa chain V-J-C region - human
Species: Homo sapiens (man)
```

DIOMIGSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS Gaps .; 0 96.8%; Score 537; DB 2; Length 125; 96.3%; Pred. No. 3.4e-39; ive 1; Mismatches 3; Indels Query Match Best Local Similarity 96.3 Matches 103; Conservative

ö

9

A;Status: preliminary; translation not shown

A;Cross-references: EMBL:X72423; NID:g441314; PIDN:CAA51091.1; PID:g441315 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;32-106/Domain: immunoglobulin homology <IMM>

Length 123; 91.0%; Score 505; DB 2;

ઠે QQ Χİ

gaJ

```
A;Gene: GDB.IGKV1
A;Gene: GDB.136264
A;Gene: Apple: Sp12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappenant disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lance; Superfamily: immunoglobulin V region; immunoglobulin Noregion; immunoglobuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S36262
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Reference number: S36262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R,Goni, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A,Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA)
A,Reference number: A93964; MUID:83273707; PMID:6410398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Residues: 1-108 <GON>
A,Cross-references: UNIPROT:P01610
C,Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated
                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain V-I region (WEA) - human
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig lambda chain V region (clone alpha-TNF-E7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb_1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                              1 DIOMIOSPSSISASVGDRVIITCRASQGIRNDLGWYQOKPGKAPKRLIYAASSLQSGVPS
                                                                                                                               1 DIQMIQSPSSLSASVGDRVTITCRESQGIRNDLGWYQQKPGKAPKLLIYGTSSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNDLIWYQOKPGTAPKRLIYGAISLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQTTSFPLTFGGGTKLEIK 107
                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.5%; Score 497; DB 2; L
90.7%; Pred. No. 7.7e-36;
iive 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.3%; Score 501; DB 1;
ilarity 89.7%; Pred. No. 3.5e-36;
Conservative 6; Mismatches 5;
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
                ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z18842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.73
Matches 97; Conservative
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-107 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Accession: A01876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A01876
                97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :Genetics:
                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                d
                                                                                              ઠે
                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)

C;Species: Homo appiens (man)

C;Species: Homo appiens (man)

C;Date: 03-Feb-1994 #text_change 21-Jan-2000

C;Accession: 536269

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from phage display libraries.

A;Reference number: S36256; MUID:93178448; PMID:7679990

A;Accession: 536269

A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Species: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01867
R;Laure, C;J; Watanabe, S; Hilschmann, N.
Hoppe-Scyler's Z; Physiol. Chem. 354, 1503-1504, 1973
A;Tille: The primary structure of a monoclonal IgM immunoglobulin (macroglobulin Gal), A;Reference number: A01867; MUID:75059122; PMID:4215718
A;Molecule Lype: protein
A;Residues: 1-108 <LAU>
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                    9
                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVTIICRASQGIRNDLTWYQQKPGKAPKELIYAASNLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID:g939915; Superfamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P01599
A;Note: the C region of this chain has the Inv (3) marker
C;Comment: This chain was isolated from a Waldenstrom's macroglobulin.
                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                 77 RFSGSGSGTEFTLTISSLQPEDFATYYCLQYNGYPRTFGQGTKVBIK 123
                                                                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGAGTEFTLTISSLQPEDFATYYCLQQNSYPRSFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.8%; Score 504; DB 1; Length 108; 91.6%; Pred. No. 2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 107;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain V-I region (Gal) - human (tentative sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
    91.6%; Pred. No. 1.8e-36; ive 3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.6%; Score 503; DB 2; 90.7%; Pred. No. 2.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;16-90/Domain: immunoglobulin homology <IMM>;23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GDB:136264; Map position: 2p12-2p12
                                                 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 91.6
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-107 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
```

Gene: GDB:IGKV1

Genetics:

Query Match

ò 셤 ઠે g

ო

```
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047 #sequent, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46377; S3865,
C;Accession: S46377; S3865,
C;Accession: S46377; S3865,
C;Accession: S46377
C;Accession: S46377
C;Accession: S46377
C;Accession: S46377
C;Accession: S46377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 IQMRQSPSSLSASVGDRVTITCRASQGIRNDLGMNQQKPGKAPKLLIYAASSLESGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-114 <BEN>
A;Cross-references: EMBL:Z27178; NID:g415971; PIDN:CAA81702.1; PID:g415972
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;22-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:9441387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: $40349

R;Klain, R.; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3248-3271, 1993

A;Title: Experessed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:9408091; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSGSGSGTDFTLTISSLQPEDFATYYCQFNTYPLTFGGGTKVEIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 FSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 FSGSGFGTDFTLTISSLQPEDFATYYCLQDYSYPLTFGGGTKVVI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 FSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPLTFGGGTKVEI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X72459; NID:9441386; PIDN:CAA51127.1; C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.2%; Score 484; DB 2; Length 12
88.7%; Pred. No. 1.1e-34;
ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                     Ig kappa chain V-J region (T33-17) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 486; DB 2;
Pred. No. 7.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88...
Best Accas 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 91.4 Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V-J region - C.Species: Homo ganiens fman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-125 < KLE>
                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
B49047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: S41809
R;Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zac Eur. J. Immunol. 23, 2868-2875, 1993
A;Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequenc A;Reference number: S41809; MUID:9403986; PMID:8223863
A;Accession: S41809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig lambda chain V region (clone alpha-THY-23) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: 836279
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: 836256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
        9
                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                   g kappa chain V region A30 - human
Species: Homo sapiens (man)
Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
23 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMIQSPSSLSASVGDRVIIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDSVT1TCQASQGIRNDLAWYQQKPGKAPKLLIYAASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X72808; NID:9415383; PIDN:CAA51328.1; PID:9415384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Cross-references: EMBL:Z18831; NID:g33418; PIDN:CAA79283.1; PID:g939911 Subperfeamily: immunoglobulin V region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin homology ife-90/Domain: immunoglobulin homology < NM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                         61 RFSGSGSGTDFTLTISSLQPEDFATYFCQQANSLPPTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTINGLQPEDFATYYCQQLGAYPLTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          introns: 19/1; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.8%; Score 493; DB 2; Length 10
Best Local Similarity 88.8%; Pred. No. 1.7e-35;
Matches 95; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: S36279
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 89.0%; Score 494; DB 2; L. Best Local Similarity 100.0%; Pred. No. 1.5e-35; Matches 95; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <HUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-108 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     α
                                                      셤
                                                                                                                                                             요
                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

ö

Gaps

61

ô

Gaps

ô

Gape

ö

9

```
C;Accession: S19674
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffithe, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunication. Human antibodies from V-gene libraries displayed on pht A;Reference number: S19663; MUID:92085276; PMID:1748994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain V-J region - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C; Accession: $4033 R; Klein, R.; Jaenichen, R.; Zachau, H.G. Eur. J. Immunol. 23, 3248-3271, 1993 A; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region (clone alpha-TEL9) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 DIQMIQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Crose-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-108/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                    A;Cross-references: EMBL:X61642; NID:937860; PIDN:CAA43823.1; PID:91335386 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                   1 DIOMIOSPSSISASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTINSLQPEDFATYYCQQTNSFPLTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSNYPLTFGGGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 108;
                                                                                    Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.6%; Score 475; DB 2;
86.9%; Pred. No. 6.7e-34;
ive 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 86.0%; Pred. No. 5.9e-34;
Matches 92; Conservative 7; Mismatches 8;
                                                                                    , DB 2;
4.8e-34;
                                                                  85.8%; bcc...
86.0%; Pred. No. ....
8; Mismatches
C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                               Best Local Similarity 86.0
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-125 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Residues: 1-108 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S19674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S19674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρ,
A,Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes A,Reference number: A49047; MUID:92387224; PMID:1516616 A,Accession: B49047 A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specificity from phage display libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Journal of Lambda chain V region (clone alpha-CEA4-8A) - human (fragment)

Iglambda chain V region (clone alpha-CEA4-8A) - human (fragment)

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Species: O3-Peb-1994 #text_change 21-Jan-2000

C.Species: O3-Peb-1994 #sequence_revision 03-Peb-1994 #text_change 21-Jan-2000

C.Species: O3-Peb-1994 #sequence_revision 03-Peb-1994 #text_change 21-Jan-2000

ENGO J. 12, 725-734, 1993

A.R.Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, PRTI-1: Human anti-self antibodies with high specificity from phage display libraries A;Reference number: S36266; MUID:93178448; PMID:767990

A.R.Gression: S36264

A.Status: preliminary; nucleic acid sequence not shown

A.Residues: L107 cRIP

A.R.Cross-references: EMBL:218845; NID:933426; PIDN:CAA79297.1; PID:9939919

C.Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 DIQLTQSPSFLSASIGDRVTITCRASQGINSYLAWYQQKPGKAPKLLIYVASTLQSGVPS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                     A.Molecule type: nucleic acid
A.Residues: 1-108 <VIC.
A.Residues: 1-108 <VIC.
A.Residues: 1-108 <VIC.
A.Residues: 1-108 <VIC.
A.Bxperimental source: thymic B lymphocytes
A.Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C.Superfamily: immunoglobulin v region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RPSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 480; DB 2; Length 132;
Pred. No. 2.7e-34;
6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                      Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                            9; Indels
                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 481; DB 2;
89.7%; Pred. No. 1.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: heterotetramer; immunoglobulin F;37-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.5%;
86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: X72444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 86.0.
Best Local 92; Conservative
                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 89.77
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-132 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S40334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
```

RESULT 12

ò g ò 8 ö

Gaps

ö

9 9 ô

Gape

ö

RESULT 13

ద

ò

g

ò

8 8

Search completed: November 16, 2005, 22:04:07 Job time : 12.7849 secs

THIS PADE BY ANK (USPTO)

P01595 home eaplen P01606 home sapien P01602 home sapien P01602 home sapien P01593 home sapien Q96pff home sapien P01612 home sapien P01612 home sapien

O6p1h4 | P01595 | P01606 | P01603 | P01603 | P01602 | P01

Q72473 P01607

mus musculu mus musculu

P01651

ı

OM protein

Run on:

Sequence:

Searched:

0B

Minimum Maximum Database

Result No.

```
1 DIQMIQSPSSLSASVGDRVTIICRASQGIRNDLTWYQQKPGKAPKELIYAASNLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTTTCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                              MEDLINE=75059122; PubMed=4215718;
MEDLINE=75059122; PubMed=4215718;
Laure C.J., Watanabe S., Hilschmann N.;
Macroglobulin Gal.), I. The amino acid sequence of the L-chain of kappa-type, subgroup I.";
HORPE-Expler's Z. Physiol. Chem. 354:1503-1504(1973).
-i. MISCELLANEQUS: The C region of this chain has the INV (3) marker.
-i. MISCELLANEQUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11814 MW; C1AD3CB0F600FF73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 504; DB 1;
Pred. No. 8.6e-44;
                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                               108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             macroglobulin.

PIR, A01867; K1HUGL.

HSSP: PO1607; 1BWW.

GO; GO:0005823; F:antigen binding; NAS.

GO; GO:0006955; P:imwune response; NAS.

InterPro; IPR007110; IG-like.
                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Framework-4
072473
... HUMAN
               KV10 HUMAN
Q6PIH4
KV1C HUMAN
KV1N HUMAN
KV1J HUMAN
KV1J HUMAN
KV1A HUMAN
                                                                                            KV1T HUMAN
KV5Q MOUSE
KV5T MOUSE
KV5R MOUSE
                                                                                   Q96PF6
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1. 2-
SMART: SMO406, IGv. 1.
PROSTTE; PS50815, IG LIKE; 1.
Direct protein sequencing; Immu DOMAIN 24 34 CC DOMAIN 35 49 FP DOMAIN 57 88 FP DOMAIN 57 88 FP DOMAIN 57 88 FP DOMAIN 57 88
                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
05-JUL-2004 (Rel. 44, Last ann
19 Kappa chain V-I region Gal.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 90.8%;
Local Similarity 91.6%;
es 98; Conservative
                                                                                                                                                                                               STANDARD;
       234
236
236
236
236
108
108
108
108
108
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
50
57
89
98
108
108
      NCBI_TaxID=9606;
                                                                                                                                                                                             KV1G_HUMAN
P01599;
      DOMAIN
DISULFID
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                       KV1G HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
       셤
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapien
sapien
sapien
sapien
sapien
sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                     sapien
sapien
sapien
sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                           sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapien
                                                                                                                                                                                                                                                                                                                                                                                                                             sapien
                                                                  November 16, 2005, 21:36:13 ; Search time 59.9908 Seconds (without alignments) 913.348 Million cell updates/sec
                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                       1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo
homo
                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q65zc8
Q96sa9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6gmx0
Q7z3y4
Q65zc9
P04430
Q9u177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P01611
P01600
P80362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P04431
P01598
Q9u181
P04432
Q6pit5
P01608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01601
P01596
P01594
P01605
P01604
P01597
                                                                                                                                                                                                                                                                                                                                                                                                          Q6gmwl
Q6gmx8
Q6pih7
                                                                                                                                                                                                                                                                                                                                                                                         P01599
                                                                                                                                                                                                                                                                                                                                                                                                  P01610
                                                                                                                                                                                                                                                                                                                                                                                                                                              26gmx9
                                                                                                                                                                                       1612378
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                    1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q6PITS
KV1P HUMAN
Q9UL79
                                                                                                                                                                                                                                                                                                                                                                                       KVIG HUMAN
KVIR HUMAN
QGGMWI
QGGMX8
QGPIH7
Q9UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q652C9
KV1V HUMAN
Q9UL77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV1E HUMAN
KV1Q HUMAN
                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV1L HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                            OGGWX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q652C8
Q96SA9
Q6GMX0
Q7Z3Y4
                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                     .. UniProt 03:*
1: uniprot sprot:*
2: uniprot trembl:*
                                                                                                                                                                                                                                                                                                                                                                       ü
                                                                                                   US-10-660-357A-14
555
                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                             438.5
438
438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432.5
430
430
429
428
428
                                                                                                                                                                                                                                                                                                                                                                                                                                                               464.5
461
461
460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456
455
4452
446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437
434
433
                                                                                                               Perfect score:
                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                         504
475
475
469
469
```

ô

Gaps

ö

Length 108,

```
Aypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O6GMX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
Q6GMX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OOC KARARAKKA KARARA KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMIQSPSSLSASVGDRVITITCRASQGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                     Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides X,30 and X33.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-1- MISCELLANEOUS: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated galactose and isolated from a patient with Waldenstrom's macroglobulinemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :
0
61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 501; DB 1; Length 108; Pred. No. 1.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11840 MW; 9249B61F094561BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00406; ĬGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region WEA.
Homo sapiens (Human).
                                                                                                                             108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Framework-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO: 0005576; C:extracellular; NAS.
GO; GO: 0003823; F:antigen binding; NAS.
GO; GO: 0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-V:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=83273707; PubMed=6410398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A01876; K1HUWE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3est Local Similarity
                                                                                                                    KV1R_HUMAN
P01610;
                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q6GMW1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6GMW1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                        KV1R HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                   RESULT 2
                                                                                                                        CORPTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,

A popking R.F., Jozdan H., Moore T., Max S.I., Wang J., Heishe F.,

B piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B brownstein M.J., Usdin T.B., Tochiyuki S., Carrinci P., Prange C.,

R aha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Wokiernan R.J., Malek J.A., Gunarate P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Mything M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 IQMIQSPSSLSASVGDRVIIITCRASQGISNDLGWYQQKRGKAPKLLIYAASSLQSGVPSR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 FSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGTKVEIX 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 236;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 499; DB 2; Length 23
Pred. No. 6.8e-43;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 protein.
236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC073791; AAH73791.1; ...
InterPro; IPR003159; Ig.
InterPro; IPR003109; Ig-like.
InterPro; IPR003597; Ig. cl.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP07554; Cl-set; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 92.5
98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISSUE=Spleen;
```

ö

ന

```
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09UL70
                 RRAPA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

TISSUB-Primary B-Cells;

MEDLINE-2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A trausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A lacchul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.R.,

Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Morley R.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Shevchenko Y., Boutfauf G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rhiting M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 1g; 2.
SMART; SM00409; 1G; 2.
SMART; SM00406; 1G: 1.
SMART; SM00406; 1G-1.
PROSITE; PS50835; 1G LIKE; 2.
PROSITE; PS00290; 1G MHC; UNKNOWN_1.
Hypochaeical protein:
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.6%; Score 475; DB 2;
86.9%; Pred. No. 1.9e-40;
tive 6; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC073764; AAH73764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q6PIH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
            용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
```

```
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeelbry B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jozdan H., Moore T., Max S.I., Wang J., Hasleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan R.J., Malek J.A., Gunsatne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Jones G.J., Marra M.B.,
Jones G.J., Jones G.J., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 RFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSSPPTFGGGTKVEIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 85.0%; Score 472; DB 2; Length 236; 1 Similarity 87.9%; Pred. No. 3.9e-40; 94; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUB-Lung;
Strauberg R.,
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25603 MW; 8BC561106861213F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003599; IG.
InterPro; IPR003109; IG.-Like.
InterPro; IPR003597; Ig_-Cl.
InterPro; IPR003506; Ig_-NHC.
InterPro; IPR003596; Ig_-NHC.
InterPro; IPR003596; Ig_-NHC.
Pfam; Pr00564; Cl-set; I.
SWART; SW00409; IG; 2.
SWART; SW00406; IG; 1.
PR0SITE; PS00290; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC034141; AAH34141.1;
HSSP; P01607; 1AR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 236 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
```

ö

```
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q652C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
Q96SA9
ID Q96SI
AC Q96SI
DT 01-DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
            SERBERE
                                                                                                                                                                                                                                                                                                                                                                                             pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Primary B.-Cells,

RX TISSUE=Primary B.-Cells,

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Romstein M.J., Wickernan K.J., Malek J.A., Gunarathe P.H.,

RA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA "Generation and initial analysis of more than 15,000 full-length human

RI mouse DDNA sequences.",

Ra Dones Nafl. Acad. Sci. N. S.
                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIOMIQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMTOSPSSLSASVGDRVTITCRASOGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107
                                                                                                                                                                                                                                                                                                                             84.5%; Score 469; DB 2; Length 108;
86.0%; Pred. No. 3.3e-40;
Live 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                          108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -.
HSSP; P01607; IBWW.
InterPro; IPR007110; Ig-like.
R InterPro; IPR007110; Ig-like.
R SMART; SM0406; IGv; I.v.
R PROSITE; PSS0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC073763; AAH73763.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig.c1.
InterPro; IPR00360; Ig MHC.
InterPro; IPR00366; Ig WHC.
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 86.0
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGMX9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7

OGGMX9

OD GGMX9

DD OS-JU

         RY REPRESENT SOLVE STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
ö
                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                     23 DIQMIQSPSSLSASVGHRVTITCRASQNVSRWLAWYQQRPEKAPKSLIYATSSLHSGVPS 82
                                                                                                                                                                                                                                                                                                           1 DIQMIQSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                    84.3%; Score 468; DB 2; Length 244; 83.2%; Pred. No. 1.1e-39; ive 10; Mismatches 8; Indels
                                                                                                                                                                                                               DB 2; Length 236;
                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-97362799; PubMed-9219263;
A KONTermann R.E., Wing M.G., Winter G.;
Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
Nat. Biotechnol. 15:629-631(1997).
RUBL; Y13057; CAA73500.1; -.
RUBL; Y13057; CAA73500.1; -.
RUBL; PRO03596; Ig.v.
RICE-Pro: IPRO03596; Ig.v.
R Pfan; PF00047; ig; 2.
SWART; SM00409; IG; 2.
RMART; SM00406; IGv; 2.
RMSCITE; PS50835; IG_LIKE; 2.
                                                                                                                                            Hypothetical protein.
SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96SA9 PRELIMINARY; PRT; 107 AA. 096SA9; Created) (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                  84.5%; Score 469; DB 2;
85.0%; Pred. No. 8e-40;
:ive 5; Mismatches 1
Pfam, PF00047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single-chain Fv (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89; Conservative
                                                                                                                                                                                                                                          Best Local Similarity 85.0
Matches 91, Conservative
```

```
Local Similarity
                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q723Y4
Q723Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7Z3Y4
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Splen;

X MEDLINE-2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

villalon D.K., Wuzny D.M., Soderspren E.J., Lu X., Gibbs R.A.,

A Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIOMIOSPSSLSASVGDRVIIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMIQSPSSLSASVGDRVIIICRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                               XEQUENCE FROM N.A.

MEDLINE=99375893; PubMed=9712075;
Adderson E.E., Shirkhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.E., Shirkhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.E., Shirkhman anti-N-acetylglucosamine/anti-myosin rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes.;
I. J. Immunol. 16:12020-2031(1998).
R. PIR; B49047; B49047.
R. PIR; PH0867; PH0867.
R. PIR; S1977; S1977.
R. PIR; S34083; S34086.
R. PIR; S34086; S34086.
R. PIR; S94086; S34086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                          Homo sapiens (Human).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYS-TLTFGGGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.7%; Score 464.5; DB 2;
88.8%; Pred. No. 9.3e-40;
Niematches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, PO1607, IBWW.
INTERFO; IPR007110; Ig-like.
INTERFO; IPR003596; Ig-v.
SMART, SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26GMXO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OKMD90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
Q6GMX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDE RELEASE DE BORT DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Richards R.L., Feingold E.A., Grouse L.H., Cherge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worden P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.W. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergene B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rahesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 DIQMTQSPSSLSASVGDRVTITCRASQNINNYLNWYQLKFGKAPNLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skeletal Muscle;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 RFSGSGSGTDFTLTISSLRPDDFATYYCQQSYNIPLTFGGGTNVEIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.1%; Score 461; DB 2; Length 236;
85.0%; Pred. No. 5.3e-39;
iive 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BC037775, AH73775.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003596; Ig.w.
Pfam; PF00549; Cl-set; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .l protein.
236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00409; IG; 2.
SMART; SM00409; IGc1; 1.
SMART; SM00406; IGc1; 1.
PROSITE; PS50875; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, C1 01-OCT-2003 (TrEMBLrel. 25, La O1-MAR-2004 (TrEMBLrel. 26, La Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Similarity 85.0%;
91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
```

ô

ø

ઠ

ò

```
133 DIQMTQSPSTLSASIGDRVTITCRASEGIYRWLAWYQQKPGKAPKLLIYKASSLASRAPS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Framework-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 82.2%;
1 Similarity 81.3%;
87; Conservative
                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
49
56
88
97
107
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
35
50
57
89
98
108
108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                              KV1V HUMAN
P04430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                            KV1V_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UL77
                                                                                                                                                                                                                          OC OC OE OF OC OC
                                                                                 요
                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                       'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIOMIOSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 DIQMTQSPSSLSASVGDTVTITCRASQDISNYLAWFQQKRGKAPKSLIYGASSLQSGVQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.9%; Score 460; DB 2; Length 240;
82.2%; Pred. No. 6.8e-39;
tive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.1%; Score 461; DB 2; Length 236;
84.1%; Pred. No. 5.3e-39;
ive 6; Mismatches 11; Indels
                                                                                                                                                                                                                 HSSP; D01834; HRZ.
InterPro; IRR07110; Ig-like.
InterPro; IRR007110; Ig-like.
InterPro; IRR003066; Ig-MrC.
InterPro; IRR003066; Ig-MrC.
InterPro; IRR003566; Ig-MrC.
InterPro; IRR003566; Ig-MrC.
InterPro; IRR003566; Ig-MrC.
InterPro; IRR00356; Ig-MrC.
InterPro; IRR00356; Ig-MrC.
InterPro; IRR00356; Ig-MrC.
InterPro; PS00290; Ig-MrC; Ig-MrC.
Irrorotein.
IRR00310; Ig-MrC; Ig-MrC; Ig-MrC.
Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig-MrC; Ig
                                                                                                                                                       Strausberg R.,
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005332; AAH05332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25569 MW; FDCFD3645F64B373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kontermann R.E., Wing M.G., Winter G.;
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97362799; PubMed=9219263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single-chain Fv (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 84.1
nes 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
Jones S.J., Marra M.A.;
                                                                                                             SEQUENCE FROM N.A.
TISSUE=Skeletal Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0652C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQLIQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIOMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dwulet F.E., O'Connor T.P., Benson M.D.;
"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
Mol. Immunol. 23:73-78(1986).
PIR; A01878; KIHUBN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Amyloid; Direct protein sequencing; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NFTGSGSGTDFILTISSLOPEDFATYYCQOYNSYPYTFGQGTKVQIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                 193 RFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLEIK 239
61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 456; DB 1; Length 108;
Pred. No. 7e-39;
9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11840 MW; CD3FD944FE96FD37 CRC64;
                                                                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
05-UDL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region BAN.
Homo sapiens (Human).
                                                                                                                                                                                                                        ż
```

ô

ઠ

```
ô
                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kratzin H., Yang C., Krusher J.U., Hilschmann N.;

"Preparative separation of the tryptic hydrolysate of a protein by high-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes).";

Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).

-! MISCELLANEOUS: The C region of this chain has the INV (3) marker. PIR, A01877; KIHUWS.

HSSP, P09362; IWTL.
                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                            Young D.C.; Wyosin-reactive autoantibodies in rheumatic carditis and normal
             SEQUENCE FROM N.A. MEDINE-9814934; DOI=10.1006/clin.1998.4531; MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; WUX X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pramework-1.
Complementarity-determining-1.
Framework-2.
                                                                                                                                                                                                                                                                                                                      81.8%; Score 454; DB 2; Length 108;
86.0%; Pred. No. 1.1e-38;
iive 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-2.
Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complementarity-determining-3.
                                                                                                                                                                                                                                                                                      108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                                      Cin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035037; AAD56273.1; -.
PIR; B49047; B49047.
PIR; S34083; S34083.
HSSP; P01607; IBWW.
InterPro; IPR007710; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv.
PROSTIE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region Wes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antrigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81092279; PubMed=6778806;
                                                                                                                                                                                                                                                                                                                                     Local Similarity 86.0 tes 92, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                      NON TER
NON TER
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                              fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
ô
                                                                                                                                                               9
                                                                                                                                                                                    1 DIQMIQSPSSVSASVGDRVIIICRASQDISHWLAWYQQKSGKARKLLIYSASSLENGVPS 60
                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                            0, Оарв
                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLQPEDFATYFCQQAHSVPLTFGGGTTVDIK 107
                                                                                      Query Match 81.4%; Score 452; DB 1; Length 108; Best Local Similarity 83.2%; Pred. No. 1.8e-38; Matches 89; Conservative 8; Mismatches 10; Indels
                                                     11608 MW; 782B14A649A60E45 CRC64;
                   By similarity.
 Framework-4
                                                                                                                                                                                                                                                                                                                           Search completed: November 16, 2005, 22:01:51 Job time : 59.9908 secs
98 1
23
108 1
108 AA;
DOMAIN
DISULFID
NON TER
SEQUENCE
 FFFS
                                                                                                                                                                                                  a
                                                                                                                                                                                                                                        ò
```

TITE PART DI ANN (USPTO)

Sequence Sequence Sequence

Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence 3 Sequence 3 Sequence 3 Sequence 3

9, A

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

н

Perfect score:

. :

Sequence:

Scoring table:

Database

```
1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 108;
                                                                                                                                                                                                                                                      ALIGNMENTS

ALIGNMENTS

US-08-378-939-32

Sequence 32, Application US/08378939

Patent No. 5876561

APPLICANT: CROWE, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER

TITLE OF INVENTION: PRODUCTION OF ANTIBODIES

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:
ADDRESSER: ROTHWELL, FIGG, ERNST & KURZ

STREET: 555 THIRTEENTH ST. N.W.

CITY: WASHINGTON

STATE: D. C.

COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 91.4%; Score 507; DB 2; L
Best Local Similarity 91.6%; Pred. No. 1.5e-40;
Matches 98; Conservative 3; Mismatches 6;
                                                US-09-540-018-1
US-08-378-939-18
US-09-125-098-9
US-09-540-018-9
US-09-540-018-9
US-09-94-373C-3
US-08-437-642B-3
                                                                                                                                                                                                              PCT-US93-07832-3
US-08-871-488A-18
                                                                                                                                                                                   US-09-705-392A-3
US-09-705-398-3
                                                                                                                                                         US-08-146-206C-3
US-09-705-686-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
REIGN APPLICATION DATE:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1608-118
TELECHONICATION INFORMATION:
TELECHONICATION INFORMATION:
TELECHONE: (202) 783-6040
TELECHONE: (202) 783-6031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTER FSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 108 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
US-08-378-939-32
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Appl
Sequence 34, Appl
Sequence 5, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 18, Appli
Sequence 29, Appli
Sequence 3, Appli
Sequence 2, Appli
                                                                                       ; Search time 18.1939 Seconds (without alignments) 439.017 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         555
1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2 6/ptodata/1/iaa/SA_COMB.pep:*
/cgn2 6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2 6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2 6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                       November 16, 2005, 21:41:29
                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                          Patents AA:*
                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                            US-10-660-357A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                          Copyright
                                                                                                                                                                                                                                                                                                                                                                                          Issued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
```

Score

Result No.

9

Gaps

o'

Indels

```
US-08-157-101A-5
                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/09240274

Patent No. 6255455
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REPERENCE: 09596-42UZ
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQLTQSPSSLSASVGDTVTITCRASQGISNNLAWYQQKPGKAPKRLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
61 RFSGSGSGTEFTLIISSLOPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                          61 RFSGSGSGTEFTLTISSLQPEDFATYYCQQDNSYPFTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTEFTLTISSLQPEDFATYYCQQDNSYPFTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 91.4%; Score 507; DB 2; Length 108; 1 Similarity 91.6%; Pred. No. 1.5e-40; 98; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,939

FLING DATE:

CLASSIFICATION DATA:

APPLICATION NUMBER: US 07/952640

FILING DATE:

CLASSIFICATION NUMBER: US 07/952640

FILING DATE: 01-DEC-1992

ATTORNEY AGENT INFORMATION:

NAME: ERNST, BARBARA G

REGISTRATION NUMBER: 1808-118

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 783-6040

TELEPHONE: (202) 783-6040

TELEPHONE: (202) 783-6031

INFORMATION FOR SEQ ID NO: 34:

SEQUIBACE CHARACTERISTICS:
                                                                                                                                                                       Sequence 34, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEMIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 108 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                     US-08-378-939-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-240-274-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-378-939-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
2 ELTQSPSSLSASVGDRVTITCRASQGFRNDLGWYQQKPGKAPKRLIYATSSLQSGVPSRF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                              3 QMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRF
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: KURHARA, TATSUYA
APPLICANT: MATSUKURA, NOBUO
APPLICANT: MATSUKURA, NOBUO
APPLICANT: NISHIHARA, TATSURO
ITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
ITLE OF INVENTION: PLASMIDS THERFOR
NUMBER OF SEQUENCES:
ADDRESSER: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                              ó.
                                                                                                                                                                                                                                                                                                                                      Query Match

90.5%; Score 502; DB 3; Length 107;
Best Local Similarity 91.4%; Pred. No. 4.3e-40;
Matches 96; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSGSGTEFTLTINSLQPEDSATYYCLQHNSFPWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 SGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 9437/204199
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ. 1371
TELEREX: 202-861-3711
TELEREX: 574-627 CUCH
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                              ; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-29
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 29
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08157101A
Patent No. 5808032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS LENGTH: 236 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
```

```
RESULT 7
US-09-490-153-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                       23 DIQMTQSPSAMAASVGDRVTITCRASQGIGNYLVWFQQKPGKVPKRLIYAASSLQSGVPS 82
                                                          Gaps
                                                            ö
                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.1%; Score 489; DB 3; Length 108; 90.7%; Pred. No. 7.38-39; Live 2; Mismatches 8; Indels
                    DB 1; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
APPLICATION NUMBER: EP 95 11 3021.0
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
ATTORNEY/AGENT INFORMATION:
NAME: MAME: MANDENDER: 27,794
ATTORNEY/AGENT INFORMATION:
NAME: MANDER: MANDENDER: 27,794
                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: James F. Haley, Jr., Esq. c/o Fish & Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
APPLICANT: Rnappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Go, Liming
APPLICANT: Go, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE ADDRESS:
                    Score 497; DB 1;
Pred. No. 3e-39;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09025769B
Patent No. 630064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                    89.5%;
ilarity 88.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
Query Match
Best Local Similarity (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                         RESULT 5
US-09-025-769B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-025-769B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                 g
                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
```

```
1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 108;
                                                                               Pack, Peter
Ilag, Vic
Ge, Limino
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
CORRESPONDENCE: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 88.1%; Score 489; DB 4; I Local Similarity 90.7%; Pred. No. 7.3e-39; les 97; Conservative 2; Mismatches 8;
                                                                                                                                                                                                                                                    STREET: 1666 K Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-490-070A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
IS-09-490-070A-14
Sequence 14, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 912-2020 INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 108 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Knappik, Achim
                                                                  APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                       COUNTRY: USA
```

```
RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMTOSPSSLSASVGDRVTITCRASOGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BEAPLE

COMPUTER: BEAPLE

COMPUTER: BAFFILD

COFFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 18-FEB-1998

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
                                                              c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c/o Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RESGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.1%; Score 489; DB 4; Length 108; 90.7%; Pred. No. 7.3e-39; tive 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Back, Peter

Ilag, Vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Ne

STREET: 1251 Avenue of the Americas

CITY: New York
TITLE OF INVENTION: Protein/(Poly)peptide libraries
             CORRESPONDENCE ADDRESS:
ADDRESSE: James F. Haley, Jr., Esq.
STRET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REGISTRATION INDRER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-153-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.7%
....hes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: USA
ZIP: 10021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-490-324-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASOSISNYLNWYQOKPGKAPKLLIYAASSLOSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
CORPOTTER: IN PC Compatible
CORPOTTER: IN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/ABGNT INFORMATION:
NAME: James F. Haley, Jr., ESQ.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 13.5 inch, 1.44 Mb floppy disk SOFFWARE: 13.5 inch (Genericch) CURRENT APPLICATION DATA: 1.40-1992 CLASSIFTCATION: 530 PRIOR APPLICATION DATA: APPLICATION DATA: 15.0 INC. 1992 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: 14.0 INC. 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

88.1%; Score 489; DB 4;
Best Local Similarity 90.7%; Pred. No. 7.3e-39;
Matches 97; Conservative 2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: procein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-324-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 108 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-934-373C-18
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHWARE: WinPatin (Geneticeh)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGBAT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
    ; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 107 amino acids TYPE: Amino Acid
                                                                                                                                     Best Local Similarity 88.8
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-146-206C-18
                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-146-206C-18
                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASOSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                               Score 481; DB 2; Length 107;
Pred. No. 4.1e-38;
3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: 07/115272
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: 07/115272
FILING DATE: 14-JUN-1991
ATPORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INPORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0709P2

TELECOMMUNICATION INFORMATION:

TELEFAX: 650/952-9881

TELEFAX: 650/952-9881

TELEFAX: 650/952-9881

TELEFAX: 650/952-9881

TELEFAX: 670/952-9881

TYPE: Amino Acid

US-07-934-373C-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P0709P2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-1994
TELEFAX: 650/952-981
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                 86.7%;
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-437-642B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                             1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIOMIOSPSSLSASVGDRVIITCRASOSISNYLAWYOOKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08146206C
Fatent No. 6407213
GRNERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta. Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUMTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                 ö
                                                                                                                                                                                                                                                                             61 RFSGSGSGTDFTLTISSLOPEDFATYYCOQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                           61 RESGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
86.7%; Score 481; DB 3; Length 107; 88.8%; Pred. No. 4.1e-38; ive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 86.7%; Score 481; DB 4; Length 107; Best Local Similarity 88.8%; Pred. No. 4.1e-38; Matches 95; Conservative 3; Mismatches 9; Indels
```

```
US-09-705-392A-18
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
APPLICANT: Baughman, Sharon A.
APPLICANT: Shak Steven
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US 60/48,067A
CURRENT FILING DATE: 2000-08-25
PRIOR PILING DATE: 1999-08-27
PRIOR PLING DATE: 1999-08-27
PRIOR PLING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 14
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 481; DB 4; Length 107;
Pred. No. 4.1e-38;
3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 31.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIPICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/146206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,378
REPREMCE/SDOCKT NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: VL consensus sequence US-09-648-067A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                         Sequence 14, Application US/09648067A
Patent No. 6627196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 88.8
Matches 95; Conservative
RESULT 12
US-09-648-067A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-705-686-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
1 DIQMIQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/09705392A
Patent No. 6719971
GENERAL INPORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFILTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVBIK 107
                                                                                                                                                                                                 Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.7%; Score 481; DB 4; Length 107;
88.8%; Pred. No. 4.1e-38;
tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
                                                                                                                                                                                             10 14; Score 481; DB 4; 10 15; Secre 481; DB 4; 16 18; Pred. No. 4.1e-38; Conservative 3; Mismatches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-No. 6719971-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, WendY M.
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18
                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-705-686-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
             INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.84
Matches 95; Conservative
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVITTCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                           APPLICANT: Catter, Paul J.

Presta, Leonard G.

TILLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                              61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.7%; Score 481; DB 4; Length 107
88.8%; Pred. No. 4.1e-38;
tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-No. 6800738-2000
CLASSIFFCATION: CURROWN>
PRIOR APPLICATION NUMBER: 07/116272
APPLICATION NUMBER: 07/115272
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/115272
FILING DATE: 14-UTN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REFERENCE/DOCKET NUMBER: 90709PID2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                           Sequence 18, Application US/09705398
Patent No. 6800738
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-1994
TELEFAX: 650/952-981
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 107 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.8
Matches 95; Conservative
                                                                                                                                                               RESULT 15
US-09-705-398-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-705-398-18
요
                                              ઠે
                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
```

පු

Search completed: November 16, 2005, 22:07:19 Job time : 19:1939 secs

THIS PACE III ANY MOREN

Sequence

0.0001 1000.0 1000.0 89.0

US-10-727-155-273 US-10-727-155-305 US-10-877-73-4-24 US-10-805-177-62 US-10-805-177-115 US-10-805-177-115 US-10-727-155-28 US-10-727-155-28 US-10-727-155-28 US-10-041-860-229 US-10-041-860-229 US-10-041-860-229 US-10-041-860-229 US-10-727-155-224 US-10-893-576-40 US-10-893-576-40 US-10-893-576-40 US-10-893-576-40 US-10-893-576-40 US-10-155-126 US-10-155-126 US-10-10-10-10-1155 US-10-10-1155-126 US-10-10-1155-126 US-10-10-1155-126 US-10-10-1155-126 US-10-10-1155-126 US-10-10-1155-126 US-10-10-1155-126 US-10-10-1155-126 US-10-727-155-256 US-10-727-155-256 US-10-727-155-256 US-10-727-155-256 US-10-727-155-256 US-10-727-155-256 US-10-727-155-256

```
5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

5555

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Ap
Sequence 231, A
Sequence 267, A
Sequence 51, Ap
Sequence 14, Ap
Sequence 16, Ap
Sequence 208, A
                                                                                                                                                        November 16, 2005, 22:02:09; Search time 65.6949 Seconds (without alignments) 681.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14,
Sequence 14,
                                                                                                                                                                                                                                                 US-10-660-357A-14
555
1 DIQMIQSPSSLSASVGDRVT.......CLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_TRW PUB_Pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_TRW PUB_Pep:*
3: /cgn2_6/ptodata/1/pubpaa/NCT_NEW PUB_Pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB_Pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB_Pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB_Pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB_Pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB_Pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB_Pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB_Pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB_Pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB_Pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB_Pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1867879
                     version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-330-613-14

US-10-330-530-14

US-10-041-860-18

US-10-041-860-267

US-10-041-860-285

US-10-041-860-285

US-10-060-357-14

US-10-660-357-14

US-10-660-357-14

US-10-67-383-16

US-10-727-155-208

US-10-727-155-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                   1867879 seqs, 418409474 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                     GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107
107
107
107
107
107
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein
                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
```

Sequence 3 Sequence 3 Sequence 1

ALIGNMENTS

Sequence Sequence Sequence Sequence

```
SEQ ID NO 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIGMIGSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 555; DB 14; Length 107; ilarity 100.0%; Pred. No. 9e-40; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Corvalant, Jose R.F.
APPLICANT: Corvalant, Jose R.F.
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Dng
APPLICANT: Tang, Xiao-Dng
APPLICANT: Gazit, Gadi
APPLICANT: Gezit, Gadi
APPLICANT: Gezebeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX: 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
                                                                 APPLICANT GUIDAS, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERNCE: ADGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 555; DB 14; Length 1
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 18, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; Sequence 14, Application US/10330530; Publication No. US20030152514A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo Sapiens
US-10-330-530-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: homo sapiens
US-10-041-860-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-041-860-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

US-10-041-860-233

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMIQSPSSLSASVGDRVIIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 555; DB 14; Length 107; Best Local Similarity 100.0%; Pred. No. 9e-40; Matches 107; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 233, Application US/10041860
| Publication No US20030157109A1
| GENERAL INFORMATION:
| APPLICANT: Corvalan, Jose R.F.
| APPLICANT: Theng, Xiao-Chi
| APPLICANT: Peng, Xiao-Chi
| APPLICANT: Peng, Xiao-Chi
| APPLICANT: Ang, Xiao-Dong
| APPLICANT: Ang, Xiao-Dong
| APPLICANT: Reagant, Gadit
| APPLICANT: Gazit, Gadit
| APPLICANT: Weber, Richard
| APPLICANT: Bezabeh, Binyam
| TITLE OF INVENTION: THEREOF
| TITLE OF INVENTION: ANGERIX 051A
| CURRENT APLICATION NUMBER: US/10/041,860
| CURRENT FILING DATE: 2002-01-07
| NUMBER OF SEQ ID NOS: 377
| SOFTWARE: FastsEQ for Windows Version 4.0
| SEQ ID NO 233
| LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Squence 267, Application US/10041860

Publication No. US20030157109A1

GENERAL INFORMATION:

APPLICANT: Corvalan, Jose R.F.

APPLICANT: Peng, Xiao-Chi

APPLICANT: Peng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Xiao-Dong

APPLICANT: Reng, Kiao-Dong

APPLICANT: Reng, Kiao-Dong

APPLICANT: Reng, Kiao-Dong

APPLICANT: Meber, Richard

APPLICANT: Weber, Richard

APPLICANT: Weber, Richard

APPLICANT: HEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: ABGENIX.051A

CURRENT APPLICATION NUMBER: US/10/041,860

CURRENT FILING DATE: 2002-01-07

NUMBER OF SEQ ID NOS: 377

SOFTWARE: FREESE FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 555; DB 14; Length
; Pred. No. 9e-40;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 107; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: homo sapiens
US-10-041-860-233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-041-860-267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 107;
                                                        61 RFSGSGSTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Floege, Juergen
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Keyt, Bruce
APPLICANT: LaRochalle, William
APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: WEING ANTI-PDGF-DD ANTIBODIES
TITLE OF INVENTION: WISING ANTI-PDGF-DD ANTIBODIES
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
CURRENT FILING DATE: 2003-09-16
PRIOR FILING DATE: 2003-09-16
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 97
SOFTWARE FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 107
                                                                                                                                                                               Sequence 14, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:

APPLICANT: Bar-Eli, Menashe

APPLICANT: Green, Larry L.

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

FILE REPERENCE: AGGENIX. 030C1

CURRENT APPLICATION NUMBER: US/10/660,357

CURRENT APPLICATION NUMBER: 10/330,580

PRIOR PILING DATE: 2002-12-26

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FestSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 555; DB 16; Best Local Similarity 100.0%; Pred. No. 9e-40; Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 555; DB 16;
100.0%; Pred. No. 9e-40;
Migmatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10665383
Publication No. US20040141969A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Homo Sapiens
US-10-660-357-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: homo sapiens
US-10-665-383-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-10-665-383-16
                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                            <u>۾</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51, Application US/10309762
| Sequence 51, Application US/10309762
| Publication No. US20040018198A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| APPLICANT: Foltz, Ian
| APPLICANT: Handa, Masahisa
| APPLICANT: Handa, Masahisa
| APPLICANT: Handa, Masahisa
| APPLICANT: Gallo, Michael
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
| CURRENT PILLING ANTISON: ANTIBONIC ANTIGEN
| CURRENT PILLING DATE: 2002-12-02
| PRIOR PELICATION NUMBER: 06/337275
| PRIOR PILLING DATE: 2001-12-03
| NUMBER OF SEQ ID NOS: 246
| SEQ ID NO SI
| LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 107;
61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFSGSGSGTEFTLISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 555; DB 15; Lengua. 100.0%; Pred. No. 98-40; Luinmarches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 555; DB 14; Length 1
100.0%; Pred. No. 9e-40;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                   APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                    Sequence 285, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
                                                                                                                                                                                            APPLICANT: Corvalan, Jose R.F.
                                                                                                                                                                                                                    Jia, Xiao-Chi
Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-041-860-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-309-762-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-309-762-51
                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
```

අ

ò 원

Gaps

၀

δ 8

Gaps

ð

```
1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                              DB 17; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RPSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lean
APPLICANT: Rathy Manchulencho
APPLICANT: Rathy Manchulencho
APPLICANT: Raffaella Faggioni
APPLICANT: Qiaojun Jane Su
ITILE OF INVENTION: ANTHEODIES DIRECTED TO TUMOR NECROSIS
ITILE OF INVENTION: ANTHEODIES DIRECTED TO TUMOR NECROSIS
ITILE OF INVENTION: ANTHEODIES DIRECTED TO TUMOR NECROSIS
ITILE OF INVENTION: APACOR AND USES THEREOF
FILE REPERENCE: ABGENIX. 073A
CURRENT PAPLICATION NUMBER: 05/430729
RIOR FILING DATE: 2003-12-02
RIOR FILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FRAELSEQ for Windows Version 4.0
; APPLICANT: Qiaojuan Jane Su

TITLE OF INVENTION: ANTHBODIES DIRECTED TO TUMOR NECROSIS;

TITLE OF INVENTION: ANTHBODIES THEREOF;

FILE REFERENCE: ABGENIX.073A;

CURRENT APPLICATION NUMBER: US/10/727,155

; CURRENT PILING DATE: 2003-12-02;

PRIOR PILING DATE: 2002-12-02;

NUMBER OF SEQ ID NOS: 320;

SOFTWARE: FastSEQ for Windows Version 4.0;

SEQ ID NO 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 555; DB 17; Lengtn ...
100.0%; Pred. No. 9e-40; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 555; DB 17; Best Local Similarity 100.0%; Pred. No. 9e-40; Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 273, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcook
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mary Haak-Frendscho
Palaniswami Rathanaswami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Larry Green
Xiao Feng
Scott Klakamp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-273
                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-10-727-155-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-727-155-273
                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 555; DB 17; Length 107; 100.0%; Pred. No. 9e-40; .ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                        61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rozama Liea
APPLICANT: Rathy Manchulencho
APPLICANT: Raffaella Faggioni
APPLICANT: Raffaella Faggioni
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: PACTOR AND USES THEREOF
FILE REPERENCE: ABGENIX: 073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT PILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 208
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NESULA 1. (18-10-120)

Sequence 220, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcook
APPLICANT: John S. Kang
APPLICANT: Orit Foord
                                                                                                                                                                                         Sequence 208, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcook
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Kiao Feng
                                                                                                                                                                                                                                                                                                                                                                                         Scott Klakamp
Mary Haak-Frendscho
Palaniswami Rathanaswami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mary Haak-Frendscho
Palaniswami Rathanaswami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kathy Manchulencho
Raffaella Faggioni
Giorgio Senaldi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Larry Green
Xiao Feng
Scott Klakamp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craig Pigott
Meina Liang
Rozanne Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craig Pigott
Meina Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rozanne Lee
                                                                                                                                                                   US-10-727-155-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
```

g

ð

g

ò

9

```
APPLICANT: Kang, Jaspal.

APPLICANT: King, Chadwick T.

APPLICANT: Su, Qiaojuan Jane

TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION

TITLE OF INVENTION: MUTANTS OF EPIDERWAL GROWTH FACTOR RECEPTOR AND USES THEREOF

FILE REFERENCE: ABGENIX. 087A2

CURRENT APPLICATION NUMBER: 06/40493,145

PRIOR TILING DATE: 2003-06-27

PRIOR PILING DATE: 2003-106-27

PRIOR FILING DATE: 2003-106-27

PRIOR FILING DATE: 2004-04-15

NUMBER: 05 EQ ID NOS: 144

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 107
                    TION: ANTIBODIES DIRECTED TO THE DELETION RICEPTOR AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 100.0%; Score 555; DB 17; Best Local Similarity 100.0%; Pred. No. 9e-40; Matches 107; Conservative 0; Mismatches 0;
               ATTLE OF INVENTION: ANTIBODIES DIRECTED TO TRITLE OF INVENTION: MUTANTS OF EPIDERMAL GRG FILE REFERENCE: ADGENTY.087.

FILE REPERENCE: ADGENTY.087.

CURRENT APPLICATION NUMBER: US/10/877,773

CURRENT FILING DATE: 2004-06-25

PRIOR FILING DATE: 2003-06-27

PRIOR FILING DATE: 2003-11-26

PRIOR FILING DATE: 2003-11-26

PRIOR FILING DATE: 2003-11-26

PRIOR FILING DATE: 2003-11-36

PRIOR FILING DATE: 2003-11-36

NUMBER OF SEQ ID NOS: 144

SOFTWARE: PESESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 24

LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/10877774 Publication No. US20050059087A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Weber, Richard
APPLICANT: Feng, Xiao
APPLICANT: Foord, Orit
APPLICANT: Green, Larry
APPLICANT: Gudas, Jean
APPLICANT: Keyt, Bruce
APPLICANT: Liu, Ying
APPLICANT: Rathanswami, Palani
     Qiaojuan Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raya, Robert
Yang, Xiao Dong
Corvalan, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foltz, Ian
Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-10-877-773-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Homo sapiens US-10-877-774-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIÓMTÓSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

100.0%; Score 555; DB 17; Length 107;
Best Local Similarity 100.0%; Pred. No. 9e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0
61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulencho
APPLICANT: Raffaella Faggioni
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Giorgio Senaldi
APPLICANT: Giorgio Senaldi
APPLICANT: Oiacjuan Jane Su
TITLE OF INVENTION: FACTOR AND USES THEREOF
FILE REFERENCE: ABGENIX:073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                             ; Sequence 305, Application US/10727155; Publication No. US20050049402A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              Mary Haak-Frendscho
Palaniswami Rathanaswami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/10877773 Publication No. US20050053608A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Weber, Richard
APPLICANT: Feng, Xiao
APPLICANT: Foord, Orit
APPLICANT: Green, Larry
APPLICANT: Grdas, Jean
APPLICANT: Keyt, Bruce
APPLICANT: Liu, Ying
APPLICANT: Liu, Ying
APPLICANT: Rathanaswami, Palani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kang, Jaspal
King, Chadwick T.
Klakamp, Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang, Xiao Dong
Corvalan, Jose
                                                                                                                                                                                                                        APPLICANT: John S. Babcook
APPLICANT: Jaspal S. Kang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foltz, Ian
Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                         Scott Klakamp
                                                                                                                                                                                                                                                                                                                                                                                                                                  Craig Pigott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raya, Robert
                                                                                                                                                                                                                                                                                                    Larry Green
Xiao Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-727-155-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-877-773-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEO ID NO 305
                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
        Query Match
        100.0%;
        Score 555;
        DB 17;
        Length 107;

        Best Local Similarity 100.0%;
        Pred. No. 9e-40;
        Additional Section S
```

Н

```
2005, 21:35:48 ; Search time 61.3676 Seconds (without alignments) 674.351 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                  561
1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                      2105692
 5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                               2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         geneseqp2000s:*geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A_Geneseq_16Dec04:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqp1980s:*
geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   geneseqp20028:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                  US-10-660-357A-18
                                                                                                           November 16,
                                                                                                                                                                                                                                                                                                                                                                                      DB seq ]
                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠.
                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                      Minimum Maximum I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                         Run on:
```

		d			SOUTHERIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	561	100.0	107	7	ADC99789	Adc99789 Anti-huma
2	561	100.0		7	ADD05393	Add05393 Anti-MUC1
m	561	100.0	107	7	ADF09831	Adf09831 Human ant
4	561	100.0	107	7	ADK18842	Adk18842 Anti-huma
S	561	100.0	107	7	ADK18916	Adk18916 Anti-huma
9	561	100.0	107	7	ADK18892	Adk18892 Anti-huma
7	561	100.0	107	7	ADK18612	Adk18612 Anti-huma
œ	561	100.0	107	7	ADK18602	Adk18602 Anti-huma
6	561	100.0		7	ADK18810	Anti
10	561	100.0		7	ADK18844	Adk18844 Anti-huma
11	561	100.0		7	ADK18808	Adk18808 Anti-huma
12	561	100.0	107	7	ADK18807	Adk18807 Anti-huma
13	561	100.0	107	7	ADK18604	Adk18604 Anti-huma
14	561	100.0	107	7	ADP03996	Adp03996 Murine-ex
15	561	100.0	107	æ	ADL25422	Adl25422 Human mAb
16	561	100.0		ω	ADL25426	Ad125426 Human mAb
17	561	100.0		ω	ADL25442	Ad125442 Human mAb
18	561	100.0		ω	AD007289	Ado07289 Human pro
19	561	100.0	107	œ	ADP22368	Adp22368 Human ant
20	561	100.0		ω	ADP22401	Adp22401 Human ant
21	561	100.0	236	Ŋ	ABG77164	Abg77164 Germline
22	561	100.0		æ	ADR28586	Adr28586 Human ant
23	558	99.5	101	7	ADK18841	Adk18841 Anti-huma
24	556	99.1	107	ω	ADP22158	Adp22158 Human ant
25	551	98.2	107	7	ADK18885	Adk18885 Anti-huma

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, ossophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

Claim 3; SEQ ID NO 18; 78pp; English

Adp22110 Human ant Adp22354 Human ant	-	_	_	•		Adk18600 Anti-huma	Adl25418 Human mAb	Adpo7905 Human imm	Adp22154 Human ant	Adp47296 Human pho	Adp03916 Murine-ex	Adp03912 Murine-ex	Adp03908 Murine-ex	Adp03913 Murine-ex	Adk52390 Human ant	Adc99785 Anti-huma	Add05389 Anti-MUC1	Adf09827 Human ant
ADP22110 ADP22354	ABG77160	ADR28582	ADK18840	ADK18879	ADK18806	ADK18600	ADL25418	ADP07905	ADP22154	ADP47296	ADP03916	ADP03912	ADP03908	ADP03913	ADK52390	ADC99785	ADD05389	ADF09827
	9							_	7 8	_	•	7 7	7 7	7 7	2 8	7 7	7 7	7 7
10	236	23	10	20	10	10	10	23	10	10	10	10	10	10	15	10	10	10
97.9	97.9	6.1	7.7	7.76	7.76	7.76	7.76	7.76	37.5	97.3	97.1	97.1	1.76	97.1	9.96	96.4	96.4	96.4
549	5.	54	54	54	54	54	54	54	54	54	54	54	54	54	54	54	54	54
26	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies. Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 18 ADC99789 standard; protein; 107 AA. 26-DEC-2002; 2002WO-US041581. 28-DEC-2001; 2001US-0346299P (first entry) (ABGE-) ABGENIX INC. WPI; 2003-587113/55 lung cancer; human. N-PSDB; ADC99791 WO2003057838-A2. 01-JAN-2004 Homo sapiens 17-JUL-2003. ADC99789; Gudas J; RESULT 1 ADC99789 ô

Gaps

.. 0

Indels

100.0%; Pred. No. 5.9e-35; ive 0; Mismatches 0;

9

1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60

61 RFSGSGSGTEFILTISSLOPEDFATYYCLOHNSYPWTFGQGTKVEIK 107

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS

```
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                        g
                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                        유
                                                                                                             ò
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a menoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-MUC18 antibody light chain variable region protein, SEQ ID No 18.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                ;
0
                                                                                                                                           100.0%; Score 561; DB 7; Length 107; 100.0%; Pred. No. 5.9e-35; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; SEQ ID NO 18; 87pp; English.
light chain protein of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD05393 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2002; 2002WO-US041582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2001; 2001US-0346460P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein of the invention.
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-577496/54.
N-PSDB; ADD05395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gudas J, Bar-Eli M;
                                                                                                                                                                            Best Local Similarity Matches 107; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastatic tumor
                                                                         Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003057006-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD05393;
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
ADD05333
ADD
                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

DB 7; Length 107;

100.0%; Score 561;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated with expression of MC18 tumour antigen. The method involves administering anti-WUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting tumour metastasis. The method carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIOMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIOMIOSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                     cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; light chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises a method for inhibiting cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 107;
RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                          Human anti-MUC18 monoclonal antibody light chain #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 561; DB 7;
100.0%; Pred. No. 5.9e-35;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 18; 83pp; English.
                                                                                             ż
                                                                                            ADF09831 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2002; 2002WO-US041580.
                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2001; 2001US-0346414P.
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-598367/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADF09833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                          WO2003057837-A2
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                             12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                          17-JUL-2003
                                                                                                                            ADF09831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sudas J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                             RESULT 3
                                                                              ADF0983
                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

us-10-660-357a-18.rag

```
Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
ADK18892
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEKZ93 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 561; DB 7; Length 107; 100.0%; Pred. No. 5.9e-35; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPWTFGOGTKVEIK 107
                                                                                                                                                                                                                                                                   antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-human PDGF-D antibody protein related sequence #142.
                                                                                                                                                                                                                          Anti-human PDGF-D antibody protein related sequence #68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 266; 255pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK18916 standard; protein; 107 AA
                                                                                   ADK18842 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-2003; 2003WO-US000398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
Les 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-587119/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                            WO2003057857-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corvalan JRF,
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                              06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK18916
                                                                                                                                 ADK18842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                             $\circ{\circ}{\circ}$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPWTFGOGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 107;
antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; immunomodulator; cytostatic; gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-human PDGF-D antibody protein related sequence #118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 561; DB 7;
100.0%; Pred. No. 5.9e-35;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 340; 255pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK18892 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JAN-2002; 2002US-00041860.
                                                                                                                                                                                                                                                                   06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                                                      07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D6-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                     (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 107 AA;
                                                                                                                                 402003057857-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-2004
```

ö

9 9

Weber R;

Gazit G,

Chen F,

Yang X,

Feng X,

```
The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188 to 99 arrising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                         New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-human PDGF-D antibody light chain protein sequence.
                                                                                                                                                                                                                             Disclosure; SEQ ID NO 316; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADK18612 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-2004 (first entry)
                                        Jia X,
(ABGE-) ABGENIX INC.
                                                                                                     WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107 AA;
                                        Corvalan JRF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                            Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK18612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60 1 DIÓMTÓSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60 Gaps ; 100.0%; Score 561; DB 7; Length 107; 100.0%; Pred. No. 5.9e-35; ive 0; Mismatches 0; Indels (RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPWTFGOGTKVEIK 107 Matches 107; Conservative Similarity

ö

WO2003057857-A2 ADK18612
XX
XX
XX
AC
ADK1
XX
AC
ADK1
XX
ADT
DE
ANT:
CO
BE
ANT:
CO
BI
BE
CO
BE
CO
BI
BE
CO
BE
CO
BI
BE

06-JAN-2003; 2003WO-US000398. 17-JUL-2003

07-JAN-2002; 2002US-00041860.

(ABGE-) ABGENIX INC.

Bezabeh B;

WPI; 2003-587119/55.

Corvalan JRF, Jia X,

Weber R;

Gazit G,

Chen F,

Yang X,

Feng X,

New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.

Disclosure, SEQ ID NO 36, 255pp, English

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
              The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                    DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gazit G, Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                    100.0%; Score 561; DB 7; Length 107; 100.0%; Pred. No. 5.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-human PDGF-D antibody light chain protein sequence.
                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen F,
                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 26; 255pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK18602 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JAN-2003; 2003WO-US000398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                          Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                               Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003057857-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bezabeh B;
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADK1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ****************
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

ഗ

ADK18810 RESULT

ò 셤 ò a

```
The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188. 0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ĎÍQMTGSPSSLSAŠVGDRVTITCRASGGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; immunomodulator; cytostatic; gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indela
                                                                                                                                                                                                                     anti-human PDGF-D antibody protein related sequence #70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human PDGF-D antibody protein related sequence #34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 561; DB 7;
100.0%; Pred. No. 5.9e-35;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 268; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ż
                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK18808 standard; protein; 107
                                                                                                 ADK18844 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                           06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                             WO2003057857-A2
                                                                                                                                                                               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bezabeh B;
                                                                                                                                         ADK18844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK18808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
ADK18808
                                                                              ADK1884
                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BXXXXXB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                ö
                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody that binds to the antibodies are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                               DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMIQSPSSLSASVGDRVTITCRASQCIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 561; DB 7; Length 107; 100.0%; Pred. No. 5.9e-35; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                  61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                           RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                        Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory; immunomodulator; cytostatic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gazit G,
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-human PDGF-D antibody protein related sequence #36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ,
                                        Score 561; DB 7;
Pred. No. 5.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen
                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 234; 255pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang X,
                                                                                                                                                                                                                                                                                                                                               ADK18810 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feng X,
                                     . Match 100.0%;
Local Similarity 100.0%;
Les 107; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JAN-2003; 2003WO-US000398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-587119/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107 AA;
  Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003057857-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corvalan JRF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004
                                                                           Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                       ADK18810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                        Query Match
```

ઠે 셤 8

Weber R;

ö

Gapa

ö

9 9

```
Corvalan JRF, Jia X,
                             Corvalan JRF, Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-587119/55.
         (ABGE-) ABGENIX INC.
                                                            WPI; 2003-587119/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                 Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402003057857-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bezabeh B;
                                      Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK18604;
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                        The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modularing collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188. O 99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                          Weber R;
                                                                                                                                                                                                            New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 561; DB 7; Length 107; 100.0%; Pred. No. 5.9e-35; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; immunomodulator; cytostatic; gene therapy
        antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                          Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-human PDGF-D antibody protein related sequence #33.
                                                                                                                                                          Chen F,
                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 232; 255pp; English
                                                                                                                                                          Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK18807 standard; protein; 107 AA
                                                                                                                                                          Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JAN-2003; 2003WO-US000398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JAN-2002; 2002US-00041860
                                                                                           06-JAN-2003; 2003WO-US000398
                                                                                                                07-JAN-2002; 2002US-00041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                          Jia X,
                                                                                                                                                                                        WPI; 2003-587119/55.
                                                                                                                                     (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003057857-A2.
                                                  WO2003057857-A2
                                                                                                                                                         Corvalan JRF,
                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 107;
                                                                       17-JUL-2003
                                                                                                                                                                     Bezabeh B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK18807;
                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1:
ADK18807
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCBP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weber R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D), useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                      New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RPSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; immunomodulator; cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gazit G,
Gazit G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-human PDGF-D antibody light chain protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen F,
   Chen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 561; DB 7;
100.0%; Pred. No. 5.9e-35;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 231; 255pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang X,
   Yang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK18604 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feng X,
Feng X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36-JAN-2003; 2003WO-US000398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-2002; 2002US-00041860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
les 107; Conservative
```

```
8888888888
                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal cell carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandiar neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; light chain variable domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody secficically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine-expressed anti-human CA IX monoclonal antibody VL protein SEQ 166.
                                 The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when HEX293 cells are transfected with the plasmid pCEPA/Sec-30664188. This sequence corresponds to a protein used in the invention.
                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                     Score 561; DB 7; Length 107; Pred. No. 5.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                        0; Mismatches
Disclosure, SEQ ID NO 28; 255pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 166; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallo M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP03996 standard; protein; 107 AA
                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-DEC-2002; 2002WO-US038550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-2001; 2001US-0337275P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Handa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                        Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-523295/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foltz I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                   Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003048328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gudas J,
                                                                                                                                                                                                                                                                       Query Match
 ઠે
                                                                                                                                                                                                                                                                                                                                                                            유
                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an antibody or its binding fragment that binds platelet derived growth factor-DD (PDGF-DD), where the antibody is useful in preparing a medicament for treating nephritis. Also described:

(1) a method of detecting nephritis; (2) a method of treating nephritis; of treating nephritis; of treating meanigal proliferative glomerulonephritis. The antibody has nephrotropic, antiinflammatory, dermactlogical, immunosuppressive and antidiabetic activities, and can be used in gene therapy. The antibody or its binding fragment, that binds pOGF-DD, can be used in preparing a medicament for treating nephritis and related disorders, e.g., mesangial proliferative glomerulonephritis. The present sequence represents a human
                          sequence
ody VL
                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
cervical intraepithelial squamous and glandular neoplasia, oesophageal tummour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VL (light chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a transgenic mouse strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD; nephritis; mesangial cell proliferation inhibition; mesangial proliferative glomerulonephritis; nephrotropic; antiinflammatory; dermatological; immunosuppressive; antidiabetic; gene therapy; human; monoclonal antibody; mAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of an antibody or its binding fragment that binds platelet derived
growth factor-DD (PDGF-DD) for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lichenstein H;
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human mAb 1.24.1 light chain variable region protein SEQ ID NO:32.
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                         Length 107;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Larochelle WJ,
                                                                                                                                                                                                                                   ;
                                                                                                                                                                                       100.0%; Score 561; DB 7;
100.0%; Pred. No. 5.9e-35;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 32; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keyt B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL25422 standard; protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gazit-Bornstein G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-2003; 2003WO-US029414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-2002; 2002US-0411137P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                   Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABGE-) ABGENIX INC. (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-269881/25.
N-PSDB; ADL25421.
                                                                                                                                                                                                               Local Similarity
                                                                                                                                                Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004024098-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ното варіелв.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floege J,
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL25422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL25422
```

```
monoclonal antibody (mAb) variable region sequence, which is used in the
 SSXS
```

	o morfor present (com) (c	1	1
exemplification of	exemplification of the present invention.		
Sequence 107 AA;			

	. 0
	Gaps
	· ·
Length 107;	Indels
	32;
Score 561; DB	Pred. No. 5.9e-; / Mismatches
lery Match 100.0%;	<pre>Heet Local Similarity 100.0%; Pred. No. 5.9e-35; Matches 107; Conservative 0; Mismatches 0; Indels</pre>

Search completed: November 16, 2005, 21:51:38 Job time : 61.3676 secs 6 6 6 6 6

```
version 5.1.6
- 2005 Compugen Ltd.
GenCore
Copyright (c) 1993
```

OM protein - protein search, using sw model

November 16, 2005, 21:37:48; Search time 12.7849 Seconds (without alignments) 805.260 Million cell updates/sec Run on:

US-10-660-357A-18

1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPWTFGQGTKVEIK 107 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		kappa	kappa	kappa	kappa	kappa c	lambda	Ig lambda chain V	Ig kappa chain V-J	kappa		kappa	lambda			kappa	Ig kappa chain V-J		kappa	kappa	kappa chain	kappa	kappa c	ti-HIV1	kappa c	Ig lambda chain V	Ig kappa chain V r	kappa	ביים ב
	S40353	KIHUWE	S40313	KIHUGL	S40333	S41809	836269	S36262	S40367	840369	S40336	S40335	S36279	S40331	S40334	846377	S40349	S40352	868698	B49047	A49134	KIHUBN	S46371	169017	S40318	836264	S44122	S19674 .	576355
DB	7	Н	~	Н	7	~	~	~	~	N	~	7	7	~	Á	~	~	7	~	~	~	-	~	~	~	N	~	N	c
% Query Match Length	:	108	123	108	125	117	107	107	127	129	124	126	108	123	132	114	125	131	95	108	141	108	117	101	124	107	108	108	107
% Query Match	93.2	92.9	91.1	6.06	88.2	88.1	87.2	87.0	86.5	86.5	85.8	85.6	85.4	84.3	84.3	84.1	83.8	83.6	83.2	83.2	83.2	83.1	82.7	82.5	82.5	82.4	82.4	82.2	201
8	523	521	511	510	495	494	489	488	485	485	481.5	480	479	473	473	472	470	469	467	467	467	466	464	463	463	462	462	461	460 5
Result No.	; ; ; ;	7	٣	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

kappa chain	kappa chain	kappa chain	Ig kappa chain V-J	light chain	kappa chain	kappa chain	• •	Ig kappa chain - h		kappa chain					
21	54	8	9/	72	33	17	æ	Þ	~		_	7	4	10	
83052	84226	S4036	S463	S463	84718	S3400	831998	KIHUH	S5279	S38646	KIHUAL	836277	840317	C2105	840314
ഗ			2 \$463					1 KIHUH					2 S4031		
2	7	7	7	7	N	0	7	-	N	~	-	N		7	~
2	.6 117 2	.6 130 2	.5 117 2	81.5 128 2	81.2 107 2	81.2 108 2	81.1 109 2	80.6 108 1	80.6 129 2	80.6 132 2	80.2 108 1	80.2 108 2	80.2 129 2	79.9 117 2	79.9 122 2
81.9 108 2 S	.6 117 2	8 81.6 130 2	.5 117 2	81.5 128 2	81.2 107 2	81.2 108 2	81.1 109 2	80.6 108 1	80.6 129 2	80.6 132 2	80.2 108 1	80.2 108 2	.2 129 2	79.9 117 2	79.9 122 2

ALIGNMENTS

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 DIQMTQSPSSLSASVGDRVTITCRASQGIGNDLGWYQQKPGKAPKRLIYAASSFQSGVPS 74
                            C'Species: Homo sapiens (man)
C'Accession: 840353
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;File: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
93.2%; Score 523; DB 2; Length 125;
Best Local Similarity 94.4%; Pred. No. 2.1e-37;
Matches 101; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                      A;Accession: S40353
A;Status: preliminary; translation not shown
A;Molecule type: mRND
A;Molecule type: mRND
A;Rosidues: 1-12 - KLEs
A;Cross-references: EMBL:X72463
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heteroteramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>
Ig kappa chain V-J-C region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>Q</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

KIHUWE

Ig kappa chain V-I region (WEA) - human

C;Species: Homo sapiens (man) C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004

wit

A; Molecule type: protein
A; Residues: 1-108 <GON>
A; Cromment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: GDB: 136264
A; Cross-references: GDB: 136264
A; Map position: 2p12-2p12
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp

```
C, Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-117 <HUB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S41809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            840333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:136264
A;Map position: 2012-2012
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
        L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01867
R;Laure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), 3, Reference number: A01867, MUID:75059122; PMID:4215718
A;Rocession: A01867
A;Rocession: A01867
A;Roselues: 1-108 cLAU>
A;Roselues: 1-108 cLAU>
A;Roselues: Le C region of this chain has the Inv (3) marker
C;Comment: This chain was isolated from a Waldenstrom's macroglobulin.
C;Genetics:
A;Gene: GDB:IGKV1
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer F;16-99/Domain: immunoglobulin homology <IVM>F;16-99/Domain: immunoglobulin homology <IVM>F;23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLAWFQQKPGKAPKRLIYDAASLLSGVPS 76
                                                                                                                                                                                                                                                                                                                       1 DIOMTOSPSSLSASVGDRVTITCRASOGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40313
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-1271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X72423; NID:g441314; PIDN:CAA51091.1; PID:g441315 C.Suberfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterottetramer; immunoglobulin Pi32-106/bomain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTEFTLTINSLQPEDFATYYCLQYSSFPWTFGQGTKVEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGSGTEFTLTISSLQPEDFATYYCLQYNGYPRTFGQGTKVEIK 123
                                                                                                                                                               Score 521; DB 1; Length 108;
Pred. No. 2.7e-37;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 511; DB 2; Lengtn 12.
Pred. No. 2.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kappa chain V-I region (Gal) - human (tentative sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.1%;
                                                                                                                                                             92.9%;
91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kappa chain V-J region - human
                                                                                                                                                               Query Match
Best Local Similarity 91.6
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-123 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
Ig kappa chain V region A30 - human C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C; Accession: S41809
Bur. J. Immunol. 23, 2868-2875, 1993
A; Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequence A; Reference number: S41809
A; Reference number: S41809
A; Reterence number: S41809
A; Reterence preparation of the L regions and the repertoire of V(kappa) gene sequence A; Reference number: S41809
A; Reterence Preparation of the L regions and the repertoire of V(kappa) gene sequence A; Reterence Preparation of the L regions and the repertoire of V(kappa) gene sequence A; Reterence Preparation of the L regions and the Reference Preparation of the Refere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNDLIWYQQKPGKAPKELIYAASNLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiDate: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
CiAccession: S40333
Rixlein R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Filte: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-125 <KLE>
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
P;34-108/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Cross-references: EMBL:X72808, NID:9415383; PIDN:CAA51328.1; PID:9415384
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGAGTEFTLTISSLQPEDFATYYCLQQNSYPRSFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RPSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 125;
                                                                                                                                                                                                                   Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.1%; Score 494; DB 2; I
100.0%; Pred. No. 5.5e-35;
                                                                                                                                                                                                       Score 510; DB 1;
Pred. No. 2.3e-36;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 88.2%; Score 495; DB 2; Local Similarity 88.8%; Pred. No. 4.8e-35; ne 95; Conservative 5; Mismatches 7,
C, Keywords: heterotetramer
F,16-90/Domain: immunoglobulin homology <IMM>
F,23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain V-J region - human
                                                                                                                                                                                                             Query Match 90.9%;
Best Local Similarity 92.5%;
Matches 99; Conservative
```

m

```
18 DIÓMTGSPSSLSASVGDRVTITCRASGSISNYLNWYGRKPGKAPKLLIYAASSLQSGVPS 77
                                                                                                         Ig kappa chain V-J-C region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Rixlein, R.; Jaenichen, R.; Zachau, H.G.
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080991; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Speciaes: Homo sapiens (man)
C.Speciaes: Homo sapiens (man)
C.Jate: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C.Accession: $40.36
Extractions 23, 3248-3271, 1993
A.Fitle: Expressed human immunoglobulin chi genes and their hypermutation.
A.Reference number: $40312; MUID:94080991; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C'Species: Homo sapiens (man)
C'Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C'Accession: 540336
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 DIOMTOSPSSLSASVGDRVTITCRASHVISNHLVWFQQKPGKAPKSLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PID:g441427 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 RFSGSGSGTDFTLTISSLOPEDFATYYCQQSYNTPWTFGQGTKVEIK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 86.5%; Score 485; DB 2; Length 129; Best Local Similarity 87.9%; Pred. No. 3.4e-34; Matches 94; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:X72477
C,Superfamily: immunoglobulin v region, immunoglobulin homology
C,Keywords: heterocteramer, immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 86.5%; Score 485; DB 2; L
Local Similarity 88.8%; Pred. No. 3.4e-34;
les 95; Conservative 3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-127 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V-J region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-129 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              840336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S36262
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. Babbo J. 12, 725-734, 199
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ה
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S36269
R;Griffiths, A.D; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. Rs. Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. Ashabo J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MuID:93178448; PMID:7679990
A;Accession: S36269
A;Status: preliminary; nucleic acid sequence not shown
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09
                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                               Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb_1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
                                                                                 1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPSSLSASVGDRVTITCRESQGIRNDLGWYQQKPGKAPKLLIYGTSSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:218838; NID:g33422; PIDN:CAA79290.1; PID:g939915 C. Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGTDFTLTISSLQPEDFATYFCQQANSLPPTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.2%; Score 489; DB 2; Length 107; 88.8%; Pred. No. 1.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig lambda chain V region (clone alpha-TNF-E7) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z18842
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Koywords: heteroterramer; immunoglobulin
F;I6-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-107 <GRI>
  ö
                                                                                                                                                           87.0%; Score 488; DB 2;
89.7%; Pred. No. 1.6e-34;
iive 3; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
Mismatches
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 89.7%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 88.83
Matches 95; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-107 <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S36262
95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Matches
                                                                                                                                                                 ò
                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

ô

Gaps

81

ö

Gaps

ô

g

ò g

ò

```
1 DIQMIQSPSSLSASVGDSVTITTCQASQGIRNDLAWYQQKPGKAPKLLIYAASTLQSGVPS 60
                                                                                                                                                                                                              1 DIOMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S40334
1g Kappa chain - human
C.Species: Homo sapiens (man)
C.Species: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMIOSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CjAccession: S4031
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;32-106/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: 840334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTEFTLTINGLQPEDFATYYCQQLGAYPLTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.3%; Score 473; DB 2; Length 123; Best Local Similarity 88.8%; Pred. No. 3.4e-33; Matches 95; Conservative 2; Mismatches 10; Indels
                                                                                            Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.3%; Score 473; DB 2; Length 13
85.0%; Pred. No. 3.6e-33;
ive 7; Mismatches 9; Indels
                                                                                                                                                     9; Indels
                                                                                     Score 479; DB 2;
Pred. No. 9.3e-34;
5; Mismatches 9;
C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: S40331
A, Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translation not shown
                                                                                     Query Match
Best Local Similarity 86.9%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-132 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-123 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S40334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig lambda chain V region (clone alpha-THY-23) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: 836279
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. A;Title: Human anti-ealf antibodies with high specificity from phage display libraries.
A;Reference number: 836256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 IQMTQSPSSLSASVGDRVTIACRASQGIRSDLSWYQQKPGKAPKLLIFAASTLHSGVPSR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIOMIOSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Species: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                              A;Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PID:g441361 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                         A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: $40335
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S36279
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-108 <GRI>
A; Cross-references: BMBL:Z18831; NID:g33418; PIDN:CAA79283.1; PID:g939911
C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.6%; Score 480; DB 2; Length 126; 85.8%; Pred. No. 8.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 FSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSGSGSGTDFTLTVSSLQPEDFATYFCLQDYSYPYTFGQGTKLEMK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reaidues: 1-126 <KLE>
A;Cross-references: EMBL:X72445
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                   85.8%; Score 481.5; DB 2; Length
88.0%; Pred. No. 6.5e-34;
tive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S40312; MUID: 94080891; PMID: 8258341
A; Accession: S40335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: immunoglobulin V region; immunos.
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                          F;31-105/Domain: immunoglobulin homology <IMM>
                                                                                                                     A;Status: preliminary; translation not shown A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V-J-C region - human C; Species . London .
                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.0
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                        A; Residues: 1-124 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: mRNA
   Immuno].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
```

RESULT 13

ò 셤 ò g

ö

16

ö

9

22 DIQLTQSPSFLSASIGDRVTITCRASQGINSYLAWYQQKPGKAPKLLIYVASTLQSGVPS 81

g & g

Search completed: November 16, 2005, 22:04:08 Job time : 13.7849 secs

TIES PARE BLAIM (USPTO)

Н

```
92.9%;
larity 91.6%;
Conservative
                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct protein seque
Monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
24
35
50
57
89
98
23
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
                                                                                                                                                                                                                         HUMAN
DOMAIN
DOMAIN
DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                         KV1R HUN
P01610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                               KV1R_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Mai
Best Loca
Matches
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapien
sapien
sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapien
                                                                   ; Search time 59.9908 Seconds (without alignments) 913.348 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo
homo
homo
homo
homo
homo
homo
                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGGGTWU
P01599
QGGTXB
Q9u177
QGU177
QGGDIP7
QGGDIP7
QGGDIP7
QGGDIP8
QG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01601
P01597
P80362
                                                                                                                                                                                                              1612378
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                       1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KV1R HUMAN
OGGWW1
KV1G HUMAN
OGGWX8
Q9UL77
Q9UL70
KV1V HUMAN
Q7Z3Y4
Q6PIH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q6GMX9
Q652C8
KV1H HUMAN
Q96SA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KV1B HUMAN
KV1F HUMAN
072473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6GMX0
KV1W HUMAN
Q652C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV1C HUMAN
KV1I HUMAN
                                                                      2005, 21:36:13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6PITS
Q9UL79
KV1L HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
HUMAN
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KV11 HUMAN
KV1E HUMAN
KV1Y HUMAN
                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                        UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                US-10-660-357A-18
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          November 16,
                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464
463
455
455
452
450
450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein
                                                                                                                                     Sequence:
                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                            Database
                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
```

```
ö
             homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3.4-pyruvylated galactose
in Klebsiella polysaccharides K30 and K33 ",
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELANBOUS: This chain was obtained from a monoclonal antibody
against 3.4-pyruvylated galactose and isolated from a patient with
Waldenstrom s macroglobulinemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region WEA.
1g kappa chain V-I region WEA.
Howo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
P04432
P01609
P01609
P01601
P01608
P01608
P01608
P01652
P01650
P01653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Framework-1.
Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pramework-1.

Complementarity-determining-
Pramework-2.

Complementarity-determining-
Rramework-3.

Complementarity-determining-
Pramework-3.

Complementarity-determining-
Pramework-4.

By similarity.

108

By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, PROSS 1 INTEL.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0008955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam, PRO047; ig; 1.
SWART; SW0047; ig; 1.
PROSITE; PSS0835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 521; DB 1;
Pred. No. 9.8e-46;
6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                              108 AA
                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                  KV1K HUMAN
KV1P HUMAN
KV1P HUMAN
KV1A HUMAN
Q96PF6
KV5S MOUSE
KV5S MOUSE
KV5T MOUSE
KV5T MOUSE
                                                                                                                                                                                                                                             KV1T HUMAN
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=83273707; PubMed=6410398;
```

N

```
NON TER
SEQUENCE
                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6GMX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                      KV1G HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6GMX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXX OCC OFF DATA
                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                    A REDLINE=22388257; PubbMed=12477932; DOI=10.1073/pnas.242603899; StraubBerg R.L., Feingold E.A., Grouse L.H., Derge J.G., Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Antochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Antochen M.J., Uddin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J., Brownstein M.J., Uddin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Anilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Ginbs R.A., Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Williand A., Young A.C., Shevchenko Y., Boutfard G.G., Aniting M.M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., A Jones S.J., Marra M.A., Green E.D., Schmutz J., Myers R.M., Butterfield Y.S., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 IQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 IQMTQSPSSLSASVGDRVTITCRASQGISNDLGWYQQKPGKAPKLLIYAASSLQSGVPSR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
              Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073791; AAH73791.1; -
InterPro; IPR001359; Ig.;
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR00356; Ig MHC.
InterPro; IPR00356; Ig MHC.
InterPro; IPR00356; Ig MHC.
InterPro; IPR00356; Ig Juhr.
Efam; PF07654; C1-set; 1.
Ffam; PF07654; C1-set; 1.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 2.
SWART; SW00406; IG; 1.
SWART; SW00406; IG; 1.
SWART; SW00406; IG; 1.
SWART; PF05111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.5%; Score 519; DB 2; Length 236; 94.3%; Pred. No. 3.7e-45; ative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGTKVEIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 236 AA; 25751 MW; SBFE6A087AFAC437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                               236 AA
                                                                                               PRT;
                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 94.3
Matches 100; Conservative
                                                                                             PRELIMINARY;
                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Spleen;
                                                                                                                                                                                                                                                                   TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                             26GMW1;
                                                                                             Q6GMW1
                                                                  RESULT 2
Q6GMW1
                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                        a
ð
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTIICRASQGIRNDLTWYQQKPGKAPKELIYAASNLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                 Laure C.J., Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), I. The amino acid sequence of the L-chain of kappa-type, subgroup I.";
Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
KVIG HUMAN STANDARD; PRT; 108 AA.
P01559;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region Gal.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 510; DB 1; Length 108;
Pred. No. 1.3e-44;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11814 MW; C1AD3CB0F600FF73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SW0047; ig; 1.
SMART; SW00406; IGv; 1.
Direct protein sequencing; Imminoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 65-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Framework-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:000576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                     WEDLINE=75059122; PubMed=4215718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 92.5%;
99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
49
56
88
97
107
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A01867; KIHUGL.
HSSP; P01607; 1BWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
35
50
57
89
98
108
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macroglobulin.
                                                                                                                                                                                                                   NCBI_TaxID=9606;
```

```
108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Fragment)
                                                                                                                                                                                  NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                              09UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
       MEDLINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Nilalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A. Marra M.A.,
Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIOMTOSPSSLSASVGDRVTITCRASOGIRNDLGWYQQKPGKAPKRLIYAASSLOSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 DIOMIQSPSSVSASVGDRVIITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.0%; Score 477; DB 2; Length 23
86.9%; Pred. No. 7.8e-41;
tive 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEOUENCE 236 AA; 25707 MW; 4FCBE14B6559EFC9 CRC64;
                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF07654; C1-6et; 1.
Pfam; PF07654; C1-6et; 1.
SMART; SM00409; IG; 2.
SMART; SM00406; IG; 2.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC073764; AAH73764.1; -. InterPro; IPR003599; Ig. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
Q9UL77
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIOMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMIQSPSSLSASVGDRVIITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%; Score 471; DB 2; Length 108; 86.9%; Pred. No. 1.3e-40; ive 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.6%; Score 469; DB 2; Length 108; 86.0%; Pred. No. 2.2e-40; ive 5; Mismatches 10; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY_2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044; AAD56280.1; -.
PIR; PH0863; PH0863.
                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AR0350373, AAD56273.1; -.
PIR; 849047; B49047.
PIR; S34083; S34083.
HSSP; PO1607; IBWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA; 11738 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01607; 1BWW.
INTERPO; IPR007110; IG-11ke.
INTERPO; IPR003596; IG-v.
SMART; SM00406; IGv; I.
PROSITE; PS50835; IG-LIKE; 1.
                                                                                                                                                                                                                                                                     InterPro; IPR007110; 19-like.
InterPro; IPR003596; 1g.v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 86.9
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
```

```
SMART, SM00406, IGV; 1.
PROSITE; PS00290; IG_IKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC005332; AAH05332.1; ...
HSSP; P01834; 1HBZ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP07654; C1-8et; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6P1H7;
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Skeletal Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT S

OF PIH

OF P
ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQLIQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKRQKRAPKSLIYDASTLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Skeletal Muscle;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                             MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2; Dwulet F.E., O'Connor T.P., Benson M.D.; "Polymorphism in a kappa I primary (AL) amyloid protein (BAN)."; MOI. Immunol. 23:73-78(1986).
PIR; A01878; KHUBN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Hypothesial protein.
Hypothesial (Hyman).
Hypothesial (Craniata; Vertebrata; Euteleostomi;
Hypothesia; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NFTGSGSGTDFILTISSLQPEDFATYYCQQXNSYPYTFGQGTKVQIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct protein sequencing; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 83.1%; Score 466; DB 1; Length 108; 1 Similarity 82.2%; Pred. No. 4.4e-40; 88; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Framework-3.
Complementarity-determining-3.
Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11840 MW; CD3FD944FE96FD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-2004 (Rel. 44, Last annotation update)
19 kappa chain V-I region BAN.
                                                                          108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003996; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS50835; IG LIKE; 1. Amyloid; Direct non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
88
97
107
108
                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                        P04430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07Z3Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7Z3Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko, L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 DIQMIQSPSSLSASVGDTVIITCRASQDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMIOSPSSLSASVGDRVIIICRASQGIRNDLGWYQQXPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDZINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.7%; Score 464; DB 2; Length 236;
85.0%; Pred. No. 1.7e-39;
ive 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypotherical protein.
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```
and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q652C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
Q652C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS 82
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A., Murly D.M., Sodergren E.J., Lu K., Gibbs R.A., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeelby R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIOMIOSPSSLSASVGDRVIIICRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubsberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Schemen C.M., Schnler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.5%; Score 463; DB 2; Length 236; Best Local Similarity 86.9%; Pred. No. 2.1e-39; Matches 93; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                               Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO34141; AAH34141.1; -.
HSSE; P01607; 1AR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             25603 MW; 8BC561106861213F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                  InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PR007654; Cl-set; I.
SWART; SW00400; IG; Z.
SWART; SW00400; IG; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein
                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6GMX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
QGGMX9
     . 8
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DIQMTQSPSSLSASVGHRVTITCRASQNVSRWLAWYQQRPEKAPKSLIYATSSLHSGVPS 82
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Maddan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywalnski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNTYPLTFGGGTKVEIK 129
                                                                                                                                                                                                                                                                                                                                               TISSUE=FILIMELY D=Celle,

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

BMBL; BC073763; AAH73763.1; -.

InterPro; IPR003599; IG.

InterPro; IPR003599; IG.

InterPro; IPR003597; IG.

InterPro; IPR003597; IG.

InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003596; Ig.

R R InterPro; IPR003596; Ig.

R R R InterPro; IPR003596; Ig.

R RART; SM00407; IG.

SMART; SM00407; IG.; 1.

SMART; SM00406; IG.; 1.

SMART; SM00406; IG.; 1.

SMART; SM00406; IG.; 1.

R PROSITE; PS00290; IG. MHC, UNKNOMN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=97362799; PubMed=9219263;

KROITE-mann R.B., Wing M.G., Winter G.;

"Complement recruitment using bispecific diabodies.";

Nat. Biotechnol. 15:629-631(1997).

EMBL; Y13057; CAA73500.1; -.

InterPro; IPR00110; Ig-like.

InterPro; IPR00110; Ig-like.

InterPro; IPR003596; Ig_v.

Fram; PR00047; Ig; 2.

SWART; SM00406; IG; 2.

SWART; SM00406; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26127 MW; 4B1F17868338F2BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 81.1%; Score 455; DB 2; 1 Similarity 83.2%; Pred. No. 1.4e-38; 89; Conservative 5; Mismatches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q652C8;
25-0CT-2004 (TrEWBLrel. 28, Cr
25-0CT-2004 (TrEMBLrel. 28, La
25-0CT-2004 (TrEMBLrel. 28, La
Single-chain FV (Fragment).
Name=BCFV;
                                                                                                                                                                                                                 cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
```

```
Q96SA9;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KV1B HUMAN P01594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVIB_HUMAN
   Q96SA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                    ö
                                                                                       9
                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
PIR; A01868; KIHUHH.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003596; Ig_v.
Pfam; PR0047; ig; 1.
PR00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
3D-etructure; Bence-Jones protein; Direct protein sequencing;
                                                                                                                                    61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                        197 RFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLIFGGGTKLEIK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPWTFGOGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFSGSGSGTDFTLTISSLOPEDFATYXCOONYITPTSFGOGTRVEIK 107
80.9%; Score 454; DB 2; Length 244; 81.3%; Pred. No. 1.9e-38; ive 10; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 452; DB 1; Length 108;
Pred. No. 1.2e-38;
6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11671 MW; 08D3A6160D8D0618 CRC64;
                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                        108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Framework-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; 1F6L; X-ray; L=1-108.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; P:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=71032830; PubMed=4097974;
                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Last seq
25-007-2004 (Rel. 45, Last ann
Ig kappa chain V-I region Hau.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.18;
                 Best Local Similarity 81.39
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [mmunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
56
88
97
107
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local b...
90;
                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                 KVIH HUMAN

ID XVIH HUMAN

YOU 21-JUL.

DI 21-JUL.

DE 19 1-JUL.

DE 19 1-JUL.

OC BUKARIY

OC BUKARIY

RA WATANA

BR PROBLI

CC -!- MI

DR PIR, A

DR PIR, A

RA SOSII

KW INTEFE

DR SWART;

DR SWART;

DR SWART;

RA JONAIN

FT DOMAIN

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                    ò
                                                                                                                                                                  원
```

RESULT 13

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIOMIGSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=72189444; PubMed=5028201; Schiechl H., Hilschmann N.; "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Ig kappa chain V-I region AU.
If howo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                           01-MAR-2004 (TrEMBLrel. 19, Last sequence update)
Anti-streptococcal. 26, Last annotation update)
Anti-streptococcal. 26, Last annotation update)
variable region (Fragment)
Homo sapiens (Human)
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Molecular analysis of polyreactive monoclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X.FAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-77022433; PubMed=1234024;
Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.3%; Score 450.5; DB 2; Length 107; 86.9%; Pred. No. 1.7e-38; ive 2; Mismatches 11; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQFBDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYS-TLTFGGGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Joppe-Seyler's Z. Physiol. Chem. 353:345-370(1972)
    107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                              antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR007110, Ig-like.
InterPro, IPR003596, Ig.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR, B49047; B49047.
PIR, PH0867; PH0867.
PIR, S16840, S16840.
PIR, S31977; S31977.
PIR, S34083; S34083.
PIR, S34086; S34086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01607; 1BWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein Au).";
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search
셤
                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMIQSPSSLSASVGDRVIITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLBSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                  Biophys. Struct. Mech. 1:139-146(1975).

-!- MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain REI.
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
PDB; 1JV5; X-ray; A=1-107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Schwager P., Steigemann W., Schramm H.J.; "The structure determination of the Bence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                              80.2%; Score 450; DB 1; Length 108; llarity 81.3%; Pred. No. 1.9e-38; Conservative 6; Mismatches 14; Indels
                                                                                                                                                                                Pramework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
                                                                                                                                                                                                                   Framework-3.
Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                               11939 MW; E8011187EE6F6FB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUJ-1986 (Rel. 01, Created)
21-JUJ-1986 (Rel. 01, Last sequence update)
21-JUJ-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region EU.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA
                                                                                                                                                                                                                                            By similarity.
                                                                                                                                                                                                                                    Framework-4
                                                                                   PDB; 1JV5; X-ray; A=1-107.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                 Jones protein Au.";
                                                                                                                                                                                                                                                                                                                                                                                                             102
108
108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 87; Conserv
Schwager P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
KV1F HUMAN
ID KV1F HUMAN
                                                                                                                                                                                                                                   DOMAIN
DISULFID
STRAND
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
SEQUENCE
                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                              STRAND
TURN
STRAND
TURN
STRAND
TURN
                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                          STRAND
                                                                                                                                                                                                                                                                                                                                                                           STRAND
HELIX
                                                                                                                                                                                                                                                                                                                                                                                            STRAND
                                                                                                                                                                                  OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                       IGRN
OE DIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
```

```
1 DIQMIQSPSTLSASVGDRVIITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                 MEDLINE=71064027; PubMed=4923144;
Gall W.E., Redeman G.M.;
Gall W.E., Redeman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Blochemistry 9:1188-1316(1970).
- !- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                              Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.7%; Score 447; DB 1; Length 108; 82.2%; Pred. No. 3.9e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-3 Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11788 MW; 9CD294F2F4D88823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0066955; P:immune response; NAS.
InterPro; IPR001310; Ig-like.
InterPro; IPR0013596; Ig-v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rch completed: November 16, 2005, 22:01:52 time : 60.9908 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Framework-3
                                                                                                                                     MEDLINE=71064023; PubMed=5489770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A90562; K1HUEU.
HSSP; P01607; 1BWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                              DISULFIDE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

(المالية المالية المال

Н

```
RESULT 2
US-07-934-373C-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-240-274-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-274-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 29
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29, Appl
118, Appl
118, Appl
118, Appl
118, Appl
118, Appl
11, Appl
12, Appl
13, Appl
14, Appl
15, Appl
16, Appl
17, Appl
18, Appl
18, Appl
11, Appl
18, Appl
19, Appl
11, Appl
19, App
                                                                                                                                                                                                                                                                  (without alignments)
439.017 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                              2005, 21:41:29 ; Search time 18.1939 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 18, sequence 18, sequence 18, sequence 18, sequence 18, sequence 37, sequence 37, sequence 1, A sequence 1, A sequence 9, A sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3,
Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3
Sequence 3
Sequence 3
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-240-274-29
US-07-934-373C-18
US-08-437-6218
US-08-146-206C-18
US-09-705-392A-18
US-09-705-392A-18
US-09-705-398-18
US-09-705-398-18
US-08-705-398-18
US-08-705-398-18
US-08-705-398-18
US-08-374-899-3
US-08-374-899-3
US-08-378-939-34
US-08-859-053-30
US-08-859-053-30
US-08-859-053-30
US-08-859-053-30
US-08-859-053-30
US-08-859-053-30
US-08-859-053-30
US-09-850-018-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-437-642B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-146-206C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US93-07832-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patents AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                    US-10-660-357A-18
561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           November 16,
                                Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2525

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

2520

                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
No.
```

```
ô
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: The D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL TITLE OF INVENTION: The D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF FILE REPERBUCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01.29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
  Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                 Sequence
Sequence
Sequence
                                                                                                                                 Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 522; DB 3; Length 107;
Pred. No. 9.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSGSGTEFTLTINSLQPEDSATYYCLQHNSFPWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 SGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPWTFGOGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; sequence 18, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
US-08-871-488A-18
US-09-025-769B-28
US-09-025-769B-28
US-09-490-070A-38
US-09-490-153-43
US-09-490-153-43
US-09-490-153-43
US-09-490-153-43
US-09-490-153-43
US-09-490-324-43
US-09-490-324-43
US-09-490-324-43
US-09-157-101A-5
US-08-157-101A-5
US-08-157-101A-5
US-08-157-101A-5
US-08-164-2066-17
US-08-146-2066-17
US-08-146-2066-17
US-09-705-686-17
US-09-705-686-17
US-09-705-686-17
US-09-705-686-17
US-09-705-686-17
                                                                                                                                                                                     US-08-378-939-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: anti-Rh(D) chain F01
                                                                                                                                                                                                                                                                           ; Sequence 29, Application US/09240274; Patent No. 6255455; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98; Conservative
  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 98; Conserv
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08146206C

Patent No. 6407213

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Method for Making Humanized Antibodies

TITLE OF INVENTION: Method for Making Humanized Antibodies

CORRESPONDENCES: 26

CORRESPONDENCES: 26

CORRESPONDENCES: ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: Soulh San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 501; DB 3; Length 107; Pred. No. 8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZUCHANTIAN STATE OF THE COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windpatin (Genetech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C FILING DATE: 17-No. 6407213-1993 CLASSIFICATION DATA:
APPLICATION DATA: TO STORY STATE OF THE STATE OF THE STORY STATE OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: 90709P2C1
TELEPHONE: 650/25-1994
TELEPHONE: 650/952-9811
TELEPHONE: 650/952-981
TELEPHONE: 650/952-981
TELEFAX: 650/952-981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P0709P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFRENCE/DOCKET NUMBER: P071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-1994
TELEPHAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.7
Marches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-437-642B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-146-206C-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDFATYXCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 501; DB 2; Length 107;
Pred. No. 8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible COMPUTER: 18M PC compatible COMPUTER: 18M STATION DATA: 18M STATION NUMBER: US/07/934,373C FILING DATE: 21-Aug-1992 CLASSIFICATION 18M STATION NUMBER: PCT/US92/05126 FILING DATE: 15-JUN-1992 PRIOR APPLICATION NUMBER: 07/715272 FILING DATE: 14-JUN-1991 FILING DATE: 14-JUN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-437-642B-18
Sequence 18, Application US/08437642B
Sequence 18, Application US/08437642B
Patent No. 6054297;
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetich, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REGISTRENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.3%;
                  South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.7°
Matches 97; Conservative
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
                                                                                                                            94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-934-373C-18
```

8

```
1 DIOMIOSPSSLSASVGDRVITICRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baughan, Sharon A.
APPLICANT: Baughan, Sharon A.
APPLICANT: Shak Steven
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P17551
CURRENT APPLICATION NUMBER: US/09/648,067A
CURRENT FILING DATE: 2000-08-25
PRIOR FILING DATE: 1999-00-27
PRIOR FILING DATE: 1999-00-27
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 14
LENGTH: 107
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OP INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGSGTDFTLTISSLOPEDFATYYCOOYNSLPWTFGOGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.3%; Score 501; DB 4; Length 107; Best Local Similarity 90.7%; Pred. No. 8e-39; Matches 97; Conservative 3; Mismatches 7; Indels
                                                                                                                                                               DB 4; Length 107;
                                                                                                                                                                                                                 7;
                                                                                                                                                          Query Match
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: VL consensus sequence US-09-648-067A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09648067A
Patent No. 6627196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/09705686 Patent No. 6639055 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                           US-08-146-206C-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-648-067A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-705-686-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ठ
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQXPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIOMIOSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MINPATIN (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

89.3%; Score 501; DB 4;
Best Local Similarity 90.7%; Pred. No. 8e-39;
Matches 97; Conservative 3; Mismatches
                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-No. 6719971-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-705-392A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

ô

Gape ö

7; Indels

9

```
1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                         1 DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGGGTKVEIK 107
                                                                                                                                       61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                               61 RFSGSGSGTDFTLTISSLQPEDFATYXCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.3%; Score 501; DB 5; Length 107; 90.7%; Pred. No. 8e-39; 7; Indels ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                     PCT-US93-07832-18
; Sequence 18, Application PC/TUS9307832
; GENERAL INFORMATION:
    TITLE OF INVENTION: Immunoglobulin Variants
; TITLE OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCENTAIN AFFILTANIAN LANGER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 107 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 90.7 97; Conservative
  97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US93-07832-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-974-899-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
Matches 9
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                     엄
                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVBIK 107
                                                                                                                                                                                                                                                                                           Score 501; DB 4; Length 107;
Pred. No. 8e-39;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.3%; Score 501; DB 4; Length 107; 90.7%; Pred. No. 8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: VS/99/705,398 FILING DATE: 02-NO. 6800738-2000 CLASSIFICATION: cUnknown>
                   REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 01/715272
FILING DATE: 14-UN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
TELECOMMUNICATION INFORMATION:
                                                                         INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18
REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/09705398 Patent No. 6800738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650/225-1994
TELEPA: 650/652-981
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.7%;
Matches 97; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-705-398-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

ò

Gaps

```
Sequence 32, Application US/08378939
Patent No. 5876561
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
ITILE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STRET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
PILING DATE: «UNKNOWN»
FILING DATE: «UNKNOWN»
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                        NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
       SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                      TELEPHONE: 650/225-1994
TELEFAX: 650/522-981
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 108 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 783-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 90.7 Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-378-939-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-795-798-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMIQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 501; DB 3; Length 108;
Pred. No. 8.1e-39;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
Genentech, Inc.
                                                                 APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUECES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-795-798-3
; Sequence 3, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
Sequence 3, Application US/08974899
Patent No. 6037454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60/031971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P10
TELECOMMINICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031:
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: 650/952-981
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.7%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 108 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
```

```
1. DIQMIQSPSSLSASVGDRVIITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLESGVPS 60
                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                            Gaps
                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                       61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSLPWTFGQGTKVEIK 107
Score 501; DB 4; Length 108;
Pred. No. 8.1e-39;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
```

ô

```
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: BOE
STATE: Ma
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-599-226-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQLTQSPSSLSASVGDTVTITCRASQGISNNLAWYQQKPGKAPKRLIYAASSLESGVPS 60
                                                                                                                                                                                                                                   1 DIQLTQSPSSLSASVGDTVTITCRASQGISNNLAWYQQKPGKAPKRLIYAASSLESGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIOMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQOKPGKAPKRLIYAASSLOSGVPS
                                                                                                                                                                                                1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                              61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTEFTLTISSLQPEDFATYYCQQDNSYPFTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFSGSGSGTEFTLTISSLQPEDFATYYCQQDNSYPFTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 500; DB 2; Length 108; Pred. No. 1e-38; 4; Mismatches 6; Indel8
                                                                                                               Score 500; DB 2; Length 108;
Pred. No. 1e-38;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                         US-08-378-939-34
| Sequence 34, Application US/08378939 |
| Sequence 34, Application US/08378939 |
| Patent No. 5876961 |
| Patent No. 5876961 |
| APPLICANT: CROWE, JAMES SCOTT |
| APPLICANT: LEWIS, ALAN PETER |
| TITLE OF INVENTION: PRODUCTION OF ANTIBODIES |
| ORRESPONDENCE ADDRESS: 46 |
| ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: STREET: 555 THIRTEENTH ST. N.W. CITY: WASHINGTON STATE: D. C. COUNTRY: D. C. STATE: D. C. STATE: D. C. STATE: D. C. COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTAATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.1%;
                                                                                                               Query Match
Best Local Similarity 90.7%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 108 amino acids
amino acid
LENGTH: 108 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                TYPE: 'amino acid'
'TOPOLOGY: linear
'MOLECULE TYPE: protein
US-08-378-939-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-378-939-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           පු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                              ò
```

```
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Teauka, Kateunarri
APPLICANT: Teauka, Kateunarri
APPLICANT: Teauka, Kateunarri
APPLICANT: Teauka, Kateunarri
APPLICANT: Hori, No. 6803039uaki
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FLIE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 DIQMTQSPSSVSASVGDRVTITCRASQGISRLLAWYQQKPGKAPKLLIYVASSLQSGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 88.4%; Score 496; DB 4; Length 236; 1 Similarity 89.7%; Pred. No. 5.3e-38; 96; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: Which, Michael
APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allen, Deborah J.
Hoogenboom, Hendricus
Kaymakcalan, Zehra
Sequence 30, Application US/09859053 Patent No. 6803039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Labkovsky, Boris
Mankovich, John A.
McGuinness, Brian T.
Roberts, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DG
SOFTWARE: Patentin Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08599226
Patent No. 6090382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salfeld, Jochen G.
```

```
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DECORDI, GUILLO A., Jr.
REFERENCE/DOCKET NUMBER: BBI-043
TELECHMONICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7401
INFORMATION FOR EGO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

FRAGMENT TYPE: internal
US-08-599-226-1
```

1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60 1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 60 0; Gaps Query Match

86.8%; Score 487; DB 3; Length 107;

Best Local Similarity 88.8%; Pred. No. 1.5e-37;

Matches 95; Conservative 5; Mismatches 7; Indels

ò

Search completed: November 16, 2005, 22:07:19 Job time : 18.1939 secs

THE PACE DLAMK (USPTO)

307, App 52, Appl 6, Appl 265, Appl 265, App 309, Appl 16, Appl 16, Appl 48, Appl 230, App 230, App 230, Appl 260, Appl 260, Appl 260, Appl 270, A

sequence seq

Sequence Seq

us-10-660-357a-18.rapb

```
1 DIQMIQSPSSLSASVGDRVIIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-330-613-18

Sequence 16, Application US/10330613

Publication VOS20030147809A1

Sequence 16, Application US/10330613

Publication VOS20030147809A1

APPLICANT: Gudas, Jean

TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN

FILE REFERENCE: ABGENIX: 022A

CURRENT APPLICATION NUMBER: US/10/330,613

CURRENT PILING DATE: 2002-12-26

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 561; DB 14;
Pred. No. 1.7e-39;
0; Mismatches 0;
US-10-041-860-340
US-10-309-762-166
US-10-665-383-32
US-10-665-383-36
US-10-665-383-52
US-10-727-155-274
US-10-727-155-307
US-10-775-444A-52
                                                                                                                                                                                                           US-10-917-073A-6
US-10-041-860-265
US-10-741-860-309
US-10-727-155-16
US-10-727-155-260
US-10-775-444A-48
US-10-775-444A-48
US-10-041-860-23
US-10-041-860-24
US-10-041-860-23
US-10-041-860-23
US-10-041-860-24
US-10-041-860-24
US-10-041-860-24
US-10-041-860-24
US-10-041-860-24
US-10-041-860-24
US-10-041-860-303
US-10-041-860-303
US-10-041-860-303
US-10-041-860-303
US-10-041-860-303
US-10-041-860-303
US-10-041-860-303
US-10-05-303-28
US-10-05-303-28
US-10-727-155-60
US-10-727-155-60
US-10-727-155-60
US-10-727-155-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-644-277-96
US-10-330-613-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
    TYPE: PRT
ORGANISM: Homo Sapiens
    0.001

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000

1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-330-613-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
    윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18, Appl
26, Appl
26, Appl
36, Appl
231, App
232, App
234, App
266, App
266, App
316, App
                                                                                                                                           November 16, 2005, 22:02:09; Search time 65.6949 Seconds (without alignments) 681.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Sequence 18, Sequence 26, Sequence 26, Sequence 28, Sequence 28,
                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVT......CLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                      5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-330-613-18
US-10-310-530-18
US-10-041-860-26
US-10-041-860-26
US-10-041-860-31
US-10-041-860-231
US-10-041-860-232
US-10-041-860-234
US-10-041-860-266
US-10-041-860-266
US-10-041-860-266
US-10-041-860-266
                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                   1867879 segs, 418409474 residues
                      GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB seq length: 0
DB seq length: 200000000
                                                                                                                                                                                                                               US-10-660-357A-18
561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107
107
107
107
107
107
107
107
                                          Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         561
561
561
561
561
561
561
561
                                                                                                     OM protein -
                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum I
Maximum I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
No.
```

ö

Gaps

ö

Indela

Length 107;

9

```
Application US/10041860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-10-041-860-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMIQSPSSISASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIÓMTÓSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
            ; Sequence 18, Application US/1033530; Publication No. US20030152514A1; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES; FILE REFERENCE: ABGENIX.031A; CURRENT APPLICATION NUMBER: US/10/330,530; CURRENT APPLICATION NUMBER: US/246414; PRIOR FILING DATE: 2001-12-18; PRIOR FILING DATE: 2001-12-18; NUMBER OF SEQ ID NOS: 40; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 561; DB 14; Length 107; 100.0%; Pred. No. 1.7e-39; tive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 561; DB 14; Length 107; Best Local Similarity 100.0%; Pred. No. 1.7e-39; Matches 107; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/10041860

Sequence 26, Application US/10041860

CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: O'LAN': Caralan, Jose R.F.
APPLICANT: Gazit, Gadi
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Rancine
APPLICANT: Gazit, Rancine
APPLICANT: Meber, Richard
APPLICANT: Meber, Richard
APPLICANT: Weber, Richar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: homo sapiens
US-10-041-860-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo Sapiens
US-10-330-530-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 107;
    US-10-330-530-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSASVGDRVIIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 561; DB 14; Length 107; Best Local Similarity 100.0%; Pred. No. 1.7e-39; Matches 107; Conservative 0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 561; DB 14; Length 107; Best Local Similarity 100.0%; Pred. No. 1.7e-39; Matches 107; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RESGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                               APPLICANT: Chen, Francine, APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: ABGENIX. 051A
CURRENT RILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Bezeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFREENCE: ABGENIX. 051A
CURRENT APPLICATION UNDER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FRSELEG for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
Publication No. US20030157109A1
GENERAL INFORMATION:
                                                      APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corvalan, Jose R.F.
                                                                                                                  Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: homo sapiens
US-10-041-860-28
```

ö

RESULT 4 US-10-041-860-28

```
Sequence 266, Application US/10041860 Publication No. US20030157109Al GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 234, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: homo sapiens US-10-041-860-234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: homo sapiens
US-10-041-860-266
                                                                                                                                                                                                                                                                                                                                                                  US-10-041-860-234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-10-041-860-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                              ò
                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGMYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGTEFTLTISSLOPEDFATYYCLOHNSYPWTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JIA. Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Peng, Xiao-Dong
APPLICANT: Peng, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Chen, Francine
APPLICANT: Bezabeh, Binyam
APPLICANT: Bezabeh
APPLICANT: Bezab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 561; DB 14; Best Local Similarity 100.0%; Pred. No. 1.7e-39; Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 561; DB 14; Best Local Similarity 100.0%; Pred. No. 1.7e-39; Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 232, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
                                                                                                                                                                                   Sequence 231, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: homo sapiens
US-10-041-860-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-232
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 561; DB 14; Length 107; 100.0%; Pred. No. 1.7e-39; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RESGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tag, AEG-CLIL
APPLICANT: Yang, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gadi
APPLICANT: Gadi
APPLICANT: Weber, Richard
APPLICANT: ABCENIX. 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
NUMBER OF SEQ ID NOS: 377
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 266
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Feng, Xiao
APPLICANT: Chen, Xiao-Dong
APPLICANT: Chen, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX OS1A
CURRENT APPLICANTON NUMBER: US/10/041,860
CURRENT PILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOTWARE: FastSEQ for Windows Version 4.0
```

```
TYPE: PRT
CRGANISM: homo sapiens
US-10-041-860-340
                                TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-041-860-340
                                                                            US-10-041-860-316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-309-762-166
         LENGTH: 107
                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          원
                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                     1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
       100.0%; Score 561; DB 14; Length 107; 100.0%; Pred. No. 1.7e-39; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 561; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7e-39;
Matches 107; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                               61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                          61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVBIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RESGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 316, Application US/10041860
; Sequence 316, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.;
APPLICANT: Feng, Xiao-Chi
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Reber, Richard
APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION THEREOF
; FILE REFERENCE: AGENIX.051A
; CURRENT FILING DATE: 2002-01-07
; WUMBER OF SEG ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                         Sequence 268, Application US/10041860
GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Siao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Yang, Xiao-Chi
APPLICANT: Chen, Francine
APPLICANT: Reng, Kiao-Chi
APPLICANT: Reng, Racine
APPLICANT: Rechard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
ITLE OF INVENTION: THEREOF
FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FESTESEQ for Windows Version 4.0
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 107; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: homo sapiens
US-10-041-860-268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 268
LENGTH: 107
                                                                                                                                                g
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                 1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVP8 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                Gapa
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 166, Application US/10309762
; Sequence 166, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: GLOBAS, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Gallo, Micchael
; TITLE OF INVENTION: (AIX) TUMOR ANTIGEN
; TITLE OF INVENTION: (AIX)
; FILE SEFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-03
Query Match 100.0%; Score 561; DB 14; Length 107; Best Local Similarity 100.0%; Pred. No. 1.7e-39; Matches 107; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                      61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jia, Xiao-Chi
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Feng, Xiao
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadi
APPLICANT: Gazit, Gadi
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: THEREOF
ITLLE OF INVENTION: THEREOF
FILE REFERENCE: AGENIX: 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SEQ ID NOS: 377
SEQ ID NOS: 377
SEQ ID NOS: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 561; DB 14; Best Local Similarity 100.0%; Pred. No. 1.7e-39; Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 340, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
```

```
g
                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMIQSPSSLSASVGDRVIIITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                              1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                     1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                   Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
                                                                                                                                                                                                                                                                                                                                                          61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTEFTLTISSLOPEDFATYYCLQHNSYPWTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/10665383

Publication No. US20040141969A1

GENERAL INFORMATION:
APPLICANT: Floege, Juergen
APPLICANT: Gazit, Gadi
APPLICANT: Lachenstein, Henri
APPLICANT: Lichenstein, Henri
TITLE OF INVENTION: WETHOD FOR THE TREATMENT OF NEPHRITIS
TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
FILE REFERENCE: ABGENIX.052A
CURRENT FLLING DATE: 2003-09-16
PRIOR PPLICATION NUMBER: 60/411,137
PRIOR FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
TITLE OF INVENTION: ANTIGEN
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT APPLICATION NUMBER: 10/330,580
PRIOR PILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 107
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                   100.0%; Score 561; DB 15; 100.0%; Pred. No. 1.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 561; DB 16;
Pred. No. 1.7e-39;
Mismatches 0;
                                                                                                                                                                                                            0; Mismatches
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 107; Conservative
                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-10-309-762-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo Sapiens
US-10-660-357-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-10-665-383-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-660-357-18
                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 107
; TYPE: PRT
; ORGANISM: how sapiens
US-10-665-383-32

Query Match

US-10-665-383-32

Query Match

Disput Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIOMTQSPSSLSASVGDRVITTCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60

OY 1 DIOMTQSPSSLSASVGDRVITTCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPS 60

OY 61 RFSGSGSGTEFTLISSLQPEDFATYCLQHNSYPWTFGQGTKVEIK 107

Db 61 RFSGSGSGTEFTLISSLQPEDFATYCLQHNSYPWTFGQGTKVEIK 107

Search Completed: November 16, 2005, 23:05:42
```

TIME WITCH THE PROPERTY (USPTO)

```
November 16, 2005, 21:35:48; Search time 64.8088 Seconds (without alignments) 674.351 Million cell updates/sec
                                                                                                                                                               1 DIVMTQSPDSLAVSLGERAT......CQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                 2105692
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    2105692 seqs, 386760381 residues
 version -
                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - protein search, using sw model
                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                   geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
 GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_16Dec04:*
                                                                                                                                                                                                                                                                                                                                                                                                           geneseqp1980s:*geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         geneseqp2004s:*
                                                                                                                                  US-10-660-357A-22
590
                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
              Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                        protein
                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                 Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	uc
-	590	100.0	113	7	ADC99793	Adc99793 #	Anti-huma
7	590	100.0	113	7	ADD05397	Add05397 P	Anti-MUC1
ю	590	100.0	113	7	ADF09835		Human ant
4	556	94.2	133	Н	AAP80894	Aap80894 V	V region
Ŋ	550	93.2	114	æ	ADO3 63 63		Intracell
9	549	93.1	122	œ	ADI26708		Human ant
7	546	92.5	114	œ	ADP03687	_	Human ant
60	546	92.5	114	8	ADP03713		Human ant
σ	546	92.5	120	4	AAG65565	ß	Amino aci
10	546	92.5	135	ო	AAB03714		Immunoglo
11	546	92.5	135	9	ADA47343		Human ant
12	546	92.5	135	7	ADB72875	Adb72875 F	Human AA
13	546	2	135	œ	ADP88458		
14	546	92.5	135	ω	ADQ87927	Adq87927 F	Human HS]
15	546		286	ω	ADP03811	_	Human ant
16	544	92.2	114	8	ADO32154		Mouse ant
17	544	92.2	114	ω	ADQ75236	Adq75236]	Immunoglo
18	544	92.2	155	~	AAW32483		Kappa lic
19	544	92.2	155	~	AAY06912	Aay06912 F	Human var
20	544	ď	342	N	AAW32482	_	Growth fa
21	544	ď	342	N	AAY06909	<u>-</u>	TLHL amir
22	544	92.2	495	~	AAW32480	081	Growth fa
23	544	ς.	495	7	AAY06908	80	CATAB-TEV
24	543	ä	114	ω	ADP03705	705 1	Human ant
25	543	92.0	114	8	ADP03709	<u>.</u>	Human ant

	AdoS8062 S2 Cell d Aau00815 Human Imm Adp03723 Human ant Abb07172 ebvHigM M Ad12660 Human ant			Adg28267 Method of Abj18724 Antibody Abj18682 Antibody Aaw27546 Human Ab
ADP03683 ADP03695 ADK52434	ADO58062 AAU00815 ADP03723 ABB07172 ADI2660	ABP43142 ADP03815 ADL91336 AAR30144	ABP98692 ABP98684 ADG43870 ADP03701	ADQ28267 ABJ18724 ABJ18682 AAW27546
14 8 79 8	252 8 240 4 113 8 119 5			114 8 8 114 9 8 114 9 8 115 2
92.0	910 910 910 910 910 910 910	91.5	91.4 91.4 91.4 91.4	91.4 91.2 91.2
543	9012 4000 4000	540 540 55 539.57 7	50.00	5.44 5.33 5.33 5.33 5.33 5.33 5.33 5.33
ก็หัห	N M M M M	เพิทีพัพ	w w 4 4	के के के के

ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 22 ADC99793 standard; protein; 113 AA (first entry) lung cancer; human. 01-JAN-2004 ADC99793;

Homo sapiens

WO2003057838-A2.

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC.

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99795.

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 22; 78pp; English.

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the pancreatic or colorectal tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and centers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody

SXS

셤 ò ద

ò

```
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                         ADF09835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gudas J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ношо
                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                  ADF09835
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                    셤
                                                                                                                                                                    8
                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                      ò
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has orytestatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                                                                                                                                         9
                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                                                       DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-MUC18 antibody light chain variable region protein, SEQ ID No 22.
                                                                                                                                                                                              DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccin
antigen; tumour metastasis; melanoma; metastatic; human; light chain.
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                           ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                Length 113;
                                                                                                                                             Indels
                                                                                                                                                ;
0
                                                                                             100.0%; Score 590; DB 7; 100.0%; Pred. No. 2.6e-42;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 22; 87pp; English.
light chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD05397 standard; protein; 113 AA
                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-DEC-2001; 2001US-0346460P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                             113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-577496/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC.
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metastatic tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADD05399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 113 AA;
                                                Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003057006-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-2003.
                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD05397;
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
ADDOS 397
ADDOS 397
ADDOS 397
ADDOS 397
ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS ADDOS
```

100.0%; Score 590; DB 7; Length 113;

Query Match

```
ô
                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanome or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                 9
                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYMASTR
                                                                                                                             1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                 1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; light chain; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                             дарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTWVEIK 113
                                                                                                                                                                                           61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYXCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                             61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation inhibition; MUC18 tumour antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human anti-MUC18 monoclonal antibody light chain #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
100.0%; Pred. No. 2.6e-42; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 590; DB 7;
100.0%; Pred. No. 2.6e-42;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 22; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               Ä
                                                                                                                                                                                                                                                                                                                                                                                               ADF09835 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2002; 2002WO-US041580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-2001; 2001US-0346414P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-598367/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADF09837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

RESULT 4

Peptide

Region

```
This invention relates to a novel method of determining the ability of an immunoglobulin single domain to bind to a target in an intracellular environment comprising assessing the intracellular interaction between the immunoglobulin domain and the target by monitoring the signal. The method comprises providing a first molecule and a second molecule, where stable interaction of the first molecule and a second molecule, where generation of a signal, providing a single minracellular immunoglobulin domains, which is associated with the first molecule, where the single communoglobulin domain is free of complementary immunoglobulin domains, providing an intracellular target which is associated with the second molecules and carget leads to stable interaction of the immunoglobulin domain and the first and second molecules and generation of the signal; and assessing the intracellular interaction between the immunoglobulin domain and the target by monitoring the signal. The methods are useful for determining the ability of an intracellular environment. The present sequence is that of a single chain variable fragment (scFV) protein which was used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTOSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the ability of an immunoglobulin single domain to bind to target in an intracellular environment by assessing the intracellular interaction between the immunoglobulin domain and the target by monitoring the signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin single domain; intracellular environment; intracellular interaction; immunoglobulin domain; scFv; single chain variable fragment.
                   Intracellular interaction-related scFv protein SeqID27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.2%; Score 550; DB 8; Lo
92.9%; Pred. No. 6.2e-39;
ive 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 27; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI26708 standard; protein; 122 AA
                                                                                                                                                                                                                                                                      14-NOV-2003; 2003WO-GB004942.
                                                                                                                                                                                                                                                                                                               15-NOV-2002; 2002GB-00026729.
                                                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity .... Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Rabbitts TH, Tanaka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-431946/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 114 AA;
                                                                                                                                                                                     WO2004046185-A2.
                                                                                                                                           Unidentified
                                                                                                                                                                                                                               03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD126708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD126708
ID AD12
XX
AC AD12
XX
DT 15-A
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence is variable region of light chain of anti-exotoxin antibody with signal sequence. AAN804988 encodes the same sequence except that its signal peptide-encoding sequence contains an intron. See also AAN80495-N8049696, AAN80498 and AAN80941-2. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New gene coding for antibody to Pseudomonas aeruginosa exotoxin - plus recombinant vectors and host cells, useful for treating infections.
                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.2%; Score 556; DB 1; Length 133; Best Local Similarity 93.8%; Pred. No. 2.3e-39; Matches 106; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                               V region of L chain of anti-P.aeruginosa exotoxin Ab #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horigome K, Noguchi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= V region of L chain

    .20
    /label= signal peptide

                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO36363 standard; protein; 114 AA.
                                                                              AAP80894 standard; protein; 133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 25; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUMO ) SUMITOMO CHEM IND KK. (SUMU ) SUMITOMO PHARM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87EP-00117760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86JP-00288340.87JP-00298513.
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      . .133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakatani T, Nomura N,
                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1988-156310/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAN80499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1986;
26-NOV-1987;
                                                                                                                                                             25-MAR-2003
03-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP270077-A
                                                                                                                        AAP80894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD036363;
```

ö 9 9

Gaps

; 0

Length 114; Indels

field.)

ઠે გ ò a RESULT 5 ADO36363 ID ADO3 XX AC ADO3 XX DT 26-A

```
communicompetent host with an antibody lul produced by injecting the antibody, where the peptide comprises a human anti-1gM antibody fragment cantibody, where the peptide comprises a human anti-1gM antibody fragment capture included are given in the specification, or active fragments. Also included are given in the specification, or active fragments. Also included are stimulating remyelination of central nervous system (CRS) axons in a mammal (comprising administering a monoclonal antibody, or mixtures, monomers, active fragments, or recombinant calls included by their ability to bind structures and cells within the CRS, treating or preventing a monoclonal antibody or mixtures, monomers, active fragments, or recombinant antibodies derived from it, characterised by their ability to bind structures and cells within the CRS, treating or preventing a monoclonal antibody, or mixtures, monomers, active fragments, or recombinant antibodies derived from it, characterised by their ability to bind structures and cells within the CRS, treating or preventing a monoclonal antibody or mixtures, monomers, active fragments, or recombinant antibodies derived from it, characterised by their ability to bind structures and cells within the CRS, and to stringleter empellination of GRS axons in a mammal, and DNA sequence (or degenerate variant of it) which encodes an antibody (or a peptide analogue, hapten, or active fragment of it, where the DNA sequence consists of a sequence encoding an antil igh antibody, and seay for screening for the antibody an assay for screening for the antibody and assay for screening demyelination and or the antibody is used to treat or prevent a production and diseases of the CRS sunging the antibody is used to treat or prevent a certival termyelination and or simulate the proliferation of glial cells in CRS axons, or a disease, other injury or dysfunction of the CRS multiple sclerosis, or a disease, other injury or dysfunction of the compliant encephalancyality is a mouse infected with Strain by The FR 
                                       Human, antibody; IgM, remyelination, neuronal growth; autoantibody; demyelination disease; multiple sclerosis; central nervous system; CNS; axon; glial cell proliferation; theiler cell proliferation; Theiler companies of murine encephalomyelitis virus infection; CNS injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human immunoglobulin M antibody for treating or preventing a demyelinating disease of the central nervous system in a human or domestic animal, such as multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to an antibody (I) produced by injecting an
Human anti IgM antibody LYM 46 Vkappa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pease LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Fig 72; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                            96US-00692084.
97US-00779784.
99US-00322862.
2000US-00580787.
                                                                                                                                                                                                                                                                                               13-NOV-2001; 2001US-00010729
                                                                                                                                                                                                                                                                                                                                           94US-00236520
                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-00730473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-119219/12.
                                                                                                                             spinal cord injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAYO-) MAYO FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADI26709
                                                                                                                                                                                                              US2003185827-A1
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodriguez M,
                                                                                                                                                                                                                                                                                                                                           29-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                 08-AUG-1996)
                                                                                                                                                                                                                                                       02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-1999
```

```
ö
                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel antibody sequences, which acts against lessioned tissue. Also claimed is a method (M1) for isolating polynucleotide encoding the antibodies, which involves (a) isolating B cells that is infiltrated into lesioned tissue, and (b) acquiring polynucleotide that encodes an antibody from the isolated B cells. The antibodies are useful for treating cancer lesions, arteriosclerosis, inflammatory disease or autolimmune disease. The present sequence was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolating polynucleotide that encodes antibody which acts against desioned tissue, involves isolating B cells that is infiltrated into lesioned tissue, and acquiring polynucleotide that encodes antibody from isolated B cells.
                                                                                                                                                                              9
                                                                                                                                                                                                              9
   can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive; human; antibody; cancer lesion; arteriosclerosis; inflammatory disease; autoimmune disease; cancer.
antibody can be used to image a portion of the CNS which can be used to diagnose or monitor demyelination and/or remyelination of the CNS. The present sequence is a variable region of a human anti-IgM antibody (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsunoda H;
                                                                                                                                                                              1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                               1 DIVNTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                 61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNTPQAFGQGTKVEIK 113
                                                                                                                                                                                                                                            61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 546; DB 8; Length 114;
Pred. No. 1.4e-38;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsubara K,
                                                                                                              Length 122;
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human antibody related protein sequence, SEQ ID 60.
                                                                                                                                              4
                                                                                                                              8.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshida K, Fujii E,
                                                                                                                Score 549; DB
Pred. No. 8.1e-
5; Mismatches
                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; SEQ ID NO 60; 200pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KK.
RES PTE LTD.
                                                                                                                                                                                                                                                                                                                                                             ¥
                                                                                                                                                                                                                                                                                                                                                             ADP03687 standard; protein; 114
                                                                                                                  93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-2003; 2003WO-JP014919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-2002; 2002JP-00339241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.5%;
Best Local Similarity 92.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                             Query Match
Best Local Similarity 92.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suzuki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHUS ) CHUGAI SEIYAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHARMALOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-450382/42.
N-PSDB; ADP03686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 114 AA;
                                                                                  Sequence 122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004048571-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isuchiya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUN-2004
                                                    tragment).
                                                                                                                                                                                                                                                                                                                                                                                             ADP03687;
                     diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHAR-)
                                                                                                                                                                                                                                                                                                                             RESULT 7
                                                                                                                                                                                                                                                                                                                                              ADP03687
                                                                                                                                                                                                                                                                                                                                                                            8X33333
                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                              ò
```

S

entry

```
Producing gene libraries and antibody libraries, involves selecting a
light chain that binds to a heavy chain product to produce a functional
formation, and producing a gene library of the light chain variable
                                                                                                                                                                                                                       Gene library; immunoglobulin; antibody library; human.
                                                                                                                                                                            Amino acid sequence of protein seq Id No.
                                          AAG65565 standard; protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; p 165; 181pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MEDI-) MEDICAL & BIOLOGICAL LAB
                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2001; 2001WO-JP001298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2000; 2000JP-00050543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akahori Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shiraki K;
                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-565420/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAH47729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                   WO200162907-A1
                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                  30-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kurosawa Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Okuno Y,
                                                                                       AAG65565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions
                                                                                                                                                                                                                                                                         Ношо
RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB037
                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel antibody sequences, which acts against lesioned tissue. Also claimed is a method (M1) for isolating polynucleotide encoding the antibodies, which involves (a) isolating B cells that is infiltrated into lesioned tissue, and (b) acquiring polynucleotide that encodes an antibody from the isolated B cells. The antibodies are useful for treating cancer lesions, arteriosclerosis, inflammatory disease or autoimmune disease. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolating polynucleotide that encodes antibody which acts against lesioned tissue, involves isolating B cells that is infiltrated into lesioned tissue, and acquiring polynucleotide that encodes antibody from
                     9
                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive; human; antibody; cancer lesion; arteriosclerosis; inflammatory disease; autoimmune disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsunoda H;
                                          DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                          ESGVPARFSGSGGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 546; DB 8; Lv
Pred. No. 1.4e-38;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                      Human antibody related protein sequence, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujii E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 86; 200pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RES PTE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshida K,
                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                    ADP03713 standard; protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-NOV-2003; 2003WO-JP014919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-2002; 2002JP-00339241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHUS ) CHUGAI SEIYAKU
(PHAR-) PHARMALOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuchiya M, Suzuki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-450382/42.
N-PSDB; ADP03712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004048571-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                              26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUN-2004.
                                                                                                          61
                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                 ADP03713;
                                                                                                                                                                                                                     RESULT 8
ADP03713
ADP03713
ADP03713
ADP03713
ADP03713
ACC ADPC
ACC
                  ઢ
                                                      g
                                                                                                        ò
                                                                                                                                              g
```

Takahashi M;

Shinohara M,

Morino K,

Iba Y,

COLLID

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aortic aneurysm-associated antigen protein; AAAP; microfibrillar protein; abdominal aortic aneurysm disease; treatment; detect; tolerance; immunoglobulin kappa; IgK.
The invention relates to producing gene libraries, comprising immunoplobulin light and heavy variable region. The method involves selecting light chain that binds with the heavy chain product to produce a functional conformation, producing a gene library comprising a function of these light chain variable genes, and combining with gene library of heavy chain variable genes. The method is used for production of gene and antibody libraries
                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                            DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAMYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                  DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                          ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                            Length 120;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin kappa2 amino acid sequence fragment.
                                                                                                                                                                                                                          Score 546; DB 4; Le
Pred. No. 1.4e-38;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB03714 standard; protein; 135 AA
                                                                                                                                                                                                                          92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                        Query Match
Best Local Similarity 92.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB03714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $$$$$$$$$$$$
```

DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60

ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYCQQYXSTPRSFGGGTMVEIK 113

61

61

ò g

요

ઠ

DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR

```
27-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB72875
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                            approximately 40kD. The protein is isolated from human acrtic tissue and binds immunoreactively with immunoglobulin purified from human abdominal acrtic aneurysm (AAA) tissue. The protein is referred to as acrtic aneurysm (AAA) tissue. The protein is referred to as acrtic aneurysm associated antigenic protein (AAAP). The protein is capable of forming a disulphide bonded dimer. The protein is immunoreactive with human kappa immunoglobulin. Also included in the invention are recombinantly produced human AAA proteins. AAAP shows regions of homology with the bovine microfibril associated glycoprotein MFAP-4 and also with fibrinogen and vironectin. The isolated microfibrillar protein is useful for alleviating abdominal acrtic aneurysm (AAA) disease and detecting the presence of AAA-associated immunoglobulin bound to the human acrtic tissue. Antibodies directed against AAAP can be used to detect AAA disease. The recombinant protein can be used to induce tolerance to aniemnoglobulin kappa2 amino acid sequence. The sequence represents an immunoglobulin kappa2 amino acid sequence. The sequence shares homology with the AAAP of the invention, it was used to identify and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                Isolated microfibrillar protein for alleviating abdominal aortic aneurysm disease is purified from human aortic tissue and binds immunoreactively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                present invention relates to an isolated microfibrillar protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; TRXI; immunosuppressive; immunomodulator; vaccine; antigen; graft rejection; autoimmune disease; humanised.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPMFGQGTKVEIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.5%; Score 546; DB 3; Length 135; 92.9%; Pred. No. 1.6e-38; Live 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human antibody HSIGKAW light chain #SEQ ID 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA47343 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                      Example 3; Col 30; 70pp; English.
                                                                                                                                                 (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                        96US-0012976P.
                                                                                              97US-00812586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 105; Conservative
                                                                                                                                                                                                                                                             with immunoglobulin.
                                                                                                                                                                                                      WPI; 2000-316895/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2002102853-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
           Unidentified
                                                                                              07-MAR-1997;
                                                                                                                        07-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003
                                      US6048704-A.
                                                                 11-APR-2000
                                                                                                                                                                              Tilson MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA47343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA4734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PXSXXXXXXXXXX
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
The invention relates to a method for treating a primary not of the invention comprises tolerance to at least one antigen. The method of the invention comprises administering at least one compound which when in a primary mixed lymphocyte reaction in vitro reduces the amount of CD4+ CD25+ cells produced. The preferred compound is a humanised antibody or its fragment, that does not bind to the FC receptor, and includes CD8s that are free of a glycosylation site. The method of the invention is useful for inducing colerance to at least one antigen, specifically for inhibiting, ameliorating or reducing an immune response to an antigen. The antibody is useful for manufacturing a medicament for inducing tolerance to an antigen (possibly in the form of a vaccine), for inhibiting an immune response, for inhibiting the rejection of a graft (such as an organ) in a human patient, and for treating an autoimmune disease. The current sequence represents the human antibody HSIGKAW light chain that was used in an example from the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating a primate to induce tolerance to at least one antigen, useful for inhibiting graft rejection or treating an autoimmune disease, comprises administering a TRX1 antibody to reduce the amount of CD4+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLAWYQQKPQQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;
AAA-associated immunoglobulin 40kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                          Kornaga T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human AAA-associated immunoglobulin related polypeptide,
                                                                                                                                                                                                                                                                                                             Rao P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 546; DB 6;
Pred. No. 1.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                          Gorman S, Hale G,
Winsor-Hines D;
                                                                                                                                                                                                                                 CAMBRIDGE TECH SERVICES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB72875 standard; protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 22; 131pp; English.
                                                                                            19-OCT-2001; 2001US-0345194P.
18-APR-2002; 2002US-0373470P.
18-APR-2002; 2002US-0373471P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.5%;
14-JUN-2002; 2002WO-GB002796
                                                      2001GB-00014517
                                                                              2001GB-00022724
                                                                                                                                                                                                           (ISIS-) ISIS INNOVATION LTD (UYCA-) UNIV CAMBRIDGE TECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                             Waldmann H,
Cobbold S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD25+ cells produced
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-175228/17.
                                                                                                                                                                                                                                                               TOLE-) TOLERRY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 135 AA;
                                                                            20-SEP-2001;
19-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                14-JUN-2001;
                                                                                                                                                                                                                                                                                                                Frewin M,
Ringler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB72875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

ô

```
The present invention relates to a process of treating a primate to induce tolerance to at least one antigen, which comprises administering to the primate at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/Kg and at least one compound that inhibits CD8+ T cells, where the anti-CD4 antibody or its fragment is present in the primate when the antigen is present in the primate. The method is useful in treating a primate to induce tolerance to at least one foreign antigen to prevent transplant rejection. The present sequence is an antibody fragment used in the exemplification of the invention.
                Treating a primate to induce tolerance to at least one antigen comprises administering at least one anti-CD4 antibody or its fragment in an initial dose of at least 40 mg/kg and at least one compound that inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primate; tolerance; antigen; mixed lymphocyte reaction; MLR; CD4+; CD25+; IL-2; IL-4; IL-12; immune response; graft rejection; immunosuppressive; antirheumatic; antiarthritic; antidiabetic; neuroprotective; antiinflammatcry; antiallergic; antisthmatic; cytostatic; antimicrobial; transplant; graft-versus-host disease; autoimmune disease; inflammation; allergy; asthma; cancer; infection; human; HSIGKAW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducing tolerance to an antigen comprises administering a CD4 antibody alone or in combination with other compounds that induce tolerance against one or more antigens.
                                                                                                                                                                                                                                                                                                                                                                                        1 DIVWTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kornaga
                                                                                                                                                                                                                                                                                                        Length 135;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human HSIGKAW variable light chain antibody protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rao
                                                                                                                                                                                                                                                                                                          92.5%; Score 546; DB 8; 92.9%; Pred. No. 1.6e-38;
                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISIS INNOVATION LTD.
UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gorman S, Hale
Winsor-Hines D;
                                                                                           Example 1; SEQ ID NO 35; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ87927 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JAN-2004; 2004WO-US002643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2003; 2003US-00353708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 92.9
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waldmann H,
Cobbold S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TOLE-) TOLERRY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-580970/56
                                                                                                                                                                                                                                                                           Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004067554-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                            CD8+ T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frewin M, V
Ringler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                     . 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ87927;
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-)
(UYCA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ87927
   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                        present invention relates to the isolation of a protein approximately ba which is purified from human aortic tissue. The protein is
                                                                                                                                                                                                                                                                                                                  40kDa which is purified from human cortic tissue. The protein is immunoreactive with abdominal aortic tissue. The protein is immunoreactive with abdominal aortic aneurysms (AAA) -associated immunoglobulin. The protein is useful for diagnosing AAA disease in a subject, e.g. human, by administering the protein or a composition comprising the protein. The inventive protein is capable of forming a fluithinget-bonded dimer of 80 kDa. The present sequence of unknown function is given in the Sequence Listing but is not mentioned elsewhere in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                             Purified protein useful in diagnosing abdominal aortic aneurysm disease in subject, e.g. human, contains specified amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transplant rejection; antigen tolerance; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPMFGQGTKVEIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 546; DB 7;
Pred. No. 1.6e-38;
2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human antibody HSIGKAW VL SEQ ID NO: 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ringler DJ;
                                                                                                                                                                                                                                                                           Disclosure; Col 73-76; 67pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP88458 standard; protein; 135
                                                                                                                                   (UYCO ) UNIV COLUMBIA NEW YORK.
                                                            28-MAR-2000; 2000US-00535832.
                                                                                         96US-0012976P
                                                                                                        97US-00812586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-2003; 2003WO-US039165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-2002; 2002US-0431839P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Windsor-Hines D, Rao P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.9
Matches 105, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRX1; human; HSIGKAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-468712/44.
                                                                                                                                                                                                  WPI; 2003-687181/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TOLE-) TOLERRY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004052398-A1
                                                                                        07-MAR-1996;
07-MAR-1997;
 US6537769-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-SEP-2004
                              25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-2004.
                                                                                                                                                                     Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP88458;
                                                                                                                                                                  Tilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
```

ö

Gaps

```
Search completed: November 16, 2005, 21:51:40 Job time : 66.8088 secs
                           The invention relates to a novel method for treating a primate to induce to least one antigen. The method comprises administering a compound, or a combination of compounds, that induces tolerance against one or more antigens. The compound or the combination being in a primary mixed lymphocyte reaction being in a primary mixed lymphocyte reaction and that come or more antigens. The compound or the combination being in a primary mixed lymphocyte reaction and that can the primary mixed lymphocyte reaction and that reduces at least one of a primary and secondary mixed lymphocyte reactions, and the amount of a primary and secondary mixed lymphocyte reactions, and the amount of a primary and secondary mixed lymphocyte reaction.

The compound or the combination being administered in an amount and for a time so as to induce tolerance of administered in an amount and for a time so as to induce tolerance of administered in an amount and for a time so as to induce tolerance of antibody given in the specification, a composition comprising the relations of the thousands of antibody given in the specification, a composition comprising the relation of a present in the primate when the antigen of arriver; inducing tolerance to an antigen in a patient; inhibiting an immune response in a patient or for inhibiting the rejection of a graft in a human patient; and screening for a compound, or a combination of at least two compounds for use in inducing tolerance. The compositions of the invention have the following activities: immunosuppressive, antiinflammatory, antiathlargatic, and antidabetic, neuroprofective, antiinflammatory, antiathlargatic, antighted to mention of a careful for inhibiting or a meliorating or ameliorating or are useful for inhibiting, preventing or ameliorating an immune response or are useful for inhibiting, such as in the inhibiting or ameliorating an immune capense or miltections. These may also be used for antibod, and inflatence represents a uncommune diseases (e.g. antiphens. The nowed the sequescent or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; Antiarteriosclerotic; Antiinflammatory; Immunosuppressive; human; antibody; cancer lesion; arteriosclerosis; inflammatory disease; autoimmune disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 546; DB 8; Length 135; Pred. No. 1.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody protein used in the novel method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human antibody related protein sequence, SEQ ID 184,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP03811 standard; protein; 286 AA
Example 1; Page 30; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2003; 2003WO-JP014919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-2002; 2002JP-00339241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.9
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MO2004048571-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP03811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
ઠે
```

```
ö
                                                                                                                                                                                                                                                          The present invention relates to novel antibody sequences, which acts against lesioned tissue. Also claimed is a method (M1) for isolating polynucleotide encoding the antibodies, which involves (a) isolating B cells that is infiltrated into lesioned tissue, and (b) acquiring polynucleotide that encodes an antibody from the isolated B cells. The antibodies are useful for treating cancer lesions, arteriosclerosis, inflammatory disease or autoimmune disease. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                               from
                                                             Tsunoda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMIQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                          tissue, involves isolating B cells that is infiltrated into tissue, and acquiring polynucleotide that encodes antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 ESGVPDRFSGSGSGTDFTLTISTLQAEDVAVYXCQQYYSTPPTFGQGTKVEIK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                               polynucleotide that encodes antibody which acts against
                                                             Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 546; DB 8; Le
Pred. No. 3.4e-38;
4; Mismatches 5;
                                                             Fujii E,
                                                                                                                                                                                                                                Example 4; SEQ ID NO 184; 200pp; Japanese.
               KK.
RES PTE LTD.
                                                             Yoshida K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 92.0
              (CHUS ) CHUGAI SEIYAKU (PHAR-) PHARMALOGICALS
                                                             Suzuki M,
                                                                                            WPI; 2004-450382/42.
                                                                                                                                                                                               isolated B cells.
                                                                                                                N-PSDB; ADP03810.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 286 AA;
                                                               Tsuchiya M,
                                                                                                                                                 Isolating
                                                                                                                                                                 lesioned (
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

- protein search, using sw model OM protein Run on:

November 16, 2005, 21:37:48; Search time 13.5018 Seconds (without alignments) 805.260 Million cell updates/sec

US-10-660-357A-22 590 1 DIWHQSPDSLAVSLGERAT......CQQYYSTPRSFGQGTMVEIK 113 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 283416 seqs, 96216763 residues

rotal number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ig kappa ch		ப	Ig kappa chain - h	ibodi	appa	Ig kappa chain V r	Ig kappa chain pre	appa chain	Ig kappa chain pre	appa chain	Ig kappa chain V-J	Ig kappa chain pre	appa chain	Ig kappa chain pre	appa chain	Ig kappa chain V r	IgA kappa rheumato	Ig kappa chain V r	Ig kappa chain V-J	appa	ppa	appa chain	appa chain	Ig kappa chain pre	appa chain	appa chain	Ig kappa chain V r	Ig kappa chain V-I
SUMMARIES	αı	S34002	K4HULN	849531	S40347	S51147	830520	S34003	K4HU17 .	S30523	K4HUJ1	844116	844119	K4HU	S40364	A53261	S46373	PH0869	A49138	PT0356	S40329	S21917	A49137	S06084	A34153	PC1214	PL0014	PL0263	S41393	B34153
	BB	7	-+	~	7	N								٦	~	~	~	~	7	~	~	~	N	~	N	7	ď	~	~	7
	Length	113	114	134	129	N	113	113	134	113	133	114	114	121	124	138	132	101	106	118	129	134	136	240	102	134	145	113	112	0
* Ouerv	Match	91.7	91.4	90.0	٥.	σ.	89.0		88.5						85.6					81.4							78.0	•	77.5	9
	Score	541	539	531	530	529	525	523	522	517	514.5	511	508	505	505	496.5	495	494	487.5	480.5	469	469	467	463	461	460	460	459	457.5	454
Result	No.	H	7	٣	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

K4HULN

Typecies: Homo sapiens (man)
C;Species: Appr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C;Accession: A01903; FG1458
R;Schneider, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, S07-557, 1975
A;Tille: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette der Subgruppe IV vc
A;Reference number: A01903; MUID:76004342; PMID:50995
A;Accession: A01903; MUID:76004342; PMID:50995
A;Reference number: A01903; MUID:76004342; PMID:50995
A;Note: this is the first completely sequenced V region of a new kappa chain subgroup, de
A;Note: this is the first completely sequenced V; Minaesco, B.
A;Note: the C region of this chain has the Inv (3) marker
B;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, B.
J;Exp. Med. 170, 1551-1559, 1989
A;Tille: Expression of a public idiotype by human monoclonal IgM directed to myelin-assoc
A;Accession: F61458

Ig kappa chain V r	antitumor monoclon	Ig kappa chain V r	Ig kappa chain pre	PL7-6 antibody lig	Ig kappa chain V-J	Ig kappa chain V r	Ig kappa chain (Ma	Ig kappa chain V r							
837529	A49260	837533	S26040	302270	809970	837532	837534	S37535	837530	S68212	G30502	F30538	E30538	A31790	PL0264
~	~	7	~	7	7	~	7	~	~	~	~	7	~	7	7
95	113	92	138	113	112	92	92	92	92	214	111	112	112	220	113
œ	œ	9	₂	6	œ	æ	œ	9	6	<u>س</u>	0	7	ø	9	4
76.	76.	76.	76.	75.	75.	75.	75.	75.	75.	75.3	75.	74.	74.	74.	74.
453	453	452	451.5	448	447.5	447	447	446	444	444	442.5	441	440	440	439
30	31	32	33	34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

```
domains of four human monoclonal 1
Sirvez
Sirvez
Sirvez
Sirvez
Sirvez
Sirvez
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S34002; S30522
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Rur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human morn
A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Accession: S34002
A;Scatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 < MAR>
A;Residues: 1-113 < MAR>
C;Superfemines: BMBL:218328
C;Superfemily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology < INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHQYYGIPRTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 541; DB 2; Length 11 Pred. No. 1.1e-41; 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.7%;
Best Local Similarity 91.2%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 89.7%;
Local Similarity 90.3%;
les 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: Z18325
                               Query Match
Best Local Similarity 90.2'
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-113 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Accession: S30520
R, Mariette, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                          ò
                                                                                                                                                                                       윤
                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
B;Molecule type: protein
C;Comment: This is a Bence Jones protein.
C;Comment: This is a Bence Jones protein.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c;Complex: An immunoglobulin heterotetramer subunits associate into la C;Superfamily: immunoglobulin , immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
F;16-94/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: O1-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
Cispecies: Massession: S4951
Ripahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Ripahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Ripahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
Ripahmoudi, M.; Edwards
Aibacciption: Molecular characterization of natural human anti-Sm autoantibodies.
A; Reference number: S48797
A; Accession: S4951
A; Status: preliminary
A; Molecule type: makina
                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
540347
540347
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C. Accession: $4034
Eur. J. Immunol. 23, 3248-3271, 1993
A. Title: Expressed human immunoglobulin chi genes and their hypermutation.
A. Reference number: $40312; MUID:94080891; PMID:8258341
A. Accession: $40347
A. Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-19 «KLE»
A;Residues: 1-19 «KLE»
A;Cross-references: EMBL:X72457; NID:g441382; PIDN:CAA51125.1; PID:g441383
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;33-113/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVWTQSPNSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                              1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:246347; NID:9560841; PIDN:CAA86466.1; PID:9560842 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;36-116/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYCQQYYSTPYSFGGGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK
                                                                                                                                                                                                                                                                                      91.4%; Score 539; DB 1; Length 114; ilarity 91.2%; Pred. No. 1.6e-41; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 531; DB 2;
Pred. No. 1e-40;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.0%;
Best Local Similarity 90.3%;
Matches 102; Conservative '
                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-134 < MAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                         Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Ride Kruif, J.; Boel, E.; Logtenberg, T. Submitted to the EMBL Data Library, January 1995
A; Description: Selection and application of human SCFV antibody fragments from a semi-syr A; Reference number: S51147
A; Reference number: S51147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMTQSPDSLAVSLGERATINCKSSQSLFYSSNNKNYLAWYQQRPGQPPKLLIYWASIR 60
                                                                                                                     9
                                                                                                                                             18 DIVMTQSPDSLTVSLGERATINCKSSQSVLYSFNNKVYLAWYQQKPQQLLIYWASTR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S51147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Roseidues: 1-120 <DEK>
A;Cross-references: BBL:X83714; NID:g633227; PIDN:CAA58689.1; PID:g633228
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIELTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPQQPPKLLIYWASTR
                                                                                                                  1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGGGTWVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEI 112
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
  Length 129,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.0%; Score 525; DB 2; Length 11 Best Local Similarity 88.5%; Pred. No. 2.9e-40; Matches 100; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 529; DB 2; Length 12
Pred. No. 1.3e-40;
4; Mismatches 7; Indels
                                                          8; Indels
Score 530; DB 2;
Pred. No. 1.2e-40;
3; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, October 1992 A;Reference number: $30520 A;Accession: $30520
                                                                                                                                                                                                                                                                                                                                                                                                                              antibody light chain V region - human (fragment)
```

셤

```
Ig kappa chain precursor V-IV region (JI) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Dacession: 30-Jun-1987 #text_change 09-Jul-2004 C;Accession: A01904 R;Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G. Nucleic Acida Res: 13, 6515-6529, 1985 A;Fitle: Subgroup IV of human immunoglobulin K light chains is encoded by a single germl; A;Reference number: A93589; MUID:86041853; PMID:2997712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-133 «KLO»
A)CTOSS-references: UNIPROT:P06313; GB:Z00022; GB:X51570; NID:933158; PIDN:CAA77317.1; P)
A,Note: the sequence was determined from the differentiated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds In some cases, such as IgA and IgM, the subunits associate into las C.Superfamily: immunoglobulin V region; immunoglobulin homology (Keywords: heterotetramer; immunoglobulin P:1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                    Ig kappa chain V region - human
C;5pecies: Homo saptens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S30523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVWIQSPDSLAVSLGERATINCKSSQSVLYSSNNKOYLAWYQQKAGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-133/Product: Ig kappa chain V-IV region (JI) #status predicted <MAT>
                                    81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYXCQQYYNLPWTFGQGTKVEIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESGSPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYLTTPPTFGGGTKVBIK 113
   61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:218329
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 517; DB 2;
Pred. No. 1.5e-39;
4; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, October 1992
A;Reference number: $30520
A;Accession: $30523
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 514.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;36-116/Domain: immunoglobulin homology <IMM>F;44-60/Region: complementarity-determining 1 F;61-75/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;115-122/Region: complementarity-determining;123-133/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76-82/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: GDB:IGKV
A,Cross-references: GDB:119341; OMIM:146980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;43-114/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83-114/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 2p12-2p12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-43/Region: framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A01904
                                                                                                                                                                                                                                                                                                                                                     R;Mariette, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
      ò
                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: the sequence was determined from the differentiated gene A; Note: the authors translated the codon TGC for residue 76 as Trp C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34000
R;Mariette, X:; Tsapis, A.; Brouet, J.C.
Bur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal
A;Reference number: S34001; MUID:93209281; PMID:7681398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain precursor V-IV region (B17) - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C;Accession: A01905
R;Marsh, P.; Mills, F.; Gould, H.
Nucleic Acids Res. 13, 6531-6544, 1985
A;Title: Detection of a unique human VkappaIV germline gene by a cloned cDNA probe. A;Reference number: A01905; MUID:86041854; PMID:2997713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DIVMTQSPDSLAVSLGERATINCKSSQSILYSSDNKNYLAWYQQKPGQPPKLLIYCASTR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKAGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: immunoglobulin V region; immunoglobulin homology
K; Keywords: heterotetramer; immunoglobulin
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-314/Product: Ig kappa chain V-IV region (B17) #status predicted <WAT>
F; 21-43/Region: framework 1
F; 36-116/Domain: immunoglobulin homology <IMM>
F; 44-60/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYLTTPPTFGGGTKVEIK 113
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNTPLTFGGGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 523; DB 2; Length 113;
Pred. No. 4.4e-40;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Righus: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <MAR>
A;Residues: 1-13 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterocetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 522; DB 1;
Pred. No. 6.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F:115-121/Region: complementarity-determining 3
F:122-134/Region: framework 4
F:43-114/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;44-60/Region: complementarity-determining 1 ;61-75/Region: framework 2 ;76-82/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sch 88.6%; 11 Similarity 89.4%; 101; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.5%;
                                                                                         RESULT 7
S34003
Ig kappa chain V region - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;83-114/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-134 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
```

a ò a

g

ö

```
Ig kappa chain precursor V-IV region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Decies: Howo sapiens (man) C;Species: 30-01un-1987 #text_change 09-Jul-2004 C;Accession: A01902 R;Klobeck, H.G.; Bornkamm, G.W.; Combriato, G.; Mocikat, R.; Pohlenz, H.D.; Zachau, H.G. Nucleic Acids Res. 13, 6515-6529, 1985 A;Aritle: Subgroup IV of human immunoglobulin K light chains is encoded by a single germl: A;Reference number: A93589; MUID:86041853; PMID:2997712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ajintrons: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
C;Complex: An immunoglobulin nome cases, such as IgA and IgM, the subunits associate into lan
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;21-121/Product: Ig kappa chain precursor V-IV region #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Spacies: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPQQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIVMIQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CjAccession: $40364
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur, J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  61 ESGVPDRFSGSGSATDFTLTISSLQAEDVAVYYCQQYYSIPLTFGGGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X72474; NID:9441416; PID:9441417
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYCQQYYSTP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTP 101
                                                                                                                                                                                                                                                                                                                                                     A; Accession: A01902
A; Molecule type: DNA
A; Residues: 1-121 «KLO>
A; Cross-references: UNIPROT: P06312
A; Note: the sequence was determined from the germline gene
A; Note: there is only one Ig kappa V-IV gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 505; DB 1;
Pred. No. 1.9e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.6%; Score 505; DB
85.8%; Pred. No. 2e-38
:ive 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;115-121/Region: complementarity-determining 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;36-116/Domain: immunoglobulin homology <IMM>F;44-60/Region: complementarity-determining 1 F;61-75/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F,26-106/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;76-82/Region: complementarity-determining 2 F;83-114/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: $40364
A, Status: preliminary; translation not shown
A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;43-114/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.8%
These 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 95.0
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;21-43/Region: framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-124 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
12 kappa chain V-J region - human
19 kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S4419
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: 1diotypic vaccination against human B-cell lymphoma: rescue of variable and A;Reference number: S44105
A;Reference number: S44105
A;Ression: S44119
A;Ression: Jreliminary
A;Ressidues: 1-114 <HAW>
                                                                                                                                                                                                                                                                                                                                                                                                                        C,Species: Homo sapiens (man)
C,Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C,Accession: S44116
R,Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL. Data Library, March 1994
A,Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable
A,Reference number: S44105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIQMIQSPDSLITVSLGERATINCKSSQSILYSSNDKNYLAWYQQKAGQPPKLLIYWASTR 60
                                                                                                                                         80
                                                                                                                    21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:231396; NID:g472973; PIDN:CAA83271.1; PID:g940530 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPDSLVVSLGERATINCKSSQSLLYSSNNKTYLAWYQQKPGQPPKLLIKWASTR
                                                                                    1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1114 <HAM>
A;Cross-references: EMBL:231391; NID:g472970; PIDN:CAAB1266.1; PID:g940527
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYCQQYYSTPRSFGQGTWVEIK 113
                                                                                                                                                                                                                             ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                   ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 511; DB 2;
Pred. No. 5.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 508; DB 2;
Pred. No. 9.7e-39;
3; Mismatches 11;
     Pred. No. 3e-39;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;16-96/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 86.1%;
Local Similarity 87.6%;
nes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V-J region - human
     89.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 86.7
Matches 98, Conservative
                                101; Conservative
Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: S44116
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                         RESULT 11
S44116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                         d
                                                                                                                                                                                                   ò
```

ö

9 8 ö

```
RESULT 15
A53261
Ighaps chain precursor V-J-C region - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-May-1994 #text_change 21-Jan-2000
C; Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C; Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
C; Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jan-2000
R; Cogne, M.; Preud' homme, J.L.; Bauwens, M.; Touchard, G.; Aucouturier, P.
J. Clin. Invest. 87, 2186-2190, 1991
A; Reference number: A53261; MUID:91250576; PMID:1904072
A; Reference number: A53261; MUID:91250576; PMID:1904072
A; Residues: 1-138 <COG>A; MUID:91250576; PMID:1904072
A; Residues: 1-138 <COG>A; MUID: A53261
A; Molecule type: mRNA
A; Residues: 1-138 <COG>A; MUID: A53261
A; Molecule type: mRNA
A; Mole
1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 84.2%; Score 496.5; DB 2; Length 138; Best Local Similarity 85.1%; Pred. No. 1.3e-37; Matches 97; Conservative 6; Mismatches 10; Indels 1
                                                                   11
                                                                   유
                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

21 DIVMTQSPDSLAVSLGERATINCKSSLSVFFSPNNKNYLAWYQQKPGQPPKLLIYWASTR 80

ઠે

d

a

Search completed: November 16, 2005, 22:04:08 Job time : 13.5018 secs

THIS PARE DESIGNATION

```
REVISION TO 9.
                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DISULFID
STRAND
                                                                                                                                                                                                                          SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAND
                                                                                                                                    KV4A_HUMAN
                                                                                                                                                  homo sapien
homo sapien
homo sapien
homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                      homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                            homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homo sapien
homo sapien
                                                                                                                                                                                                                                                                                               P01625 homo sapien
                                                                                                                                                                                                                                                                                                             homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                            homo sapien
                                                                                                                                                                                                                                                                                                                                          homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                         mus musculu
                                                                                                                                                                                                                                                                                                                                                               homo sapien
                                                                                                                                                                                                                                                                                                                                                                                     homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                               musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                      mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mus musculu
                                                                                                                                                                                                                                                                                                                                    mus musculu
                                       November 16, 2005, 21:36:13 ; Search time 63.3548 Seconds (without alignments) 913.348 Million cell updates/sec
                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    US-10-660-357A-22
590
1 DIVWTQSPDSLAVSLGERAT.......CQQYYSTPRSFGQGTWVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                              mus
                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                           P83593
Q6kb05
P01665
P01667
P01667
P01667
P01667
P01666
P18135
Q9u179
P01624
P01629
P01629
                                                                                                                                                                                                                                                                                                                                                                                                                                     P01669
Q9ul77
P01620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                P04431
Q66j87
P01622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01664
Q920e9
P04206
Q9ul78
P18136
                                                                                                                                                                                                                                                                                                             P06313
P06312
                                                                                                                                     1612378
5.1.6
Compugen Ltd.
                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                      1612378 segs, 512079187 residues
GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                      KV4C_HUMAN
KV4B_HUMAN
KV4D_HUMAN
KV4D_HUMAN
Q6KBGF
KV1M_HUMAN
KV3O_MOUSE
                                                                                                                                                                                                                                                                                                                                                                     KV3H HUMAN
KV3N MOUSE
                                                                                                                                                                                                                                                                                                                                                                                          Q9UL79
KV3F HUMAN
KV1H HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                KV3E_HUMAN
KV3R_MOUSE
KV3H_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                     KV3Q MOUSE
Q9UL77
KV3B HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KV3D HUMAN
KV3L MOUSE
Q920E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV3G HUMAN
Q9UL78
KV3M HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                    KV3L_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV3U MOUSE
                           protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                KV4A HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KV1W HU
Q66JS7
                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                 UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                          Query
Match Length DB
                                                                                                                                                                                                                                                                                               Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.3
65.1
64.9
64.9
                                                                                                                                                                                                                                                                                                                                                                                                                                     389
386
385.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          385
383
383
383
383
383
382
55
382
55
                                                                     Title:
Perfect score:
                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                          3947
3947
3947
3947
3937
3937
3937
3907
390
                                                                                                                      Searched:
                                                                                    Sequence:
                                                                                                                                                                                                     Database
                                         Run on:
                                                                                                                                                                                                                                                                                                                                                         Result
```

Q9ul83 homo sapien P01671 mus musculu P01668 mus musculu Q6plt5 homo sapien Q8nek0 homo sapien Q901662 mus musculu Q9ul85 homo sapien P01603 homo sapien P01603 homo sapien P01603 mus musculu P01663 mus musculu P01661 mus musculu	26gmwl homo sapien
000 000 000 000 000 000 000 000 000	Ö9Ö
Q9ULB3 KV3S_MOUSE KV3S_MOUSE Q6F1T5 Q8NEKO Q9GSA9 KV3Z_MOUSE KV1K_HUMAN KV1K_HUMAN KV1K_HUMAN KV3K_MOUSE KV3I_MOUSE	Q6GMW1
44444444444444444444444444444444444444	N
11100111001100110011001100110011001100	236
44444466666666666666666666666666666666	63.6
382 381.53 381.53 379.53 376.53 376.53 376.53 376.53	375
шшшшшшшш 4 4 4 4 4 пшшшшшш 4 4 4 4 4 пш 4 10 10 10 00 00 11 01 14 4	45

ALIGNMENTS

```
RESULT.

YOUR HIGHWAN STANDARD, PRT; 114 AA.

TO TOTAL-1996 (Rel. 34, Last sequence update)

DY 25-OCT-2004 (Rel. 45, Last sequence update)

DY 25-OCT-2004 (Rel. 45, Last sequence update)

DY 25-OCT-2004 (Rel. 45, Last sequence update)

DY 13-OCT-2004 (Rel. 45, Last sequence update)

DY 13-OCT-2004 (Rel. 45, Last sequence update)

DY 14-OCT-1996 (Rel. 45, Last sequence update)

DY 15-OCT-2004 (Rel. 45, Last sequence update)

DY 15-OCT-2004 (Rel. 45, Last sequence update)

DY 16-OCT-1996 (Rel. 45, Last sequence update)

NUBL TAXID-9606;

NUBL TAXID-9606;

NUBL TAXID-9606;

DY 16-OCT-1996 (Rel. 45, Last sequence)

RE SIGNORC.

RE SIGNOR.

RE SIGNORC.

RE SIGNORC.

RE SIGNORC.

RE SIGNORC.

RE SIGNOR.
```

ô 9 8

Gapa

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVWTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIVWTQSPDSLAVSLGERATINCKSSQSILYSSDNKWYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYNLPWTFGQGTKVEIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Subgroup IV of human immunoglobulin K light chains is encoded by single germline gene.";
Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                               Ig kappa chain V-IV region B17.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                       90.7%; Score 535; DB 1; Length 134; 91.2%; Pred. No. 2.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V-IV region JI. Framework-1.
                                                                                                                                                    Complementarity-determining-1.
                                                                                                                                                                                                 Complementarity-determining-2.
                                                                                                                                                                                                                                                Complementarity-determining-3. Framework-4. By similarity.
                                                                                                                                                                                                                                                                                                                                                     14966 MW; 6413A22FD0738B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-IV region JI precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 2.4e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, 200022; CAA77317.1; -.. PTR, A01904; K4HUJI. HSPP, PO1625; LLVE. GO; GO:0005576; C:extracellular; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00047; 1g, 1.
MARAT; 8M00406; IGV; 1.
PROSTTE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 91.2
Matches 103, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                               134
43
60
75
114
1133
134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zachau H.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KV4B HUMAN
                                                                                                                                                                                                                                                                                                     DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                    CHAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P06313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
KV4B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE STATE OF THE S
     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection of a unique human V kappa IV germline gene by a cloned cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGGGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-IV region B17 precursor.
Homo sapiens (Human).
Pukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 544; DB 1; Length 114;
Pred. No. 2.3e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marsh P.;
Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12640 MW; 0647F1D17F236485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune responee; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 13:6531-6544 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=86041854; PubMed=2997713;
Marsh P., Mills F., Gould H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X02990; CAA26733.1; -. HSSP; P01625; 1LVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
     InterPro; IPR003596;
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISION TO 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KV4C HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marsh P
                                                                       STRAND
TURN
STRAND
TURN
                                                                                                                                                                              STRAND
TURN
TURN
                                                                                                                                                                                                                                                      STRAND
TURN
STRAND
HELIX
                                                                                                                                                                                                                                                                                                                                                          STRAND
STRAND
STRAND
STRAND
TURN
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
```

DATA PART REPLANTED DE LA PROPERTICA DEL PROPERTIC

요

ò

ò

```
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                              KV4D
    FFFFS
                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                 SO THE FEFFFF WAR AND COLOR STANDARD SO THE ST
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                           21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 80
                                                                                                                                                                                                                                                                                     1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE PROM N.A.
MEDLINE=86041853; PubMed=2997712;
Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
                                                                                                                                                                                                                                                                                                                                                                                         81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDTIP-TFGGGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                 61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Subgroup IV of human immunoglobulin K light chains is encoded by
                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                     Score 514.5; DB 1; Length 133; Pred. No. 3.1e-45; 1ndels 1
  Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-1.
Framework-2.
                                        Complementarity-determining-2.
                                                                        Complementarity-determining-3. Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V-IV region.
Framework-1.
                                                                                                                                                              5FB3953066744AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-IV region precursor (Fragment)
Name-IGKV4-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AA
                                                                                                                        By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, PO1625; ILVE.
Genew; HGNC:5834; IGKV4-1.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003596; Ig_v.
                                                             Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART: SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                 14632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z00023; CAA77318.1; -. PIR; A01902; K4HU.
                                                                                                                                                                                                                        Best Local Similarity 89.4%;
Matches 101; Conservative
                                                                                                                                                                                                       87.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single germline gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 >121
60
75
82
114
122
132
                                                                                                                                         133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
21
44
61
76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KV40 HUMAN
P06312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zachau H.G.
                                                                                                                    DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                     Query Match
                                    DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
5777777
                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
ô
                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                     DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.
           Complementarity-determining-3. By similarity.
                                                                               Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.5%; Score 481; DB 1; Length 10
86.0%; Pred. No. 7.2e-42;
ive 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                         61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTP 101
                                                                                                                                                                                                          81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12060 MW; 0C4F31EA11E12A0B CRC64;
                                                    13380 MW; 9586AD4188D33974 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin V region.
                                                                              85.6%; Score 505; DB 1;
95.0%; Pred. No. 2.7e-44;
iive 2; Mismatches 3.
                                                                                                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-IV region STH (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                          109 AA
Framework-3.
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct protein sequencing;
                                                                                           Best Local Similarity 95.0
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
114
121
114
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
40
62
62
101
109
23
23
                        43 1
121 1
121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109
109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                        HUMAN
          DOMAIN
DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
SEQUENCE
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                          KV4D HUM
P83593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNSURE
                                                                                                                                                                                                                                                                           HUMAN
```

1;

Gaps

. 9

9

54

```
1 DIVMTOSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMIQSPSSLSVSVGDRVTITCQASQNV-----NAYLNWYQQKPGLAPKLLIYGASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                         Framework-1.
Complementarity-determining-1.
                                                                                                                                                     Complementarity-determining-2. Framework-3.
                                                                                                                                                                                                                                                                                                                                          Score 397; DB 1; Length 108;
Pred. No. 3.4e-33;
                                                                                                                                                                                                       Complementarity-determining-3
                                                                                    Pramework-1.

Complementarity-determining-
Pramework-2.

Complementarity-determining-
Pramework-3.

Complementarity-determining-
Pramework-3.

Complementarity-determining-
Pramework-4.

By similarity.

By similarity.

108

A; 11834 MW; 739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 67.3%; Fred. No. 3.4e-33;
Best Local Similarity 67.3%; Fred. No. 3.4e-33;
Matches 76; Conservative 14; Mismatches 17; Indels
                                                                   Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL 1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-JUL-2004 (Rel. 44, Last annotation update)
19 kppa chain V-III region PC 6308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 276:785-790(1978).
PIR; C01937; KVMS08.
HSSP, P01665; 1QNZ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Direct protein sequencing;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
60
92
101
111
92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KV30 MOUSE
                                                                                                                                                                                                                                                   DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                      DOMAIN
                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                          DOMAIN
                                                                                                                 DOMAIN
                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV30_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 DIVMAQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAWYQQKPGQSPKLLIYGASTR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capra J.D., Klapper D.G.;

"Complete amino acid sequence of the variable domains of two human IgM anti-gamma globulins (Lay/Pom) with shared idiotypic specificities."; Scand. J. Immunol. 5:677-684(1976).

-! MRSCELLANBOUS: The second and thintd hypervariable regions of this chain are identical with those of the human PoW V-III kappa chain, with which it shares certain idiotypic determinants.

-! MSCELLANBOUS: This chain was isolated from an IgM with anti-gamma pIR; A01871; KIHULY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                    STRAIN=Balb/c;
A Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
Briand J.P., Hoebeke J.;
Briand J.P., Hoebeke J.;
Briand J.P., Hoebeke J.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL; AJ746180; CAG34081.1; -..
R INSP; PO1837; IKCR.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR007110; Ig-like.
R InterPro; IRR00409; IG, Z.
R SMART; SM00409; IG, Z.
R SMART; SM00406; IGV; Z.
R RRSITE; PS50835; IG_LIKE; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;; Score 428; DB 2; Length 255;
;; Pred. No. 5.6e-36;
11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B68BD38395DF713B CRC64;
                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA
                        255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, PO1607, IBWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq.
05-JUL-2004 (Rel. 44, Last and
19 kappa chain V-I region Lay.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 AA; 27445 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.5%;
                                                                                                                                    ScFv B8E5 protein (Fragment)
Name=scFv B8E5;
                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 73.5
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV1M HUMAN
P01605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                             Q6KB05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVIM HUMAN

ID KVIM HI

NO 101605

DT 21-JUL

DE 19 ADU

DE 19 ADU

OC BURANA

OC BURANA

OX NCBI_T

RN (101

R
  Q6KB05
ID Q6KB05
```

셤 ò

ò

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                        Weigert M., Gatmairan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.3%; Score 397; DB 1; Length 11
68.1%; Pred. No. 3.5e-33;
ive 13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7A4ADE4D6C256D29 CRC64;
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM0406; IGv; 1.
ProSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DOMAIN
```

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV3H_HUMAN
P04207;
                                                                                                                                                                                                                                                                       SEQUENCE
                                                       fetus.";
                                                                                                                                                                                                                                  NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
KV3H_HUMAN
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQOKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                59 ESGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQOSNEDPWTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure; Direct protein sequencing; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                             Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.1%; Score 396; DB 1; Length 111; 68.1%; Pred. No. 4.4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111
12002 MW; 7ASFCB586C306D29 CRC64;
                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
19 kappa chain V-III region PC 7043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=79073152; PubMed=103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, A01937; KVMS43.
PDB; IQNZ; NNR; L=1-111.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 68.1
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38
53
60
92
101
111
                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111
111 AA;
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        diversity.";
                                                                                                                                                  KV3M_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
Q9UL70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOTTO DOLL TO THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
              ઠે
                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatic and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCRASQGI-----SNYLAWYQQKPGKVPKSLIYAASTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=86177570; PubMed=3083417; Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P., Goldfien R., Carson D.A.; "Cloning and sequence determination of a human rheumatoid factor light-chain gene."; Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVBIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 OSGVPSRFSGSGSGTDFTLTISSLOPEDVATYYCOXYNSAPRTFGPGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C., ^{\text{Myosin-reactive autoantibodies in rheumatic carditis and normal}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain V-III region CLL. Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.9%; Score 395; DB 2; Length 10 Best Local Similarity 68.1%; Pred. No. 5.5e-33; Matches 77; Conservative 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                      Citi. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035044, AAD56280.1; -.
FIR; PH0663; PH0663.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-0.
InterPro; IPR007110; Ig-0.
InterPro; IPR007110; Ig-1.
InterPro; IPR007110; Ig-0.
InterPro; IPR07110; IRR07110; Ig-0.
InterPro; IPR07110; IRR07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR001596; Ig_V.
Pfan; PF00047; Ig; 1.
PROSITE; PS50835; IG_IKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-1987 (Rel. 04, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M12740; AAA58992.1; -. HSSP; P01625; 1LVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
129
43
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA;
```

7;

```
KV3L HUMAN P18135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09UL79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                 CV3L_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                  1 DIVMTOSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                              1 DIVMTOSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                             61 ESGUPARFSGSGSGTDFTLTINSLOAEDVAVYYCOOYYS-TPRSFGOGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGVPARFSGSGGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                  66.9%; Score 394.5; DB 1; Length 129; 70.2%; Pred. No. 7.5e-33; ive 15; Mismatches 12; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.8%; Score 394; DB 1; Length 111; 67.3%; Pred. No. 7.2e-33; ive 14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-1.
Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complementarity-determining-2.
                 Complementarity-determining-2.
Framework-3.
                                               Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-3
                                                                                                                                 14275 MW; 5C13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11952 MW; 2058BB50CE306D31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-2004 (Rel. 44, Last annotation update)
19 kappa chain V-III region PC 7183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
                                                                                              By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Framework-1.
   Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Framework-4
                                                                              segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, B01937; KWMS83.
HSSP; P01665; 1QNZ.
INTERPRO; IPR007110; Ig-like.
InterPro; IPR005596; Ig-v.
Pfam; PF00047; ig: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          llarity 67.3%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE;
Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 276:785-790(1978).
                                                                                                                                                                                                         80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
 69
76
108
118
129
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111
111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 76; Conserv
                                                                                                                                                                                      Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV3N MOUSE
                                                    DOMAIN
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                           NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct
                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 KV3N_MOUSE
TD ACAN MG
AC 21-JUL.
DT 21-JUL.
DE 19 AJUL.
DE 19 AJUL.
DE 19 AJUL.
DE 19 AJUL.
OC BURARY
OC BURARY
OC BURARY
OC BURARY
RA WEIGET
RY WEIGET
RY WEIGET
RY MEDLIN
RA WEIGET
RY MEDLIN
RY WEIGET
RY MEDLIN
RY DOWN
RY DIRECT
DOWN
RY DIRECT
DOWN
RY DIRECT
RY DOWN
RY DIRECT
RY DOWN
RY DIRECT
RY DOWN
RY DIRECT
RY DOWN
RY DIRECT
RY DOWN
RY DIRECT
RY DOWN
RY DOWN
RY DOWN
RY DIRECT
RY DOWN
RY DIRECT
RY DOWN
RY DIRECT
RY DOWN
RY DIRECT
RY DOWN
RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                  g
FFFFFFS
                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                       ò
```

```
21 BIVLTQSPGTLSLSPGERATLSCRASQSV----SSSYLAWYQQKPGQAPRLLIYGASSR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=89171307; PubMed=3127527;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Mutcantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-i. DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V-III region HAH. Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09UL79;
01-MAY-2000 (TEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MAR-2004 (TEMBLrel. 26, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14073 MW; D3C55292772774D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 393.5; DB 1
65.5%; Pred. No. 9.6e-33;
ive 20; Mismatches 14
                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JK1 segment.
By similarity.
                                                                                                            g kappa chain V-III region HAH precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; PL0022; K3HUHA.
HSSP; P01625; 1EEQ.
GO; GO:000557; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
1129
43
43
55
70
77
77
1109
1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129
129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukemia.
```

```
g
                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Klapper D.G., Capra J.D.;

The amino acid sequence of the variable regions of the light chains
of idiotyplically cross reactive IgM anti-gamma globulins.";

The num idiotyplically cross reactive IgM anti-gamma globulins.";

L. Ann. Immunol. (Paris) 127C:261-271(1976)

C. -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

R. PIR; A01897; K3HUPM.

R. PIR; A01897; K3HUPM.

R. PIR; A01897; K3HUPM.

R. GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005576; C:extracellular; NAS.

R. GO; GO:0006955; F:amtigen binding; NAS.

BR GO; GO:0006955; F:immune response; NAS.

DR GO; GO:0006995; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIVMTQSPSLLSASTGDRVTISCRMSQGI-----SSYLAWYQQKPGKAPELLIYAASTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                   "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.
[1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.5%; Score 392.5; DB 1; Length 109; Best Local Similarity 68.1%; Pred. No. 1e-32; Matches 77; Conservative 16; Mismatches 15; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.6%; Score 393; DB 2; Length 108; 68.1%; Pred. No. 8.8e-33; Live 11; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11922 MW; 62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEAM, PF00047; 19; 1.
SMART; SM00406; IGV; 1.
Direct protein sequencing; Immunoglobulin V region.
DISULFID: 23 89 Similarity.
                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192 (1998).
EMBL; AF035035; AAD56271.1; -.
EMBL; A53638; S23638.
PIR; S23638; S23638.
PIR; S34090; S34090.
HSSP; P01607; IBWW.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
SMART; SM00406; IGV.
SMART; SM00406; IGV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
18 kappa chain V-III region POM.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
MEDLINE=76276460; PubMed=60899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA; 11787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 68.13
les 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV3F HUM
P01624;
                                                                                                                                                                                 fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SO DE RELEVENTA DE LA PORTE DEL PORTE DE LA PORTE DEL PORTE DE LA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

Search completed: November 16, 2005, 22:01:52 Job time : 63.3548 secs

THIS PAGE BLANK (CEPTO)

31, 49,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

```
Sequence 80, Application US/08525339A

Patent No. 6309636

TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE

TITLE OF INVENTION: MATHODS OF HUMANIZING ANTIBODY PEPTIDES

NUMBER OF SEQUENCES: 81

CORRESPONDENCE NORALSON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STREET: 755 Page Mill Road

CITY: Palo Alto

STREET: 755 Page Mill Road

CITY: Palo Alto

STREET: 194304-1018

COMPUTER REAABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBE

SOOFWARE: PetentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 37,612

RECISTRATION NUMBER: 37,613

TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 550; DB 3; Length 11 Pred. No. 3.8e-47; 3; Mismatches 5; Indels
                             US-09-025-769B-31
US-09-025-769B-49
US-09-490-070A-31
US-09-490-153-31
US-09-490-153-49
US-09-490-324-49
PCT-US3-08435-8
US-09-80-324-49
US-09-810-502-38
US-09-810-502-38
                                                                                                                                                                                                                                           US-07-935-695-4
US-08-961-309-58
US-08-961-309-66
                                                                                                                                                                                                                               US-08-463-903-4
                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92.9%;
Matches 105; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 706141
INFORMATION FOR SEQ 1D NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acide
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-525-539A-80
                                                                                                                                                                                                                                                                                                                                                                                                US-08-525-539A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
RESULT 1
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               November 16, 2005, 21:41:29 ; Search time 19.2142 Seconds (without alignments) 439.017 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                            1 DIVMTQSPDSLAVSLGERAT......CQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11
Sequence 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-525-539A-80
US-09-0490-070A-17
US-09-490-070A-17
US-09-490-153-17
US-09-490-153-17
US-09-10-12-18-17
US-09-11-18-11
US-09-11-18-11
US-09-11-18-11
US-09-11-18-11
US-09-11-19-11
US-09-11-19-19-11
US-09-11-19-11
US-09-11-19-11
US-09-11-19-11
US-09-11-19-11-19-11
US-09-11-19-11-19-11
US-09-11-19-11-19-11
US-09-11-19-11-19-11-19-11
US-09-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-19-11-1
                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                              513545 segs, 74649064 residues
                 version -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                  GenCore
(c) 1993
                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                              US-10-660-357A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
```

ö 9

0; Gaps

Length 113

```
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 BSGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                  61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPXTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: B 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELEPHONE: (212)596-9000

TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 549; DB 3; Length 11-7
Pred. No. 4.9e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
APPLICANT: Pluckthun, Andreas
APPLICANT: Pluckthun, Protein/(Poly) peptide libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-00-490-070A-17
Sequence 17, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    Sequence 17, Application US/09025769B Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.1%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 114 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.1
Best Local Similarity 92.9
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10021
                                                                                                                                                  RESULT 2
US-09-025-769B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-025-769B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
요
                                          ઠે
                                                                                g
```

```
1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYCQQYYSTPPTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT Knappik, Achim
APPLICANT Rappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
                                  Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
Mhite & McAuliffe
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARE: Patentln: Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.1%; Score 549; DB 4; Length 114; 92.9%; Pred. No. 4.9e-47; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                       STREET: 1666 K Street, N.W., Suite 300 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEPHONE: (202) 912-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-490-070A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 114 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               ZIP: 20006
COMPUTER READABLE FORM:
Ilag, Vic
Ge, Liming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.99
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-490-153-17
```

```
LENGTH: 135 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knappik, Achim
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESONDENCES: 373
CORRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: USA
                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EL PLOPSY MISH
COMPUTER: EL PROPERIED FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: PAPENTINE PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION: TO FEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.1%; Score 549; DB 4; Length 114; Best Local Similarity 92.9%; Pred. No. 4.9e-47; Matches 105; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAYE. (212)596-9000
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 114 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-490-324-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-490-153-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
Patent No. bugo. comparation:
GENERAL INFORMATION:
APPLICANT: Marin David Tilson
TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AI
TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
TITLE OF INVENTION: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVWIQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: 0.C...

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,586
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P:
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/53862-A
TELECOMMUNICATION INPORMATION:
TELECOMMU
FRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PAPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-ANG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELECHONE: (212)596-9090
TELECHONE: (212)596-9090
TELECHONE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.1%; Score 549; DB 4;
92.9%; Pred. No. 4.9e-47;
trive 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-490-324-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
COADER & ADDRESSE:
COADER & AVENDEM LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Application US/08812586 Patent No. 6048704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.9
Matches 105; Conservative
```

```
US-08-828-741B-11
                                                                                                                                                                                                                                                                                                                            US-08-828-741B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-160-567-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                셤
                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7

US-09-535-812A-43

US-09-535-812A-43

US-09-535-812A-43

Sequence 43, Application US/09535832A

Patent No. 6537769

GENERAL INFORMATION:

TITLE OF INVENTION: With Abdominal Antigenic Proteins Associated

TITLE OF INVENTION: With Abdominal Antigenic Proteins Associated

TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof

TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof

CURRENT APPLICATION NUMBER: US/09/535,832A

CURRENT PILING DATE: 2000-03-28

CURRENT FILE PATENTION ONS: 57

SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                             9
                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                      21 DIVWTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                             1 DIVMIQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPMFGQGTKVEIK 133
                                                                                                                                                                                                                                                                                 61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                          ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPMFGQGTKVEIK 133
                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09274163E
Fatent No. 6485943
GENERAL INFORMATION:
APPLICANT: STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: MAFPEN, Rosematie
FILE REFERENCE: 0518370224
CURRENT APPLICATION NUMBER: US/09/274,163E
CURRENT FILING DATE: 1999-03-22
FRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.5%; Score 546; DB 4; Length 135; 92.9%; Pred. No. 1.2e-46;
                                                                                                                                                     6; Indels
                                                                                                       Score 546; DB 3;
Pred. No. 1.2e-46;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                          92.5%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT , ORGANISM: Bscherichia coli US-09-274-163E-16
                                                                                                       Query Match
Best Local Similarity 92.9
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 105; Conservative
                  TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-812-586-46
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-535-832A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-274-163E-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                   ò
```

```
ô
                                                                                                                                                  1 DIVWTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAMYQQKPQQPPKLLIYMASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                 1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYCQQYXSTPXSFGQGTKLEIK 113
                                                                                                                                                                                                                               61 ESGVPARPSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.2%; Score 544; DB 3; Length 155; 92.0%; Pred. No. 2.2e-46; Live 4; Mismatches 5; Indel8
Length 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Suess, Gabriele M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ACULLY, SCOTT, MURPHY & PRESSER
                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Didgilo, FRANCAS:
REGISTATION NUMBER: 31,346
RETERRENCE/DOCKET NUMBER: 31,346
RELEFAX: 01616/742-4343
TELEFAX: (516) 742-436
TELEFAX: (516) 742-436
TELEFAX: (516) 742-436
TELEFAX: 1059 O1 SANS UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHRRACTERISTICS:
LENGTH: 155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City Plaza CITY: Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States of America ZIP: 11530 COMPUTRY READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMpatible COMPUTER: IBM PC COMpatible COMPUTER: PLOPS MS. TO COMPATING SYSTEM: PC-DOS/MS-DOS COMPATING SYSTEM: PC-DOS/MS-DOS
  Score 544; DB 4;
Pred. No. 1.5e-46;
4; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11, Application US/08828741B ; Patent No. 6043069
     Query Match
Best Local Similarity 92.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
```

```
Sequence 11; Application US/09509031
; Sequence 11; Application US/09509031
; Patent No. 6590800
; GENERAL INFORMATION:
; APPLICANT: States, Gabriele M.
; APPLICANT: Tarbinton, David M.
; APPLICANT: Treutlein, Herbert R.
; APPLICANT: Treutlein, Herbert R.
; TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
; TITLE OF INVENTION NUMBER: US/09/509,031
; CURRENT FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; SEQ ID NO 11
; LENGTH: 155
; TYPE: PRT
CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTWVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGQGTKLEIX 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC Compatible
COMPUTER: Talm PC Compatible
COMPUTER: Talm PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/710,299
FILING DATE: 09-No. 6521741-2000
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION NUMBER: 08/828,741
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAMME: DIGIGIOL. FTANK S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 544; DB 4; Length 155; Pred. No. 2.2e-46; 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence:Kappa
protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 544; DB 4; Le
Pred. No. 2.2e-46;
4; Mismatches 5;
                                                   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 155 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 92.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 92.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
       CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
COTHER INFORMATION:
COTHER INFORMATION:
US-09-509-031-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-710-299-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 BSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGGGTKLEIK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, APE---
Ratent NO. 6521741
GENERAL INPORMATION:
APPLICANT: Koengen, Frank
Suess, Gabriele M.
Tarlinton, David M.
Trantlenon, David M.
Trantlenon, David M.
Trantlenon, Perbert R.
Treutlein, Herbert R.
Treutlein, Peroducing SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 544; DB 3; Length 155;
Pred. No. 2.2e-46;
4; Mismatches 5; Indels
                                            GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tauess, Gabriele M.
APPLICANT: Treatlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                       ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                            United States of America
Sequence 11, Application US/09160567
Patent No. 6326179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4346
TELEPHONE: (516) 742-4366
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 155 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                           CITY: Garden Ci
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-160-567-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-710-299-11
                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
US-09-710-299-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
9
                      30 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR
DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGQGTKLEIK 142
                                                                                  ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTWVEIK 113
                                                                                                           92.2%; Score 544; DB 3; Length 342; 92.0%; Pred. No. 5.3e-46; Live 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                        APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlain, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-AMR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DiG1910, Frank S.
ATTORNEY/AGENT INFORMATION:
NAME: DiG1910, Frank S.
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHRACTERISTICS:
LENGTH: 342 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                   Sequence 6, Application US/08828741B; Patent No. 6043069 GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-828-741B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                             RESULT 13
US-08-828-741B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-160-567-6
-
                                      30
                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                      g
                                                                                  8
ठ
```

Sequence 6, Application US/09160567 Patent No. 6326179 GENERAL INFORMATION: APPLICANT: Koenegen, Frank

```
10 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSTNYLAWYQQKPGQPPKLLIYWASTR 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Koentgen, Frank
Suess, Gabriele M.
Tarlinton, David M.
Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 342
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSER: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 544; DB 3;
Pred. No. 5.3e-46;
4; Mismatches 5.
                                                                                                                            ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFA: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09710299; Patent No. 6521741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 342 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.09
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-160-567-6
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                              11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
```

30 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAMYQQKPGQPPKLLIYMASTR 89.

8 & 8

Search completed: November 16, 2005, 22:07:20 Job time : 20.2142 secs

TIES PASS DE DE SUS (USPTO)

```
US-10-330-613-22
 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 80, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 35, Appli
Sequence 16, Appli
Sequence 16, Appli
                                                                              November 16, 2005, 22:02:09; Search time 69.3787 Seconds (without alignments) 681.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                            US-10-660-357A-22
590
1 DIVMTQSPDSLAVSLGERAT......CQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                       PUDLISHER AGAPTICATIONS AND TO THE COME. PDP: *

(SGNZ_6/ptodata///pubpaa/US6/PW PUB.pep:*

(SGNZ_6/ptodata///pubpaa/US6/PW PUB.pep:*

(SGNZ_6/ptodata///pubpaa/US66_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US67_NEW_PUB.pep:*

(SGNZ_6/ptodata///pubpaa/US68_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US68_NEW_PUB.pep:*

(SGNZ_6/ptodata///pubpaa/US68_NEW_PUB.pep:*

(SGNZ_6/ptodata///pubpaa/US69_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US69_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US69_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US69_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US69_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US69_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US10_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US10_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US10_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US10_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US10_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US10_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US10_PUBCOMB.pep:*

(SGNZ_6/ptodata///pubpaa/US10_NEW_PUB.pep:*

           5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 US-10-330-613-22

4 US-10-330-530-22

6 US-10-660-357-22

US-09-956-206A-80

9 US-10-965-616-80

1 US-10-10-729-51

1 US-10-171-452A-1

2 US-10-318-353-112

3 US-10-371-984-35

3 US-10-371-984-35

3 US-10-274-163E-16
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                1867879 seqs, 418409474 residues
            version 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
                                                           sw model
                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
            GenCore (c) 1993 .
                                                         protein search, using
                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4114
9114
9114
9115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                       Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000.0
1000.0
1000.0
933.2
933.2
923.1
923.5
923.5
                                                                                                                               Title:
Perfect score:
                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                       Sequence:
                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20010001110
                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

```
Sequence 10, Appl
Sequence 11, Appl
Sequence 14, Appl
Sequence 140, App
Sequence 17, App
Sequence 27, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 13, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 11, Appli
Sequence 26, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 26, Appli
Sequence 16, Appli
Sequence 18, Appli
Sequence 112, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Appl
Sequence 4266, Ap
Sequence 136, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKVYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 590; DB 14; Length 113; 100.0%; Pred. No. 1.9e-45; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/10330613
Publication No. US20030147809A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENTX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 22
LENGTH: 113
B US-10-880-028-29
B US-10-880-028-29
T US-10-345-618-11
T US-10-345-618-11
T US-10-345-618-11
T US-10-345-618-11
US-10-345-618-11
US-10-345-618-4
US-10-345-618-4
US-10-345-618-4
US-10-345-618-4
US-10-345-618-4
US-09-274-163E-2
US-09-274-163E-4
US-09-274-163E-4
US-09-274-163E-4
US-10-26-049-4274
US-10-483-993-8
US-10-483-993-8
US-10-996-191-11
T US-10-996-191-11
T US-10-991-56-26
US-10-991-576-26
US-10-991-576-26
US-10-991-576-26
US-10-991-576-26
US-10-991-576-26
US-10-991-576-26
US-10-991-576-26
US-10-644-277-108
US-10-644-277-108
US-10-644-277-112
US-10-644-277-112
US-10-644-277-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                      Query Match
Best Local Similarity 100.0
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo Sapiens
US-10-330-613-22
```

```
PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 706141
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-965-616-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIVMTÓSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESGVPARFSGSGSGTDFTLTINSLOAEDVAVYYCOOYYSTPRSFGGGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
Sequence 22, Application US/10330530

Publication No. US20030152514A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TILE OF INVENTION:

FILE REFERENCE: ABGENIX.031A

CURRENT APPLICATION NUMBER: US/10/330,530

CURRENT APPLICATION NUMBER: US/00/330,530

CURRENT APPLICATION NUMBER: US 60/346414

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/10660357
Publication No. US20040115205A1
GENERAL INFORMATION:
APPLICANT BAR-TIL, Menashe
APPLICANT BAR-TIL, Menashe
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastsEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 590; DB 14; 100.0%; Pred. No. 1.9e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 590; DB 16; 100.0%; Pred. No. 1.9e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/09956206A Patent No. US20020164339A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-956-206A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-10-660-357-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-660-357-22
                                                                                                                                                                                                                                                                                                                                                                                      US-10-330-530-22
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

APPLICANT: DO COUTO, FERNANDO J.R.

```
APPLICANT: DO COUTO, FERNANDO J.R.
CERLANI, ROBERTO L.
PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
MC3 AONTINATION ROAD ANTIBODY, METHODS OF USE THEREOF, AND
METHODS OF HUMANIZING ANTIBODY PEPTIDES
RECOMBINANT PEPTIDES DERIVED FROM THE MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND METHODS OF HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKYYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 113;
                                                                                                                                                                                                                                                                 ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1900py disk
COMPUTER: PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206A
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.2%; Score 550; DB 9; Le Best Local Similarity 92.9%; Pred. No. 7.4e-42; Matches 105; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/525,539
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 1-10-58-1995
APPLICATION NUMBER: 08/487,598
FILING DATE: 1-1095
APPLICATION NUMBER: 08/307,868
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-956-206A-80
                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 44,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 80, Application US/10965616; Publication No. US20050169915A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 81
```

ô

```
1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DIVMTOSPDSLAVSLGERATIICKSSOSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ESGVPDRFSGSGSGTDFTLTISSLOAEDVAVYYCOOXYNTPQAFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 549; DB 14;
Pred. No. 9.9e-42;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 548; DB 17;
Pred. No. 1.1e-41;
3; Mismatches 5;
              PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR PILING DATE: 1999-05-28
PRIOR FILING DATE: 1997-01-07
PRIOR FILING DATE: 1997-01-07
PRIOR FILING DATE: 1997-01-07
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-08-08
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 51
LENGTH: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BEDIAN, VAHE
APPLICANT: BEVALARAJA, MADHAV NARASIMHA
APPLICANT: PGLTZ, IAN
APPLICANT: HAAK-FRENDSCHO, MARY
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: LOW, JOSEPH EDWIN
APPLICANT: MOBLEY, JAMES LESLIE
TITLE OP INVENTION: ANTIBODIES TO M-CSF
FILE REFERENCE: ABX-PF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/938,353
CURRENT FILING DATE: 2004-09-09
PRIOR APPLICATION NUMBER: 60/502,163
PRIOR FILING DATE: 2003-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 112, Application US/10938353
Publication No. US20050059113A1
GENERAL INFORMATION:
APPLICATION NUMBER: 09/580,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/10171452A
                                                                                                                                                                                                                                                                                                                                                                                                                           93.1%;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.9%;
Best Local Similarity 92.9%;
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 92.0°
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 112
LENGTH: 114
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-010-729-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo sapiens
US-10-938-353-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-938-353-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-10-171-452A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
Manual APPLICANT: Miller, David J.
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKYYLAWYQQKFQQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 BSGVPDRFSGSGSGSTDFTLTISSLQAEDVAVYYCQQYYSTPXTFGQGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                            COUNTRY: USA
ZIP: 94304-1018
COMPUTER READBLE FORDY
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/965,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.2%; Score 550; DB 18; Best Local Similarity 92.9%; Pred. No. 7.4e-42; Matches 105; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION WINBER: 44,408
REFERENCE/DOCKET NUMBER: 276332000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 494-0792
                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-0ct-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/956,206
FILING DATE: 17-Sep-2001
APPLICATION NUMBER: US 08/525,539
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11683
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: 08/497,598
FILING DATE: 7-UUNE-1995
APPLICATION NUMBER: 08/497,598
FILING DATE: 7-UUNE-1995
APPLICATION NUMBER: 08/497,598
FILING DATE: 7-UUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
                   ADDRESSEE: MORRISON & FOERSTER
STREET 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-SEPT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-965-616-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-010-729-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ö

9

```
9
                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                21 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                  1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPMFGQGTKVEIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPMFGQGTKVEIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

92.5%; Score 546; DB 16; Length 135;
Best Local Similarity 92.9%; Pred. No. 2e-41;
Matches 105; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                    92.5%; Score 546; DB 15; Length 135; 92.9%; Pred. No. 2e-41; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: STEVENS, Fred J.
APPLICANT: STEVENS, Fred J.
APPLICANT: WILKINS STEVENS, Priscilla
APPLICANT: RAFEN, ROSEMATIE
APPLICANT: RAFEN, ROSEMATIE
APPLICANT: SCHIFFEN, Marianne
TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
FILE REFERENCE: 051583/0224
CURRENT FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: US 08/373,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: RAO, Patricia
APPLICANT: RAO, Patricia
APPLICANT: RAO, Patricia
APPLICANT: RINDSOR-HINES, Dawn
APPLICANT: RINGLER, Douglas J.
TITLE OF INVENTION: INDUCING TOLERANCE IN PRIMATES
FILE REFERENCE: TLN-022
CURRENT APPLICATION NUMBER: US/10/731,984
CURRENT PILING DATE: 2003-12-09
PRIOR APPLICATION NUMBER: 60/431839
PRIOR PILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Synthetic Oligonucleotide US-10-731-984-35
PRIOR APPLICATION NUMBER: GB0114517.6
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 60
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 16, Application US/09274163E; Patent No. US20020137897A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/10731984; Publication No. US20040175381A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                  Best Local Similarity 92.9
Matches 105; Conservative
                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-274-163E-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-731-984-35
                                                                                                                                                                                          US-10-353-708-1
                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kornaga, Tadeusz
APPLICANT: Ringler, Douglas
APPLICANT: Cobbold, Stephen
APPLICANT: Winsor-Hines, Dawn
TITLE OF INVENTION: Compositions and Methods of Tolerizing a Primate to an Antigen
FILE REFERENCE: 695458-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESGVPDRFSGSGSGTDFTLTISSLOAEDVAVYYCOOYYSTPPMFGGGTKVEIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQOYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ze-41;
~ham 6; Indels
                                                                                                                                                                    APPLICANT: RAD, FALLELS
APPLICANT: KOTTAGGA, Taddeusz
APPLICANT: Kornaga, Taddeusz
APPLICANT: Cobbold, Stephen
APPLICANT: Cobbold, Stephen
TITLE OF INVENTION: TRX1 and Uses Therefor
TITLE REPRENCE: 69548-59
CURRENT APPLICATION NUMBER: US/10/171,452A
CURRENT PELING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR FILING DATE: 2002-04-18
PRIOR PILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-10-19
PRIOR FILING DATE: 2002-10-19
PRIOR FILING DATE: 2002-10-19
PRIOR FILING DATE: 2001-09-20
PRIOR PILING DATE: 2001-09-20
PRIOR PILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 60

**NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 92.5%; Score 546; DB Best Local Similarity 92.9%; Pred. No. 2e-4 Matches 105; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/353,708
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: USI0/11,452
PRIOR FILING DATE: 2002-06-13
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US60/373,471
PRIOR PLILNG DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR APPLICATION NUMBER: US60/373,470
PRIOR PLILNG DATE: 2002-10-19
PRIOR PLILNG DATE: 2002-10-19
PRIOR PLILNG DATE: 2001-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/10353708
; Publication No. US20030219403A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Frewin, Mark
APPLICANT: Waldmann, Herman
APPLICANT: Gorman, Scott
APPLICANT: Hale, Geoff
APPLICANT: Rao, Patricia
APPLICANT: Roo, Patricia
     US20030108518A1
                                                                               Waldmann, Herman
Gorman, Scott
Hale, Geoff
Rao, Patricia
                                                      APPLICANT: Frewin, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-171-452A-1
                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
```

8 ò

```
BRASLAWSKY, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-700-632-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR 60
                                                                                                                                                                                                                                                                               1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                              61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGGGTKLEIK 113
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GLASER, SCOTT
APPLICANT: GLASER, SCOTT
APPLICANT: MAGE, Teung-Horng
APPLICANT: HANG, Teung-Horng
APPLICANT: HOPP, Jennifer
TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
FILE REFERENCE: 1DV-001
FILE REFERENCE: 1DV-001
CURRENT APPLICATION NUMBER: US/10/880,028
CURRENT FILING DATE: 2003-06-28
PRIOR APPLICATION NUMBER: 60/508810
PRIOR APPLICATION NUMBER: 60/508810
PRIOR APPLICATION NUMBER: 60/51531
PRIOR APPLICATION NUMBER: 60/515351
PRIOR APPLICATION NUMBER: 60/515351
PRIOR FILING DATE: 2003-10-28
PRIOR FILING DATE: 2003-10-30
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.2%; Score 544; DB 18; Length 113; 92.0%; Pred. No. 2.6e-41; tive 4; Mismatches 5; Indels
                                                                                                                                                                                         Query Match 92.2%; Score 544; DB 9; Length 113; Best Local Similarity 92.0%; Pred. No. 2.6e-41; Matches 104; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29, Application US/10880028 Publication No. US:0050163782A1 GENERAL INFORMATION: APPLICANT: BRASLAWSKY, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/10880320
Publication No. US20050163783A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1995-01-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
                                                                                                     TYPE: PRT

ORGANISM: Escherichia coli

US-09-274-163E-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-10-880-028-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-880-028-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-10-880-320-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
GENERAL INFOGUEDATION:

GENERAL INFOGUEDATION:

TITLE OF INVENTION: ANTI-CD33 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID

TITLE OF INVENTION: LEUKEMIA USING THE SAME
TITLE OF INVENTION: LEUKEMIA USING THE SAME
TITLE OF INVENTION: LEUKEMIA USING THE SAME
CURRENT APPLICATION NUMBER: US/10/700,632

CURRENT FILING DATE: 2003-11-07

NUMBER OF SEQ ID NOS: 94

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

SEQ ID NO 70

LENGTH: 114

TYPE: PRT

GRANISM: Mus musculus

US-10-700-632-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPQQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVMIQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIVMTQSPDSLAVSLGERATIICKSSQSILYSSNNKNYLGWYQQKPGQPPKLLIYWASTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 'ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYXCQQYYSTPYSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ESGVPARFSGSGSGTDFTLTINSLQAEDVAVYYCQQYYSTPRSFGQGTMVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                          Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.2%; Score 544; DB 17; Length 114; 92.0%; Pred. No. 2.6e-41; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.2%; Score 544; DB 18; Best Local Similarity 92.0%; Pred. No. 2.6e-41; Matches 104; Conservative 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic construct US-10-880-320-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 70, Application US/10700632; Publication No. US20050118183A1
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
YANG, Tzung-Horng
HOPP, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
```

```
RESULT 15
US-10-345-618-11
Sequence 11, Application US/10345618
Publication No. US2003014848431
GENERAL INFORMATION:
APPLICANT: Koengen, Frank
APPLICANT: Teatlinton, David M.
APPLICANT: Treutlelin, Herbert R.
APPLICANT: Treutlelin, Herbert R.
TILE REFERENCE: 13474
CURRENT PILLOR DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR PILLING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 155
TYPE: PRT
CORRANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
92.2%; Score 544; DB 14; Length 155;
Best Local Similarity 92.0%; Pred. No. 3.5e-41;
Matches 104; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:Kappa; OTHER INFORMATION: protein sequence US-10-345-618-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

Search completed: November 16, 2005, 23:05:43 Job time : 70.3787 secs

Н

```
Add05401 Anti-MUCI
Add08499 Human ant
Add02412 Human ant
Aav025412 Human ant
Aav91284 Anti-HIV
Aav91848 Anti-Gpl2
Aay5189 Anti-Gpl2
Aay51892 Antino aci
Add2271 Human het
Add22241 Human het
Add22245 Kuman ant
Add22245 Kuman ant
Add32575 Human het
Add38275 Human het
Add38275 Human het
Add38275 Human net
Add28275 Human ant
Add28246 Human ant
Add28246 Human ant
Add28246 Human ant
Add28246 Human ant
Add38275 Human ant
Add392780 Anti-Gpl2
Aay98247 Anti-Gpl2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adc99797 Anti-huma
Add05401 Anti-MUC1
                                                                                                   ; Search time 61.3676 Seconds (without alignments) 674.351 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                           US-10-660-357A-26
562
1 DIOMIQSPSSLSASVGDRVT......CQQYDTLPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                   2105692
              version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                  2105692 seqs, 386760381 residues
                                                                                                   November 16, 2005, 21:35:48
                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC99797
ADD05401
ADD05401
ADP22412
AAV02534
AAV982139
AAX9821892
AAX92139
AAX21882
ADD28243
ADD28248
ADD28271
ADD28275
ADD28275
ADD28275
ADD28275
ADD28275
ADD28275
AAX911880
AAX911880
AAX911880
AAX911880
AAX911880
AAX911880
AAX911880
AAX911880
                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                               Geneseq_16Dec04:*
    geneseqD1980s:*
    geneseqD280s:*
    geneseqD200s:*
    geneseqD200s:*
    geneseqD200s:*
    geneseqD200s:*
    geneseqD200s:*
    geneseqD200s:*
              GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                             Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.00000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.0000

0.00000

0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ģ
```

Adp22224 Adf90904 Ad60452 Ab010817 Adn4187 Adr40134 Adr40341 Abg11908 Aaw86804 Aaw86804 Aaw76275 Abu10148 Abu10148	Ø				light chain protein SEQ	/; heavy; light chain variable pancreatic; colorectal tumour; neoplasia; colorectal; breast;									odies, useful for treating on of MUC18 in a patient, (es.		ates to a novel isolated monoclonal antibody comprising chain amino acid or a heavy or light chain variable antibody binds to MUC18. The monoclonal antibody of the	vicy and may be useful the expression of MUCI ally melanoma, oesophag	reatic or colorectal tumours, carcinomas, particularly cervical inomas and cervical intraepithelial neoplasia and cancers includicectal, breast or lung cancer, as well as other malignancies. The cectal, the control of the cancer, and well as other malignancies. The control of the cancer, the cancer and cancer and cancer and cancer and cancer and cancer and cancer the cancer and cancer the cancer and canc
ADP22224 ADF990904 ADF990904 ADF9090904 ADF90908177 ADF9081164 ADF8011908 AAR81329 AAR86804 AAR86804 AAR86804 AAR86804 AAR96804 AAR96833 AAY78328 AAY78328 AAY78328 AAY78328 AAY78328 AAY78328 AAY78328 AAY78328 AAY78328	ALIGNMENT	107 AA.			antibody 1	oclonal antibody; ; oesophageal; pan intraepithelial ne					ъ.				monoclonal antibodi ted with expression other malignancies.	; English.	novel isola cacid or a inde to MUC	static acti siated with s, specific	nours, carcinom raepithelial ne cancer, as well
∞ − ∞ ∙ ∞ ⋅ 0 ∞ 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		in;		3	nal	nal sopl aepj				1583	462991				ocle with	78pp;	A min y	yto: 8800 our:	int.
1039 1039 1039 1007 1007 1007 1007 1007) }	protein		t entry)	monoclonal	monoclonal ioma; oesop ia; intraep n.				2002WO-US041581	n	<u>ن</u>		ώ	118 monoc tiated wi	26;	tes to	tion a	orectal rvical t or lu
88888888888888888888888888888888888888	;	standard;		(firs	MUC18 m	TUC18 mo melanom cinoma; human.	<i>:</i>	-A2.			2001US-0	NIX INC		71113/5 19799.	anti-MUC18 on associat ncers, and	ID NO	n rela ight c	condi	ic or colcas and cer
0 4 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		JT 1 9797 ADC99797 Bta	, 16166	-JAN-2004	-human	anti-human MUC18 mone cytostatic; melanoma cervical carcinoma; : lung cancer; human.	o sapiens	WO2003057838	-JUL-2003.	-DEC-2002;	-DEC-2001;	GE-) ABGENIX	as J;	WPI; 2003-587 N-PSDB; ADC99	human conditi ors, ca	aim 3; SEQ	0 6	encion de isease or 1 surface	pancreatic c carcinomas a colorectal,
00000000000000000000000000000000000000	2		ADC99	01-	Anti	anti cytor cerv lung	Ношо	WO2	17-	-92	28-	(ABGE	Gudas	MPI N-PI	New or o	Cla	The dom	a dis	pan car col
		RESUI ADC99	¥¥!	1	X E	X M M M M	X 8 3	Y A X	6 X	P X	1 K X	PA XX	PI	883	E E E E	AA PS	\$888	888	8888

2.1e-34;

SXS

셤 ò 셤

à

```
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gudas J;
                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                        ઠ
                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has overstant and an be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting cumour growth (e.g. melanoma, lung tumour or tumour metaersais), inhibiting call invasion associated with melanoma, or increasing survival of an animal having a metaetatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                                                          9
                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
                                                                                                                                                                                   DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-MUC18 antibody light chain variable region protein, SEQ ID No 26.
                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
                                                                                                                   Gaps
                                                                                                                   ö
                                                                                                                                                                                                                                                           RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
                                                                            Length 107;
                                                                                                                                                                                                                                         RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVBIK 107
                                                                                                                   Indels
                                                                          100.0%; Score 562; DB 7;
100.0%; Pred. No. 2.1e-34;
iive 0; Mismatches 0;
  light chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 26; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                               ADD05401 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-2002; 2002WO-US041582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-2001; 2001US-0346460P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein of the invention
                                                                                              Best Local Similarity 100.
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gudas J, Bar-Eli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-577496/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metastatic tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-577496
N-PSDB; ADD05403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003057006-A2
                                       Sequence 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-2004
                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                    ADD05401;
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                            ADD05403
                                                                                                                                                                                                                                                                                                                                       RESULT
```

DB 7; Length 107;

100.0%; Score 562;

Query Match

```
ö
                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a method for inhibiting cell proliferation associated with expression of NUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                     9
                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIOMIQSPSSLSASVGDRVIITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
                                                                                                                       1 DIOMIQSPSSLSASVGDRVTITCQASQDINNYLAWYQQKPGKAPKLLIYDASNLETGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
                                                                                     1 DIOMTOSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell proliferation inhibition, MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; light chain; human.
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 0
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPSGSGSGTDFTFISGLOPEDIATYYCOOYDTLELFFGGGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
                                                                                                                                                                                                                                61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVBIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human anti-MUC18 monoclonal antibody light chain #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 562; DB 7;
100.0%; Pred. No. 2.1e-34;
iive 0; Mismatches 0;
                                      ö
100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 26; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      ADF09839 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-DEC-2001; 2001US-0346414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2002; 2002WO-US041580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 107; Conservative
                                    Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-598367/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABGE-) ABGENIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADF09841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003057837-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

ന

```
anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthitic; antibacterial; antiantial antibacterial; antiantial antial cancer; ovarian cancer; Indiader cancer; unq cancer; aliablastoma; stomach cancer; and antial cancer; endometrial cancer; colon cancer; pancreatic cancer; prostrate cancer; immuno-mediated inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis, glomerulonephritis; atherosclerosis; psoriasis; restenosis; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; anorexia; multiple sclerosis.
                                                                                                                                                                                                                                         Human anti-TNFa antibody light chain variable region SEQ ID NO:318.
                                                                                                                                                                                                                                                                                                            human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee
Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
                                   ADP22412 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-2003; 2003WO-US038281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-2002; 2002US-0430729P
                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-480601/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004050683-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fumor Necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domo sapiens.
                                                                                                                                                                         09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2004
                                                                                                      ADP22412;
ADP22412
ADP22412
ADP22412
ADP22412
ADP2ADP2
AXX ADP2
XXX ```

Buch \* recombinant human monoclonal antibody that specifically binds to nor Necrosis Factor-alpha, useful for treating neoplastic disease such cancers, or immuno-mediated inflammatory diseases such as rheumatoid arthritis

Example 10; SEQ ID NO 318; 213pp; English.

The present invention describes a human monoclonal antibody (1) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined 5 amino acid sequence (81, ADP22417) or (82, ADP22421);

and (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (83, ADP2242424). Also described: (1) assaying (M1) the level of TNFa in a patient sample, comprising contacting with (1), and detecting the level of binding between the antibody and TNFa in the sample; (2) a composition comprising the antibody or its functional fragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (1); antibacteriosclerotic, antiarthitic, antiarteriosclerotic, antiarthitic, antiarteriosclerotic, antiarteriosclerotic, antiartened (2); antiarteriosclerotic, antiartened (2); antiartened (2); antiartened (2); antiartened (2); antiartened (2); antiartened (3); antiartened (3) stomach cancer, endometrial cancer, kidney cancer, colon cancer,

```
ö
 AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain. light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese
 9
 9
pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory diseases such as rheumatoid arthritis, glomerulonophritis, atherosclerosis, psortasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the exemplification of the present invention.
 Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMIQSPSSLSASVGDRVIITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 0; Gaps
 Antibody; adipocyte; heavy chain; light chain; obesity; fat; heart disease; complementarity determining region; CDR.
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Length 107;
 Score 530; DB 8; Length 10 Pred. No. 4.9e-32; 4; Mismatches 3; Indels
 Anti-adipocyte monoclonal antibody light chain, FAT 22.
 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 Claim 1; Page 113-114; 182pp; English.
 AAU02534 standard; protein; 108 AA
 Vaughan TJ;
 11-OCT-2000; 2000WO-GB003900.
 99US-0158812P.
 Query Match
Best Local Similarity 93.5%;
Matches 100; Conservative
 (first entry)
 Edwards BM, Main SH,
 WPI; 2001-282031/29.
N-PSDB; AAS03434.
 Sequence 107 AA;
 WO200127279-A1.
 Homo sapiens.
 12-OCT-1999;
 29-AUG-2001
 19-APR-2001.
 AAU02534;
 diseases
 RESULT 5
 AAU02534
 888888888888
 ઠે
 셤
 ð
 셤
```

ö

62 9

SXSSS

g

8

8

8

```
using primers specific for heavy and light chain variable regions. The amplification products were inserted into a dicistronic vector to produce a library of fragments. E.coli XL1 Blue cells were transformed with the library. Filamentous phage were produced which expressed the MAD regions on their surface. Panning with gpl20 and gp41 resulted in the recovery of immunoreactive clones. The light chain VK region sequence AARS4319 neutralises HIV1 gpl20. (Updated on 25-MAR-2003 to correct PN field.)
 Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in passive immuno:therapy and detection of HIV infection.
 Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone; virus infectivity assay; precursor gp160; immunocompetence; human; anti-HIV antibody; detection; HIV infection.
 3 OMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 Gaps
 ;
 Length 107;
 63 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Score 525; DB 2; Length 10.
Pred. No. 1.2e-31;
 VL region of HIV neutralising MAb, clone B26.
 4; Mismatches
 Location/Qualifiers
 Ā
 Ŗ
 AAW01287 standard; protein; 107
 Lerner
 /label= CDR3
96..107
/label= FR4
 93.4%;
 94US-00276852
 22. .32
/label= CDR1
 48. .54
/label= CDR2
 33. .47
/label= FR2
 55. .86
/label= FR3
 l. .21
/label= FR1
 (first entry)
 Ouery Match
Best Local Similarity 94.3.
Local Similarity 94.3.
Local Similarity 94.3.
 (SCRI) SCRIPPS RES INST
 CF,
 WPI; 1996-179601/18.
 Barbas
 Sequence 107 AA;
 WO9602273-A1
 18-JUL-1994;
 Homo sapiens
 29-JAN-1997
 DR,
 01-FEB-1996
 AAW01287;
 Burton
 Region
 Region
 Region
 Region
 Region
 Region
 Region
 RESULT 7
 Key
 AAW01287
 셤
 g
 ઠે
 ö
 Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
 9
 9
 Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope; neutralisation; monoclonal antibody; kappa light chain; variable region; framework; complementarity determining region.
 patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intraabdominal fat associated with heart disease
 or
 DIQLTQSPSSLSASVGDRVTITCQASQDISNYLMWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 New human monoclonal antibodies neutralising HIV - react with gp120 gp41 and nucleic acid encoding them, useful for in vivo or in vitro diagnosis and for passive immuno-therapy.
 ö
 Anti-HIV gp120 immunoglobulin light chain variable region B26
 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Score 527; DB 4; Length 108; Pred. No. 8.3e-32; 5; Mismatches 3; Indels
 Location/Qualifiers
 AARS4319 standard; protein; 107 AA
 Š
 Example; Page 192; 248pp; English.
 Lerner
 88. .95
/label= CDR3
96. .107
/label= FR4
 CDR2
 93.8%;
 49. .55
/label= CDR2
56. .87
/label= FR3
 93WO-US009328
 92US-00954148
 CDR1
 FR2
 .. .21
'label= FR1
 (first entry)
 Local Similarity 92.5
les 99; Conservative
 22. .33
/label= (
 34. .48
/label= .
 (SCRI) SCRIPPS RES INST
 Barbas CF,
 (revised)
 WPI; 1994-135516/16.
 Sequence 108 AA;
 30-SEP-1992;
 30-SEP-1993;
 Homo sapiens
 WO9407922-A1
 25-MAR-2003
10-NOV-1994
 14-APR-1994
 Burton DR,
 61
 AAR54319;
 Query Match
 Region
 Region
 Region
 Region
 Region
 Region
 Region
 RESULT 6
AAR54319
 že
Š
```

S

```
second polynucleotide encoding a light chain immunoglobulin amino acid sequence; (b) inscrting the first and second polynucleotide sequences into a host cell; (c) maintaining the host cell in conditions which allow the amino acid sequences encoded by the polynucleotides to be expressed in the host cell; and (d) isolating the antibody comprising the heavy and light chain immunoglobulin amino acid sequences from the host cell; The arti-HIV gp-120 monoclonal antibody is used for providing passive anti-HIV gp-120 monoclonal antibody is used for providing passive carti-HIV gp-120 monoclonal antibody is used for providing passive anti-HIV gp-120 monoclonal antibody is used for patients to reduce the likelihood and/or severity of HIV-induced disease and to patients who are already HIV-infected. The antibodies are used for neutralising field isolates which provides information about the meunocompetence of an immune response in HIV patients, for detecting HIV in a biological fluid or tissue sample e.g. by radioimmunosssay, for producing anti-idiotypic antibodies which can be used for active immunisation and to screen human monoclonal antibodies to identify those with the same binding specificity and to monitor the course of HIV present in the body or in body fluides by immunosssay. The anti-HIV gp-120
 ö
 The sequences given in AAW01261-92 represent the light chain variable regions (VL) of a series of monoclonal antibodies (MAb's) which are immunoreactive with HIV glycoprotein gp120 and are capable of neutralising HIV. This sequence represents the sequence of the JK4 gene clone, B26. A MAb containing this VL sequence has the capacity to reduce HIV infectivity titre in an in vivo virus infectivity assay by 50 % at a concentration of less than 700 ng of antibody/ml, and binds mature gp120 preferentially over the precursor gp160. The MAb may be used for detection of HIV infection
 62
 9
 3 QMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 Gaps
 ö
 Anti-gp120 antibody light chain variable region from clone b26
 Antibody; anti-HIV monoclonal antibody; glycoprotein-120; human immunodeficiency virus type 1; HIV-1; infectivity titre; passive immunotherapy; reduce severity; HIV-induced disease; immunocompetence; active immunisation.
 Score 525; DB 2; Length 107;
Pred. No. 1.2e-31;
4; Mismatches 2; Indels
 63 SGSGSGTDFTFTISGLQPEDIATYXCQQXDTLPLFFGGGTKVEIK 107
 SGSGSGTDFTFISSLQPEDIATYXCQQYDNLPLTFGGGTKVEIK 105
 AAY98248 standard; protein; 107 AA.
 Lerner RA;
 Example, Fig 11; 366pp; English
 99AU-00048754.
 99AU-00048754.
 93.4%;
 04-JUL-2000 (first entry)
 99; Conservative
 (SCRI) SCRIPPS RES INST.
 Burton DR, Barbas CF,
 WPI; 2000-246867/22
 Best Local Similarity
 Sequence 107 AA;
 Homo sapiens
 16-SEP-1999;
 16-SEP-1999;
 AU9948754-A.
 17-FEB-2000
 AAY98248;
 Query Match
 Matches
 RESULT AAY9824
 8X0000000000X8
 g
 음
 ઠ
 ઠ
```

monoclonal antibodies are encoded by a human polynucleotide sequence and when used in vivo for disgnosis and immuncherapy of HIV-induced disease reduce the problems of significant host immune response to the antibodies associated with monoclonal antibodies of xenogeneic or chimeric

```
ö
 62
 9
 Novel human monoclonal antibodies which immunoreact with and neutralize human immunodeficiency virus useful for treating HIV infections.
 3 QMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise; reduce HIV infection; diagnosis; immunotherapy; HIV induced disease; glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 0; Gaps
 Anti-gp120 antibody light chain variable region from clone b26.
 93.4%; Score 525; DB 3; Length 107; 94.3%; Pred. No. 1.2e-31;
 61 SGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIK 105
 63 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVBIK 107
 2; Indels
 4; Mismatches
 AAY95139 standard; protein; 107 AA
 Ŗ,
 Example 9; Fig 11; 366pp; English.
 99AU-00048756
 99AU-00048756
 30-JUN-2000 (first entry)
 99; Conservative
 (SCRI) SCRIPPS RES INST
 Barbas CF,
 WPI; 2000-293393/26.
 Best Local Similarity
Sequence 107 AA;
 16-SEP-1999;
 16-SEP-1999;
 Homo sapiens
 AU9948756-A
 Burton DR,
 Query Match
 Matches
 AAY95139
 g
 B X 1 1 X B X B X B X B X B X B X X B X X B X
 셤
 ઠે
```

This sequence represents a fragment of the antibodies of the invention. The invention relates to the production of an anti-HIV (human immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable of reducing an HIV infectivity titre in an in vitro virus infectivity assay by 50% at a concentration of less than 70 mg/ml. The method for the production of the antibody comprises: (a) providing a first polynucleotide encoding a heavy chain immunoglobulin amino acid sequence (which does not comprise the sequence represented by AAY99206) and a

Human neutralizing monoclonal antibodies to human immunodeficiency virus (HIV) used for providing passive immunotherapy to HIV are specific for

Example 9; Fig 11; 374pp; English.

glycoprotein-120

```
immunodeficiency virus types 1 (HV-1) antibody. The invention relates to a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV mature glycoprotein ppl20 preferentially over HIV precursor glycoprotein ppl20 preferentially over HIV precursor glycoprotein ppl20 preferentially over HIV precursor glycoprotein in vitro virus infectivity assay by 50%, at a concentration of less than in vitro virus infectivity assay by 50%, at a concentration of less than in vitro virus infectivity assay by 50%, at a concentration of less than in vitro virus infectivity assay by 50%, at a concentration of less than in vitro virus infectivity assay by 50%, at a concentration of less than in vitro virus infectivity as eagents for the diagnosis and immunocompetence of an immune response in HIV infected patients. The immunocompetence of an immune response in HIV infected patients. The immunocompetence of an immune response in HIV infected patients. The immunocompetence of an immune response in HIV infected patients which can be used to screen human monoclonal antibodies to identify whether the antibody has the same binding specificity as the antibodies of the HIV gp120 and gp41 glycoproteins, thus increasing the availability of new immunotherapeutic human monoclonal antibodies. A major advantages of the monoclonal antibodies derives from the fact that they are encoded by a
 human polynucleotides sequence. Thus in vivo use of the monoclonal antibodies for diagnosis and immunotherapy of HIV induced disease greatly reduces the problems of significant host immune response to the passively administered antibodies which is a problem commonly encountered when monoclonal antibodies of xenogeneic or chimeric derivation are utilized. An additional major advantage of the monoclonal antibodies described derives from the fact that they immunoreact with a unique determinant present on mature HIV glycoprotein gpl20. This class of antibodies is particularly effective at neutralising field isolates of HIV
 62
 1 ELTQSPSSLSASVGDRVTITCQASQDISNHLNWYQQKPGKAPKLLIYDASNLETGVPSRF 60
 Prostate-specific antigen; PSA; anti-chymotrypsin; ACT; antibody; diagnostic assay; PSA-ACT; prostate cancer; tumour; immunotherapy; ITA7.
 3 QMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 Gaps
 ..
0
 present sequence represents a fragment of an anti-human
 93.4%; Score 525; DB 3; Length 107; 94.3%; Pred. No. 1.2e-31; ive 4; Mismatches 2; Indels
 SGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIK 105
 63 SGSGSGTDFTFTISGLOPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 /label= unknown
/note= "encoded by NAG"
 Amino acid sequence of antibody ITA7
 Location/Qualifiers
 AAY21882 standard; protein; 241 AA.
 (BOEF) BOEHRINGER MANNHEIM CORP.
 98EP-00122546.
 97US-0067428P.
 (first entry)
 99; Conservative
 Local Similarity
 Sequence 107 AA;
 Misc-difference
 01-DEC-1998;
 03-DEC-1997;
 Homo Bapiens
 24-SEP-1999
 EP934953-A2
 11-AUG-1999
 AAY21882;
 Query Match
 Matches
 AAY21882
рp
 ò
 g
 8
```

```
prostate-specific antigen (PSA) and anti-chymotrypain (ACT), and has an affinity for the complex which is at least 10 fold higher than the affinity for the complex which is at least 10 fold higher than the affinity for either PSA or ACT alone. The antibody is used in diagnostic assays to detect PSA-ACT alone. The antibody is used in diagnostic compared to the levels in patients suffering from prostate cancer compared to the levels in patients with benign or no growths in the prostate. Therefore detection of PSA in complex with ACT is useful for the early detection of prostate tumours, by distinguishing between benign and malignant conditions of the prostate as well as for the management of patients with prostate cancer, such as the disclosure of metastasis and the monitoring of the PSA levels after treatment. The antibodies may also be used in immunotherapy, affinity chromatography and isolation or purification of PSA-ACT. Unlike prior art antibodies which bind to PSA-ACT complexes but may also bind PSA or ACT alone, the present antibody is specific for PSA-ACT alone. Diagnostic assays using the antibodies are incore accurate in diagnosing prostate cancer as they only detect the cintact complex of PSA-ACT. Sequences AAV21880-884 represent specific examples of antibodies directed against PSA-ACT. The present sequence represents the amino acid sequence of antibody ITA7
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 human heterodimeric antibody; human; antibody; binding affinity; protective antigen; Bacillus anchracis; anchrax infection; cell recept edema factor; lethal factor; virucide; antibacterial; immunotherapy; anti-toxin; anti-infective; anthrax; botulinum; smallpox; verexelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
 Gaps
 Human heterodimeric antibody light chain kappa region SEQ ID NO:49.
 The invention relates to an antibody that binds a complex between
 New anti-complex antibody useful for diagnosing prostate cancer,
 1;
 Length 241;
 61 RESGSGSGTDFTFTISGLQPEDIATYXCQQYDTLPLTFGGGTKVEIK 107
 RFSGSGGTDFTFTISSLQPEDIATYYCQQYDNLP-TFGQGTKVEIK 240
 Indels
 93.1%; Score 523.5; DB 2; 95.3%; Pred. No. 3.1e-31; ive 1; Mismatches 3;
 Claim 27; Page 23-24; 42pp; English.
 ADD28271 standard; protein; 113 AA
 11-FEB-2002; 2002US-0356086P.
29-APR-2002; 2002US-0376408P.
27-SEP-2002; 2002US-0414053P.
 11-FEB-2003; 2003WO-US004206
 15-JAN-2004 (first entry)
 Conservative
Winter GP, Mahoney W,
 WPI; 1999-432068/37.
 Query Match
Best Local Similarity
Matches 102; Conserv
 N-PSDB; AAX86938
 Sequence 241 AA;
 WO2003076568-A2
 Homo sapiens.
 18-SEP-2003
 Synthetic.
 ADD28271;
 RESULT 11
 셤
 ð
 셤
```

```
Matches
 RESULT 13
 g
 8
 ð
 The present invention describes a human heterodimeric antibody (I) (fragment) having a binding affinity of at least 1x10-8 M to the protective antigen of Bacillus anthracis or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to cell receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities, and can be used in immunotherapy. The antibacterial activities, and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as anthrax, botulinum, smallpox, Venezuelan expense of the compalance represents a human heterodimeric antibody light chain kappa region amino acid sequence, which is used in the exemplification of
 New human heterodimeric antibodies or their antibody fragments, useful as anti-toxins or anti-infectives with respect to infective agents, e.g. anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 9
 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS 62
 monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic; Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic; Vasotropic; Immunosuppressive; Neuroprotective; neoplastic; inflammatory condition; cancer; arthritis; multiple sclerosis; anti-MCP-1; heavy chain; light chain.
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Ahluwalia K;
 ..
0
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Query Match 93.1%; Score 523; DB 7; Length 113; Best Local Similarity 93.5%; Pred. No. 1.7e-31; Matches 100; Conservative 3; Mismatches 4; Indels
 Liang ML,
 Human anti-MCP-1 variable region light chain #14.
 Haak-Frendscho M, Foord O,
 Claim 9; SEQ ID NO 49; 67pp; English.
 ADK52350 standard; protein; 152 AA
25-NOV-2002; 2002US-0428807P.
 19-AUG-2003; 2003WO-US026232
 19-AUG-2002; 2002US-0404802P
 20-MAY-2004 (first entry)
 (ALEX-) ALEXION PHARM INC
 the present invention
 Bowdish KS, Wild MA;
 WPI; 2003-722327/68.
 (ABGE-) ABGENIX INC
 Sequence 113 AA;
 WO2004016769-A2
 Homo sapiens
 26-FEB-2004
 Nile virus.
 Gudas JM,
Bhakta S;
 ADK52350;
 요
 ð
```

```
The present invention relates to a human monoclonal antibody that binds to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful for the preparation of a medicament useful for treating neoplastic or inflammatory conditions. The neoplastic disease is selected from breast cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer, pancreatic cancer or prostrate cancer. He inflammatory condition is selected from rheumatoid arthritis, glomerulonephritis, atherosoclerosis, psoriasis, restenosis, autoimmune disease or multiple sclerosis. The antibodies are also useful for diagnosing the above diseases. It is also useful for the determining the level of MCP-1 and MCP-1 family members in patient samples. The present sequence represents a human anti-MCP-1 variable region light chain sequence.
 ö
 9
 9
 New human monoclonal antibody that binds to monocyte chemo-attractant protein-1 and is immobilized on an insoluble matrix, useful for diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer, rheumatoid arthritis or psoriasis.
 1 DIQMIQSPSSLSASVGDRVIITCQASQDITTYLNWYQQKPGKAPKLLIYDASNLEIGVPS
 1 DIOMIQSPSSLSASVGDRVITITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 human heterodimeric antibody; human, antibody; binding affinity; protective antigen; Bacillus anthracis; anthrax infection; cell recept edema factor; lethal factor; virucide; antibacterial; immunotherapy; anti-toxin; anti-infective, anthrax; botulinum; smallpox; Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
 Gaps
 Human heterodimeric antibody light chain kappa region SEQ ID NO:21
 ö
 61 RESGSGSGTDFTFISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPITFGGGTRLEIK 107
 Claim 2; SEQ ID NO 56; 154pp; English.
 ADD28243 standard; protein; 164 AA
 11-FEB-2003; 2003WO-US004206.
 2002US-0356086P.
2002US-0376408P.
2002US-0414053P.
 25-NOV-2002; 2002US-0428807P.
 15-JAN-2004 (first entry)
 (ALEX-) ALEXION PHARM INC.
 Wild MA;
WPI; 2004-203794/19.
N-PSDB; ADK52349.
 Best Local Similarity
 Sequence 152 AA;
 WO2003076568-A2
 11-FEB-2002; 2
29-APR-2002; 2
27-SEP-2002; 2
 Homo sapiens.
 18-SEP-2003
 Bowdish KS,
 Synthetic
 Query Match
```

```
New antibody or its antigen-binding fragment that specifically binds
 /note= "Light chain"
23. .130
 Location/Qualifiers
 Ä
 ADD93785 standard; protein; 236
 "CDR1"
 "CDR2"
 /note= "CDR3"
 27-MAR-2003; 2003WO-US009260
 29-MAR-2002; 2002US-0369044P
 92.7%;
 ٦,
 .119
 (first entry)
 Query Match
Best Local Similarity 92.5
Matches 99; Conservative
 . 78
 23. .236
 46. .119
 . 56
 Corvalan
 /note=
 /note=
 (SCHE) SCHERING CORP
 WPI; 2003-804302/75.
N-PSDB; ADD93784.
 (ABGE-) ABGENIX INC
 Misc-difference
 Misc-difference
 WO2003085089-A2
 Sequence 502 AA
 Greenfeder S,
 Homo sapiens
 29-JAN-2004
 16-OCT-2003
 ADD93785;
 83
 Peptide
 Protein
 Region
 Region
 Region
 RESULT 15
 Kev
 ADD93785
 858888888888
 염
 8
 요
 ò
 ö
 The present invention describes a human heterodimeric antibody (I) fragment) having a binding affinity of at least 1xx10-8 M to the protective antigen of Bacillus anthracis or a molecule involved in anthrax infection that blocks binding of the antigen or molecule to receptors, edema factor and lethal factor. (I) has virucide and antibacterial activities, and can be used in immunotherapy. The antibodies (I) are useful as anti-toxins or anti-infectives with respect to infective agents, such as anthrax, botulinum, smallpox, Venezuelan equine encephalomyelities virus (VEEV), or West Nile virus (WNV). The present sequence represents a human heterodimeric antibody light chain kappa region amino acid sequence, which is used in the exemplification of
 New human heterodimeric antibodies or their antibody fragments, useful as anti-toxins or anti-infectives with respect to infective agents, e.g. anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 62
 9
 for
 DIQMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 peptide sequences, useful
in eukaryotes.
 The invention relates to an artificial proprotein comprising three
 artificial proprotein; propeptide; protein engineering; antibody
 ö
 RESGSGSGTDFTFISGLQPEDIATYYCQQYDTLPLTFGGGTKVBIK 107
 Length 164;
 4; Indels
 Score 523; DB 7;
Pred. No. 2.4e-31;
3; Mismatches 4;
 protein construction protein #16.
 New artificial proprotein comprises three artificial multimeric protein engineering
 Example 2; SEQ ID NO 88; 244pp; English
 Claim 7; SEQ ID NO 21; 67pp; English
 (LARG-) LARGE SCALE BIOLOGY CORP.
 ADN97515 standard; protein; 502
 03-OCT-2003; 2003WO-US031420
 03-OCT-2002; 2002US-0415940P
 93.1%;
93.5%;
 (first entry)
 Conservative
 the present invention
 Edwards P;
 2004-330170/30.
 WPI; 2003-722327/68
 Local Similarity
 N-PSDB; ADN97514
 Sequence 164 AA;
 WO2004031362-A2
 Unidentified
 01-JUL-2004
 15-APR-2004.
 100;
 Nile virus.
 Artificial
 Reini SJ,
 n
 61
 ADN97515;
 Query Match
 Matches
 RESULT 14
 ADN9751
ID AD
 ద
 ò
 g
 ઠ
```

```
ö
peptide sequences: a first peptide sequence of interest, a propeptide sequence attached to the C-terminus of the first peptide sequence of interest, and a second peptide of interest attached to the C-terminus of the propeptide sequence. The artificial proprotein and polynucleotides are useful for artificial multimeric protein engineering, e.g. antibodies and antibody fragments in eukaryotes. This sequence corresponds to a protein used in the generation of the protein of the invention.
 09
 82
 23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYHQKPGKAPELLIYDASNLETGVPS
 1 DIQMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Monoclonal antibody; antibody; antiasthmatic; antiallergic; antiinflammatory; immunosuppressive; dermatological; gastrointestinal-gen.; antihelminthic; cytostatic; ophthalmological; bronchodilator; interleukin-5; human; gene therapy.
 ~
 /note= "Region specifically described in Claim 2"
 ;
0
 'note= "Region specifically described in Claim
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Indels
 Length
 Score 521; DB 8; Le
Pred. No. 9.3e-31;
2; Mismatches 6;
 2; Mismatches
 Monoclonal antibody 20.13.3 light chain.
 1. .22
/note= "Signal peptide"
```

interleukin-5, useful for diagnosing, treating or preventing a condition associated with undesired interleukin-5 activity, e.g. asthma or allergic

Claim 2; Page 26; 75pp; English

The present sequence is the protein sequence of the light chain of anticuman interlewin-5 (IL-5) human monoclonal antibody (MAD) 20.13.3 To obtain this 1964 MAD. XenoMice (TW) were immunised with human IL-5; obtain this 1964 MAD. XenoMice (TW) were immunised with human IL-5; obtain this 1964 MAD. XenoMice (TW) were immunised with human IL-5; spleen and/or lymph nodes were then fused with myeloma 9-X63-Ag8.653 or resents equence. Or nucleotides 1-707, 1102-1137, 126-1585, 1683-2002, 58-709, and I48-381 of it, are claimed and used in methods of the invention relates to antibodies or their antigen-binding crayments that specifically bind IL-5. Human anti-IL-5 antibodies are provided, including chimeric, bispecific, derivatised, single chain crathent. The invention also provides gene therapy methods using nucleic antibodies or private the appendication of displace therapy methods using nucleic creatment. The invention also provides gene therapy methods using nucleic creatment. The invention also provides gene therapy methods using nucleic creatment. The invention also provides gene therapy methods using nucleic caids encoding the heavy and/or light chain molecules that comprise the undealted IL-5 antibodies, and transgenic animals. The antibodies can be used to prevent or inhibit a condition or disorder characterised by undealted IL-5 antibodies, and transgenic animals. The antibodies and callergic rhinitis, allergic bronchopulmonary aspergillosis, hypercosinophilis, churg-Strauss syndrome, atopic dermatitis, presentionphilis, churg-Strauss syndrome, atopic dermatitis, presention of disease, eosinophilic gastroenterits, chimically hypercosinophilic myalage engles of simusitis, creaponse in a subject confluentivitis, by decreasing or inhibiting the infilitration of simusitis, creaponse in a subject confluentivitis, by decreasing or inhibiting the indicated event, such as eosinophilis activation, migration into the bloodstream, adhesion to confluention, airway hyperresponsiveness, pulmonary epithelial and servived al 

Sequence 236 AA;

Query Match 92.2%; Score 518; DB 7; Length 236; Best Local Similarity 93.5%; Pred. No. 7.8e-31; Matches 100; Conservative 1; Mismatches 6; Indels

Gaps ö 1 DIOMIOSPSSLSASVGDRVIITCOASODINNYLNWYQQKPGKAPKLLIYDASNLEIGVPS 60

23 DIQMTQSPSSLSASVGDRVTITCQASQDIINYLNWYQQKPGKAPKLLIYSASNLETRVPS 82

g

8

ò

61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPFGGGTKVEIK 107

83 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNHPLTFGGGTKVEIR 129

Search completed: November 16, 2005, 21:51:41 Job time : 62.3676 secs

THIS PAGE BLANK (COPTO)

```
kappa chain V r
kappa chain V J
kappa chain V r
kappa chain - h
kappa chain V J
kappa chain V r
kappa chain pre
kappa chain pre
kappa chain V r
kappa chain Pre
kappa chain Pre
kappa chain Z J
 kappa chain V-1
kappa chain V-1
kappa chain V-1
kappa chain V-1
kappa chain - h
kappa chain (BR
kappa chain V I
 kappa chain V-J
lambda chain V
kappa chain - h
 November 16, 2005, 21:37:48; Search time 12.7849 Seconds (without alignments) 805.260 Million cell updates/sec
 kappa chain V
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 US-10-660-357A-26
562
1 DIQMIQSPSSLSASVGDRVT......CQQYDTLPLTFGGGTKVBIK 107
 Description
 5.1.6
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 283416 segs, 96216763 residues
 version 5
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 SS2789
X1HUMG
X1HUMU
X1HUMU
X1HUMU
X20365
X40365
X40349
X1HULY
X340349
X1HULY
X36264
X1HULY
X36264
X
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 S40333
S36269
 840316
 GenCore (c) 1993
 seq length: 0
seq length: 200000000
 Query
Match Length DB
 Copyright
 PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 Title:
Perfect score:
 Scoring table:
 OM protein -
 Minimum DB
Maximum DB
 Database :
 Searched:
 Sequence:
 Run on:
 Result
 Š.
```

Agree chain V-I region (Ag) - human
C;Species: Homo sapiens (man)
C;Accession: A01861
R;Titani, K.; Shinoda, T.; Putnam, F.W.
J;Biol. Chem. 244, 3550, 1360, 1369
A;Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete f A;Reference number: A92047; MUID:69234734; PMID:4893682
A;Accession: A01861
A;Molecule type: protein
A;Residues: 1-108 <TIT>
A;Cross-references: UNIRROT:P01593
A;Note: the sequence of the C region, which has the Inv (3) marker, is also given C;Comment: This is a Bence Jones protein.
C;Comment: This is a Bence Jones protein.
A;Genetics:
C;Genetics:
A;Genetics: 20B:136264
A;Map position: 2012-2012

| 130 455 81.1 102 2 80134 |
|--------------------------|
|--------------------------|

```
요
 8
 셤
 ð
 Kilfury
Ig kappa chain V-I region (Roy) - human (tentative sequence)
C; Species: Homo sapians (man)
C; Species: Homo sapians (man)
C; Date: 24-Apr-1984 #sequence revision 02-Jul-1998 #text_change 09-Jul-2004
C; Accession: A91638; B94417; A01874; S02575
R; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 349, 1077-1080, 1967
A; Title: Die chemische Struktur von zwei Bence-Jones-Proteinen (Roy und Cum.) vom kappa-A; Reference number: A91638; MUID:68362076; PMID:5595110
A; Reference number: A91638
A; Molecule type: protein
A; Residues: 1-38, 'GPK', 42-108 < HIL>
A; Rosidues: 1-38, 'GPK', 42-108 < HIL>
A; Coss-references: UNIPROT: P01608
A; Coss-references: UNIPROT: P01608
A; Coss-reference of the C region, which has the Inv (1,2) marker, is also given R; Hillschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, A. Christen reading to residing 39 and 41
 A; Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable A; Reference number: 4410
A; Recession: $44118
A; Accession: Stating
A; Returns: preliminary
A; Molecule type: DNA
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer F;16-90/Domain: immunoglobulin homology <IMM>F;16-90/Domain: immunoglobulin homology <IMM>F;23-88/Disulfide bonds: #status experimental
 944118

19 kappa chain V-J region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C;Datession: 544118

R;Hawkins, RE.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K. submitted to the EMBL Data Library, March 1994
 ö
 1;
 9
 9
 9
 9
 DIOMTOSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS
 1 DIQMIQSPSSLSASVGDRVTSTCQASQDISNYLMWYQQKPGKAPKLLIXDASNLETGVPS
 DIOMTOSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 A;Cross-references: EMBL:Z31395; NID:g472972; PIDN:CAAB3270.1; PID:g940529
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hererotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
 Gaps
 Gaps
 ő
 2;
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLP--LTFGGGTKVEIK 107
 RFSGSGSGTDFTFTISSLOPEDIATYYCOOYDNLPPGVTFGPGTKVDIK 109
 RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK 107
 RESGSGSGTDFTFTISGLOPEDIATYYCOOYDTLPLTFGGGTKVEIK 107
 Length 110;
 Score 517; DB 1; Length 108;
Pred. No. 8.1e-38;
3; Mismatches 5; Indels
 4; Indels
 Score 515; DB 2;
Pred. No. 1.2e-37;
 3; Mismatches
 A; Contents: revisions to residues 39 and 41 A; Accession: B94417
 91.6%;
ilarity 91.7%;
Conservative
 Query Match
Best Local Similarity 92.5%;
Matches 99; Conservative
 A; Molecule type: protein
 Similarity
 A; Residues: 1-110 <HAW>
 100;
 Query Match
 Local
 g
 ò
 g
 8
 g
 g
 ò
```

```
A; Residues: 39;41 <HI2>
R; Stainer, V.; Chang, J.Y.
FRBS Lett. 222, 6-10, 1987
A; Title: Chemical modification of the carboxyl groups of protein substrates enhances their A; Reference number: 802572; MUID: 88005152; PMID: 3115831
C; Comments: annotation content of the district of their comments of their contents.
 A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp costal an immunoglobulin heterotetramer subunit subunits associate into law c;Complex: an immunoglobulin v region; immunoglobulin homology
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology v IMM>
F;16-90/Domain: immunoglobulin homology v IMM>
 R.Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A,Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Subg
A,Reference number: A91653; MUID:72189444; PMID:5028201
 AjCross-references: UNIPROT: P01594
AjNote: the C region of this chain has the Inv (3) marker
RjFehlhammer, H; Schiffer, M; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Steigle Biophys: Struct. Mech. 1, 139-146, 1975
AjTitle: The structure determination of the variable portion of the Bence-Jones protein PajReference number: A90729; MUID:77022433; PMID:1234024
AjContents: annotation; X-ray crystallography
AjNote: the structure of the V region was determined by molecular replacement methods using RjSteiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
 A,Title: Chemical modification of the carboxyl groups of protein substrates enhances thei
A,Reference number: S02572; MUID:88005152; PMID:3115831
 C.Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into land issulfide bonds; in some cases, such as IgA and IgM, the subunits associate into land; superfamily: immunoglobulin vegion; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology < IMM>
F;23-88/Disulfide bonds: #status predicted
 ö
 ö
 9
 9
 C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A91653; A01862; S02573
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS
 Gaps
 Gaps
 ö
 ö
 61 RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Query Match 89.9%; Score 505; DB 1; Length 108; Best Local Similarity 90.7%; Pred. No. 8.7e-37; Matches 97; Conservative 3; Mismatches 7; Indels
 Length 108;
 Indels
 Score 508; DB 1; Le
Pred. No. 4.8e-37;
 A;Contents: annotation
C;Comment: This is a Bence Jones protein.
 [g kappa chain V-I region (Au) - human
 90.4%;
 A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
 Query Match
Best Local Similarity 89.7
Matches 96; Conservative
 A, Accession: A91653
A, Molecule type: protein
A, Residues: 1-108 <SCH>
 A; Gene: GDB: IGKV1
 C;Genetics:
A;Gene: GDB:IGKV1
 C;Genetics:
```

ന

```
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Tille: Die Primaerstruktur einer kristsallinen monoklonalen Immunglobulin-L-Kette vom ke vollstaendige Aminosaeurseequenz des Proteins.
A;Reference numbor: A91663, MUID:6023758; PMID:809329
 Ajaccession: Ap1663
Ajmolecule type: protein
Ajrogalus: 1-108 cPAL>
Ajmolecule type: protein
Ajrogalus: 1-108 cPAL>
Ajmolecule type: protein
Ajmolecules: 1-108 cPAL>
Ajmolecules: 1-108 cPAL>
Ajmolecules: Lattmann, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Bjopp, O.; Lattmann, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Ajmolecular structure of a dimer composed of the variable portions of the Bence Ajmolecular: A9032; MUID: 76039968; PMID: 1182131
Ajmolecular sunnotation; X-ray crystallography, 2.0 angstroms
Cj.Comment: This is a Bence Jones protein.
 C. Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lan C; Superfamily: immunoglobulin V region; immunoglobulin homology
 Riscott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Quer J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus infl A;Reference number: 842263; MUID:92043792; PMID:1940382
 C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42263
 C.Species: Homo sapiens (man)
C.Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 09-Jul-2004
C.Accession: Apl663; Apl673
R.Palm, W.; Hilschmann, N.
 1 DIQMIQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQIPGKAPKLLIYEASNLQAGVPS
 DIOMIQSPSSLSASVGDRVIITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLEIGVPS
 A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: EMBL:M64855; NID:g185963; PIDN:AAA58925.1; PID:g185964
C;Genetics:
 Gaps
 ö
 ö
 61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
 61 RESGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEI 106
 Length 108;
 Length 117;
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;38-112/Domain: immunoglobulin homology <IMM>
 Score 486; DB 1; Length 10
Pred. No. 3.8e-35;
6; Mismatches 8; Indels
 Indels
 RESULT 8
KIHURE
Ig kappa chain V-I region (Rei) - human (tentative sequence)
 2.
 DB 2;
 86.3%; Score 485; DB 2;
96.8%; Pred. No. 5e-35;
iive 1; Mismatches
 F;23-88/Disulfide bonds: #status experimental
 Ig kappa chain V region (08) - human
 Query Match .86.5%;
Best Local Similarity 86.8%;
Matches 92; Conservative
 A;Cross-references: GDB:136264
 Local Similarity 96.8
les 92; Conservative
 :Keywords: heterotetramer
 A, Map position: 2p12-2p12
 A; Accession: S42263
 A, Gene: GDB: IGKV1
 A; Introns: 19/1
C; Superfamily:
 Query Match
 Genetics:
 Matches
 셤
 ð
 ઠે
 g
 Ig kappa chain (BRE) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: 139154 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: 139154 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
B;Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed A;Reference number: 139154 MUID:96003804; PMID:7568160
A;Reference number: 139154
A;Status: preliminary; translated from GB/EMBL/DDBJ
 ö
 9
 16 DIQMTQSPSSLSASVGDRVTITCQATQDIGNYLNWYQHKPGKAPNLLIYDASNLETGVPS 75
 9
 9
 9
 1 DIOMIQSPSSLSASVGDRVIITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLEIGVPS 60
 Ig kappa chain - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40365
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
 Nittle: Krivaenius, A. 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40365
A;Accession: S40365
A;Actaus: preliminary; translation not shown
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:X72475; NID:g441418; PIDN:CAA51143.1; PID:g441419
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 A;Cross-references: EMBL:U31344; NID:g944925; PIDN:AAA79238.1; PID:g944926 (S.Ugerfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-90/Domain: immunoglobulin homology <IMM>
 Gaps
 Gaps
 ö
 ö
 61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGGGTKVEIK 107
 61 RFSGSGSGTEYTFTISSLOPEDIATYYCOOYDDLPYTFGGGTKVEIK 107
 RFSGSGSGTDFTFISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 88.3%; Score 496; DB 2; Length 139; 88.8%; Pred. No. 6.7e-36; ive 1; Mismatches 11; Indels
 87.2%; Score 490; DB 2; Length 108; 88.8%; Pred. No. 1.7e-35; ive 4; Mismatches 8; Indels
 Best Local Similarity 88.8%;
Matches 95; Conservative
 95; Conservative
 Best Local Similarity
Matches 95; Conserv
 A; Molecule type: mRNA
A; Residues: 1-108 < RES>
 Query Match
 RESULT 7
 원
 g
 g
 셤
 ò
 ઠે
 8
 ઠ
 ଚ
 В
 8
```

ö

09 9

```
9
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLFTGVPS
Gaps
```

ö

```
(monoclonal striational autoantibody StrAB SA-1A) - human (fragme
 R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.

Bur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
 ö
 ö
 19 IQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVPSR 78
 9
 Ig kappa chain V-I region (Lay) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
 1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGRAPKLLIYAASSLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 CjAccession: $40349

RjKlein, R.; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3348-3271, 1993

Ajritle: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: $40312; MUID:94080891; PMID:8258341
 A,Molecule type: mRNA
A,Residues: 1-125 <KLE>
A,Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
 2 IQMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSR
 A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology < IMM>
 Gapa
 Gaps
 ;
0
 ô
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 FSGSGSGTDFTLTISSLQPEDFATYYCQQFNTYPLTFGGGTKVEIK 124
 FSGSGSGTDFTFTISGLOPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Length 108;
 Length 125;
 Query Match 84.7%; Score 476; DB 2; Length 12 Best Local Similarity 85.8%; Pred. No. 3.2e-34; Matches 91; Conservative 8; Mismatches 7; Indels
 Indele
 Match 85.2%; Score 479; DB 2; L. Local Similarity 86.0%; Pred. No. 1.5e-34; es 92; Conservative 7; Mismatches 8;
 61 RISGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP
 A;Status: preliminary; translation not shown
 A,Accession: B49047
A,Status: preliminary
A,Molecule type: nucleic acid
A,Residues: 1-108 <VIC>
 g kappa chain V region
 62
 79
 Query Match
 RESULT 14
 RESULT 13
 셤
 ⋩
 엄
 a
 ò
 d
 ð
 셤
 ò
 RESULT 11
PH0862
Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C.Accession: PH0862
R.Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A; Fitle: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype A; Reference number: PH0862; MUID:92078875; PMID:1660528
A; Recession: PH0862
A; Residues: 1-95 < MAN>
C; Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F; 1-23 /Region: framework I
F; 16-90/Domain: immunoglobulin homology < IMM>
F; 24-34 /Region: complementarity-determining I
 RESULT 10
S43528
Light and the second (018) - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: S43528
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que submitted to the EMBL Data Library, December 1991
A;Reference number: S43528
 ö
 ö
 82
 9
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS 82
 1 DIQMIQSPSSLSASVGDRVIITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIOMTOSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 0; Gaps
 Gaps
 ö
 Length 117;
 A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-112/Domain: immunoglobulin homology <IMM>
 Length 95;
 ch 85.2%; Score 479; DB 2; Length 95 I Similarity 95.8%; Pred. No. 1.3e-34; 91; Conservative 1; Mismatches 3; Indels
 2; Indels
 RFSGSGSGTDFTFISSLOPEDIATYYCOOYDNLP 117
 RESGSGSGTDFTFTISGLOPEDIATYYCQQYDTLP 95
 DB 2;
 Score 485; DB 2
Pred. No. 5e-35;
 RESGSGSGTDFTFTISGLQPEDIATYYCQQYDTLP
 1; Mismatches
 F;57-88/Region: framework 3 F;89-95/Region: complementarity-determining 3
 complementarity-determining 2
 86.3%;
96.8%;
 A;Cross-references: EMBL:M64856
C;Genetics:
 92; Conservative
 Best Local Similarity
 A, Accession: S43528
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-117 <SCO>
 F;50-56/Region:
 F;35-49/Region:
 61
 61
 61
 Query Match
 Local
 Matches
 Matches
 a
 엄
 ò
 ð
 g
 ò
 g
 à
 ò
 g
```

```
Search completed: November 16, 2005, 22:04:09 Job time : 13.7849 secs
 A; Molecule type: protein
A; Residues: 1-108 < CAP-
A; Cross-references: UNIPROT: P01605
A; Cross-references: UNIPROT: P01605
A; Note: the second and third hypervariable regions of this chain are identical with thos
B; Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
A; Timmunol. 142, 3158-3163, 1989
A; Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A; Reference number: A30601; MUID: 89215279; PMID: 2496160
Arceapra, J.D.; Klapper, D.G.
Scand, J. Immunol. 5, 677-664, 1976
A.Title: Complete amino acid sequence of the variable domains of two human IgM anti-gamm
A.Reference number: A01871; MUID:77038198; PMID:824717
 C;Accession: S36264
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. Bmbn J. 125-734, 1993
A;Title: Human anti-ealf antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36264
A;Accession: S36264
A;Accession: Speciminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
 A)Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k: c:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k: c:Complex: An immunoglobulin heterotetramer; immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology cIMM>
F;23-88/Disulfide bonds: #status predicted
 A;Residues: Î-104 <GON>
C;Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
 ö
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 1 DIQMIQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60
 DIQMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 Species: Homo mapiens (man)
Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
 Gaps
 A;Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g939919
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <1MM>
 Gaps
 ;
0
 ;
0
 61 RFSGSGSGTDFTLTISSLOPEDFATYYCQQYSNYPLTFGGGTKVDIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Score 475; DB 1; Length 108; Pred. No. 3.3e-34;
 ; DB 2; Length 107;
4.9e-34;
ches 9; Indels
 12; Indels
 ; Score 473; DB
; Pred. No. 4.9e-
9; Mismatches
 4; Mismatches
 85.0%;
 Query Match
Best Local Similarity 83.2%;
Matches 89; Conservative
 91; Conservative
 A; Molecule type: protein
 Query Match
Best Local Similarity
 A; Gene: GDB: IGKV1
 g
 a
 ઠે
 ઠે
 요
 ઠે
 ò
```

THIS PART DLAME (USPTO)

```
KV1A HUMAN
P01593;
 DOMAIN
DOMAIN
DISULFID
NON TER
SEQUENCE
 Query Match
 Local
 DOMAIN
DOMAIN
DOMAIN
 DOMAIN
 DOMAIN
 KV1A_HUMAN
 Best Loc
Matches
 RESULT 1
 셤
 ò
 ò
 sapien
sapien
sapien
sapien
 sapien
sapien
 sapien
sapien
sapien
 sapien
sapien
 sapien
 sapien
 sapien
 sapien
 homo sapien
 sapien
 sapien
 sapien
 sapien
 Bapien
 sapien
 sapien
 sapien
 November 16, 2005, 21:36:13; Search time 59.9908 Seconds (without alignments) 913.348 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 DIQMTQSPSSLSASVGDRVT......CQQYDTLPLTFGGGTKVEIK 107
 homo
homo
homo
 homo
 homo
homo
 homo
 homo
homo
 рошо
рошо
 рошо
 рошо
 homo
 homo
 homo
 homo
 homo
 homo
 homo
 homo
 Description
 Q723y4 | P01611 | P04811 | P04431 | P04431 | P04431 | P01597 | P01597 | P01613 | P04430 | P04430 | P04430 | P0460 | P0660 | P0
 P01605
P01609
Q6gmx0
Q96sa9
Q9u170
P01603
 Q6gmw1
P01598
P01610
Q6pih4
 1612378
5.1.6
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1612378 seqs, 512079187 residues
 SUMMARIES
 GenCore version
Copyright (c) 1993 - 2005
 KVIW HUMAN
OGGMX8
QG5ZC8
KVIE HUMAN
KVIU HUMAN
 Q9UL81
KV1V HUMAN
Q96PF6
 KV1F HUMAN
KV1R HUMAN
Q6PIH4
 KV1Y HUMAN
KV1P HUMAN
KV1B HUMAN
KV1O HUMAN
KV1M HUMAN
 KV1K HUMAN
KV1C HUMAN
Q7Z3¥4
 Q652C9
KV1H_HUMAN
 KV1S HUMAN
Q9UL77
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 KV1A_HUMAN
 Q6GMX0
Q96SA9
Q9UL70
 OGGMX9
 Gapop 10.0 , Gapext 0.5
 26GMW1
 UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
 seq length: 0
seq length: 200000000
 US-10-660-357A-26
 Query
Match Length DB
 107
 BLOSUM62
 467.5
 448
446.5
446
 Title:
Perfect score:
 Scoring table:
 Score
 1
 OM protein
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Database
 Run on:
 Result
 Š.
```

```
ö
 homo sapien
homo sapien
homo sapien
homo sapien
mus musculu
homo sapien
 9
 9
sapien
sapien
 mus musculu
homo sapien
 mus musculu
 homo sapien
 mus musculu
 mus musculu
 1 DIOMIOSPSSLSASVGDRVIIITCOASQDINNYLNWYQQKPGKAPKLLIYDASNLEIGVPS
 Titani K., Shinoda T., Purasayan t., Titani K., Shinoda T., Purasayan t.
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 ö
 P01644
P01645
 P01612
P01599
P04432
P01647
Q72473
P01643
Q6pit5
P01648
 P01606
P01604
 61 RPSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
 Complementarity-determining-3. Framework-4.
 Length 108;
 Indels
 11992 MW; E3B3B246C18F0C4F CRC64;
 92.0%; Score 517; DB 1; Lv 92.5%; Pred. No. 2.6e-43; ive 3; Mismatches 5;
 Pfan; PP00047; ig; 1.
SWART; SM00406; IGV; 1.
PROSITE; PSSOBS5; IG_LIKE; 1.
BENCE-Jones protein; Direct protein sequencing; Immunoglobulin V region.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Kappa chain V-I region AG.
Homo sapiens (Human).
 108 AA
 ALIGNMENTS
 Framework-3.
KV1D HUMAN
KV1L HUMAN
KV1L HUMAN
KV1G HUMAN
KV1G HUMAN
KV1X HUMAN
 KV5K MOUSE
 MOUSE
 MOUSE
 KV50 MC
Q9UL79
 072473
 SEQUENCE.
MEDLINE=69234734; Pubmed=4893682;
 99; Conservative
 STANDARD;
 34
434
88
107
107
 108 AA;
 Similarity
```

108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

```
SEQUENCE
 ð
 염
 8
 g
 A SEQUENCE OF 1-35.

MEDLINE-81267384; PubMed=6167731;
Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Schomon A.,

Telared England of the human Ki Bence Jones protein Wat.",

I. J. Mol. Biol. 147:185-193(1981).

- I. MISCELLANEOUS: This is a Bence-Jones protein.

R DS. HWTL, X-ray, A/B=1-108.

R GO; GO:0005576; C:extracellular; NAS.

GO; GO:0005537; F:immune response; NAS.

R GO; GO:0006955; P:immune response; NAS.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007596; Ig-v.
 MEDLINE=95086080; PubMed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Scolmon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Ig kappa chain V-I region WAT.
If homo saplanna (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 PERM, PF60047; ig. 1.
SMART; SM00406; IGV; 1.
PROSTE; PS58135; IG_LIKE; 1.
JD-structure; Psce-Jones protein; Direct protein sequencing; Immunoglobulin V region.
61 RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK 107
 Complementarity-determining-1
 Complementarity-determining-2.
 Complementarity-determining-3.
 [1]SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 By similarity.
TN -> SD (in Ref. 2)
 Framework-3.
 Framework-1,
 Framework-4
 Biochemistry 33:14848-14857(1994).
 STANDARD;
 23
34
49
56
88
88
97
107
31
 SEQUENCE OF 1-35.
 NCBI_TaxID=9606;
 KV1Y HUMAN
P80362:
a
```

```
ô
 ô
 9
 9
 REVISIONS TO 39 AND 41.
Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Matanabe S.; (In) Franek F., Shugar D. (eds.); Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
 1 DIQMIQSPSSLSASVGDRVIITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Gaps
 Eukaryota; Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
 ö
 ö
 -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Framework-1.
Complementarity-determining-1.
Length 108;
 Complementarity-determining-2.
 Complementarity-determining-3.
 Length 108;
 4; Indels
 6; Indels
 11782 MW; FSACEDESA313DF3A CRC64;
 Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967)
 marker.
-!- MISCELLANBOUS: This is a Bence-Jones protein.
10.7%; Score 510; DB 1; 11arity 89.7%; Pred. No. 1.3e-42; Conservative 7; Mismatches 4;
 Score 508; DB 1;
Pred. No. 2e-42;
5; Mismatches 6
 SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
 108 AA
 Framework-4.
By similarity.
 Framework-3.
 Framework-2
 PIR; A91638; KIHURY.
HSSP; PO1607; 1BWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
 PRT;
 MEDLINE=68362076; PubMed=5595110;
 Ig kappa chain V-I region Roy.
Homo sapiens (Human).
 90.4%;
nilarity 89.7%;
Conservative
 STANDARD;
 [mmunoglobulin V region
 49
56
88
97
107
108
 Pfam; PF00047; ig; 1.
 108 1
108 AA;
 Query Match
Best Local Similarity
Matches 96; Conserv
 Local Similarity
les 96; Conserv
 NCBI_TaxID=9606;
 Hilschmann N.;
 HUMAN
 NON TER
SEQUENCE
 Query Match
 DISULFID
 SEQUENCE
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 KV1P_HUMAN
 Matches
 RESULT
```

m

```
HUMAN
 STRAND
STRAND
STRAND
NON TER
SEQUENCE
 Query Match
 SEQUENCE
TURN
 DOMAIN
 DOMAIN
 T 5
HUMAN
 HELIX
 Best Loc
Matches
 RESULT
KV10_HU
STATETOS
 ઠ
 임
 ò
 g
 Jones protein Au.";

Biophys. Struct. Mech. 1:139-146(1975).

L. MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain REI.

C. -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

C. -I- MISCELLANEOUS: This is a Bence-Jones protein.

PIR; A91653; K.HIUAU.

R PDB; 1JV5; X-ray; A=1-107.

R QC) GC:0005376; C:extracellular; NAS.

R QC) GC:0005576; P:antigen binding; NAS.

R QC) GC:0005555; P:antigen binding; NAS.

R DR: InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.
1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60
 monoclonal
 MEDLINE=77022433; PubMed=1234024; Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E., Schwager P., Schigmann W., Schramm H.J.; Reigemann W., Schramm H.J.; "The structure determination of the variable portion of the Bence-
 Schiechl H., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclona
immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 Pfam; PF00047; ig; 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
Prammon 1 23 Frammon's 1.
 61 RFSGSGSGTDFTFTISGLOPEDIATYYCOOYDTLPLTFGGGTKVEIK 107
 61 RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK 107
 Complementarity-determining-1. Framework-2. Complementarity-determining-2. Framework-3.
 Complementarity-determining-3.
 protein Au).";
Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972)
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
8 Kappa chain V-I region AU.
Homo sapiens (Human).
 108 AA
 By similarity
 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 MEDLINE=72189444; PubMed=5028201;
 STANDARD;
 NCBI_TaxID=9606;
 KV1B HUMAN
 DOMAIN
DISULFID
STRAND
STRAND
 SEQUENCE
 STRAND
TURN
STRAND
TURN
TURN
 901594;
 DOMAIN
DOMAIN
DOMAIN
 STRAND
TURN
STRAND
TURN
 DOMAIN
 DOMAIN
 FGRN
유
 ò
 셤
```

```
ö
 1 DIOMIOSPSSLSASVGDRVTITCOASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 9
 1 DIQMIQSPSSLSASVGDRVTITCQASQDISDYLMWYQQKPGKAPKLLIYDASNLESGVPS
 "The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their
 X.TAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=76039968; PubMed=1182131;
Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
Biochemistry 14:4943-4952 (1975).
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ö
 -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 SMARY, SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
3D-structure; Bence-Jones protein; Direct protein sequencing;
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGGGTKVEIK 107
 Complementarity-determining-1. Framework-2.
 Length 108;
 Complementarity-determining-2.
 7; Indels
 11939 MW; E8011187EE6F6FB9 CRC64;
 marker.

1. MISCELLANEOUS: This is a Bence-Jones protein.
PIR, A39.663; KIHUUR.
PDB; 1AR2; X-ray; Ø=1-107.
PDB; 1BWW; X-ray; A/B=1-107.
PDB; 1RBI; X-ray; A/B=1-107.
PDB; 1RBI; X-ray; A/B=1-107.
PDB; 1RBI; X-ray; A/B=1-107.
PDB; 1RBI; N-ray; A/B-1-1
 combining site.";
Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 DB 1;
 89.9%; Score 505; DB 1; 90.7%; Pred. No. 4e-42; ive 3; Mismatches
 P01607;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
1-JUL-1986 (Rel. 45, Last annotation update)
19 kappa chain V-I region Rel.
Homo sapiens (Human)
 108 AA
 Framework-1
 MEDLINE=76023758; PubMed=809329;
Palm W., Hilschmann N.;
 Local Similarity 90.7
nes 97; Conservative
 STANDARD;
69
75
90
106
108
 Immunoglobulin V region.
 23
34
56
56
68
70
80
85
97
102
108 AA;
 Pfam; PF00047; ig;
 NCBI_TaxID=9606;
```

```
sequencing;
 Query Match
Best Local Similarity
 108 AA;
 108 AA;
 Similarity
 NCBI_TaxID=9606;
Direct protein DOMAIN 1
 KV10 HUMAN
P01609;
 DISULFID
NON TER
SEQUENCE
 DISULFID
NON TER
 SEQUENCE
 SEQUENCE
 Query Match
 Local
 DOMAIN
DOMAIN
DOMAIN
 DOMAIN
 DOMAIN
 KW
FT FT FT S
S
S
S
S
S
S
S
 ò
 MEDLINE=77038198; PubMed=824717;
Capra J.D., Klapper D.G.;
Capra J.D., Klapper D.G.;
Capra J.D., Klapper D.G.;
Complete amino acid sequence of the variable domains of two human IgM
complete amino acid sequence of the variable domains of two human IgM
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
Cand. J. Immunol. 5:677-684(1976).
Chain are identical with those of the human Pom V-III kappa chain,
with which it shares certain idiotypic determinants.
C-I- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
DR GO: Go: 000576; C:extracellular; NAS.
GO: GO: 0005576; C:extracellular; NAS.
GO: GO: 0006555; P:immune response; NAS.
RISEPPRO; IPR007110; Ig-like.
DF InterPro; IPR007110; Ig-like.
DF InterPro; IPR007110; Ig-like.
DF INTERPROSAT: ig-1.
 ö
 9
 9
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region Lay.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ö
 Length 108;
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEI 106
 Complementarity-determining-3.
Pramework-4.
 8; Indels
 11902 MW; 9E8143E1188BCE2A CRC64;
 DB 1;
 Score 486; DB 1;
Pred. No. 3e-40;
 108 AA
 6; Mismatches
 Framework-3.
 Pfam, PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
 86.5%;
86.8%;
 Query Match
Best Local Similarity 86.8'
 STANDARD;
 102
108
108 AA;
 NCBI_TaxID=9606;
 KV1M HUMAN
 DOMAIN
DISULFID
STRAND
 NON TER
SEQUENCE
 SEQUENCE
 STRAND
 STRAND
 STRAND
 STRAND
 STRAND
 STRAND
 TRAND
 TRAND
 STRAND
 IURN
 IURN
 TURN
 TURN
 TURN
 IURN
 DDT TELEMENT TO THE POLICY OF
g
 ò
 셤
```

```
ö
 9
 9
 "The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scw.), II: the chymotryptic peptides and the
 1 DIQMIQSPSSLSVSVGDRVIITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS
 1 DIOMIOSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 complete amino acid sequence.";
Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
-!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 ö
 Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
Framework-3.
Complementarity-determining-3.
Framework-4.
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Length 108;
 Length 108;
 Framework-1.
Complementarity-determining-1.
 Complementarity-determining-2
 Complementarity-determining-3
 23 Framework-1.
34 Complementarity-determining-
49 Framework-2.
56 Complementarity-determining-
88 Framework-3.
97 Complementarity-determining-
107 Framework-4.
88 By similarity.
108
1, 11764 MW; 32CECDDDF9644414 CRC64;
 Indels
 11834 MW; 739993A95431434A CRC64;
Immunoglobulin V region.
 12;
 marker.

-I MISCELLANBOUS: This is a Bence-Jones protein.
PIR, A01875, KIHUSW.
HSSP, P01607, IBWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005825; P:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
 Score 473; DB 1;
Pred. No. 5.8e-39;
 Score 475; DB 1;
Pred. No. 3.7e-39;
 Pfam; PF00047; ig; 1. __
SMART; SM00406; IGv; 1. IG LIKB; 1.
PROSITE; PS50835; IG LIKB; 1.
BENGE-JONES protein; Direct protein sequencing;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Improper chain V-I region Scw.
Homo sapiens (Human).
 Ā
 4; Mismatches
 By similarity.
 MEDLINE=75059271; PubMed=4435756;
Eulitz M., Hilschmann N.;
 84.2%;
84.1%;
 84.5%;
 91; Conservative
 STANDARD;
 Immunoglobulin V region.
 23
34
34
88
97
107
```

ഗ

```
RESULT
 Q96SA9
 ò
 셤
 ò
 셤
 ò
 셤
 Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Morer T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Boat S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
 ö
ö
 9
 1 DIOMIOSPSSLSASVGDRVIITCQASQDIRKHLNWYDQKPGKAPRLLIYGASTLETGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 1 DIOMIOSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
Gaps
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
.;
0
 .;
0
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 61 RFSGSGSGTDFTLTISTLQPEDIGNYYCQQYDNVPITFGGGTRVENK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Score 468; DB 2; Length 236;
Pred. No. 4.3e-38;
 10; Indels
12; Indels
 Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, BC073775, AAH73775.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003596; Ig.wh.C.
InterPro; IPR003596; Ig.w.
Pfam; PF00647; Ig.2.
 25807 MW; 864EA08C7E92BF8F CRC64;
 Last sequence update)
Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 236 AA
Mismatches
 8; Mismatches
 PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 236 AA; 25807 MW, economics
 Created)
 PRT;
5;
 83.3%;
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 27,
27,
 and mouse cDNA sequences."
 SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
 89; Conservative
90; Conservative
 PRELIMINARY;
 05-JUL-2004 (TrEMBLrel.
 Hypothetical protein
 Homo sapiens (Human)
 Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 Query Match
 Local
 QGGMX0;
 Q6GMX0
Matches
 Matches
 RESULT 8
Q6GMX0
 g
 ò
 ઠે
 셤
```

```
ä
 9
 9
1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
 1 DIOMTOSPSSLSASVGDRVTITCOASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 3; Gaps
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
 Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 83.2%; Score 467.5; DB 2; Length 107;
86.1%; Pred. No. 2e-38;
ive 6; Mismatches 6; Indels 3;
 61 RFSGSGSGTDFTFISGLOPEDIATYXCQQ-YDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYST--LTFGGGTKVEIK 106
 61 RFSGSGSGIDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 83 RFSGSGSGTDFTLTISSLRPDDFATYYCQQSYNIPLTFGGGTNVEIK 129
 4BB43E9C5B577F16 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Myosin-reactive immunoglobulin light chain variable
 Ź
 æ
 108
 Created)
 PRT;
 PRT;
 antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
ENBL; U96396; AAB66785.1; -.
PIR; B49047; B49047.
PIR; PH0867; PH0867.
PIR; S16840; S16840.
PIR; S31977.
PIR; S34083; S34086.
HSSP; PO1607; IBWW.
 MEDLINE=98375893; PubMed=9712075;
 107 AA; 11520 MW;
 InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
 PROSITE; PS50835; IG_LIKE; 1.
 variable region (Fragment).
 01-MAY-2000 (TrEMBLrel, 13,
 Local Similarity 86.1 nes 93; Conservative
 PRELIMINARY;
 PRELIMINARY;
 107
 (Human)
 SMART; SM00406; IGV
 SEQUENCE FROM N.A.
 [1]
SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 Homo sapiens
 (Fragment)
 NON TER
NON TER
SEQUENCE
 23
 Query Match
 Q96SA9;
 Q9UL70
 Q96SA9
 RESULT 10
Q9UL70
```

```
KV1C HUMAN
P01595;
 SEQUENCE
 Query Match
 Query Match
 DOMAIN
DOMAIN
DOMAIN
 DOMAIN
 DOMAIN
 KV1C HUMAN
 a
 ò
 · 원
 ò
 ò
 ð
 9
 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQRPGRVPKSLIYAASTLQSGVPS
 1 DIOMTOSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 "Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
J. Biochem. 77:127-1296 (1975).
I MISCELLANEOUS: The C region of this chain has the INV (3) marker.
MISCELLANEOUS: This is a Bence-Jones protein.
 Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 ö
MEDLINE-98277139; PubMed-9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 61 RFSGSGSGTDFTFTISGLOPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Length 108;
 Complementarity-determining-2.
 Complementarity-determining-3.
 Complementarity-determining-1.
 11; Indels
 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
 11900 MW; 768839FBED5A2F4B CRC64;
 Score 459; DB 2;
Pred. No. 1.4e-37;
 Pfam; PF00047; 1g; 1.
SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; 1G_LIKE; 1.
Bence-Jones protein; Direct protein sequencing;
 Clin. Immunol. Immunopathol. 87:184-192(1998).
BMBL; AF035044, AAD56280.1; -.
BMSL; PH0863; PH0863.
HSSP; P01607; IBWW.
InterPro; IPR007110; Ig-like.
InterPro; IPR00596; Ig-v.
SWART; SM00406; IGv; 1.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
15 Azppa chain V-I region Ka.
Homo sapiens (Human)
 By similarity.
 9; Mismatches
 Framework-1.
 Framework-2
 PIR, A01669; KIHUKA.
HSSP; P80362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007586; Ig-v.
 MEDLINE=76189985; PubMed=818073;
Shinoda T.;
 PROSITE; PS50835; IG_LIKE; 1.
 81.7%;
 87; Conservative
 STANDARD;
 mmunoglobulin V region.
 57
89
98 1
23
108 AA;
 Query Match
Best Local Similarity
 NCBI_TaxID=9606;
 KV1K HUMAN
 NON TER
SEQÜENCE
 DISULFID
NON TER
SEQUENCE
 etus.";
 SEQUENCE
 DOMAIN
 P01603;
 KVIK HUMAN

ID KVIK HI

DT 21-JUL.

DT 21-JUL.

DE 19 *JUL.

OX BURALIN

RA Shinod

RA Sh
 DOMAIN
 DOMAIN
 Matches
 RAY RAY RAT RAT OF BOTH OF BOT
 8
 ò
 g
```

```
ö
 ô
 Tormation.";
Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
Li. Hoppe-Seyler's The C region of this chain has the INV (3) marker.
C -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
N. PTR; A01863; K1HUBI.
N. FTR; A01863; K1HUBI.
N. GO; GO:0003823; F:antigen binding; NAS.
N. GO; GO:0006955; C:extracellular; NAS.
N. GO; GO:0006955; P:immune response; NAS.
N. GO; GO:0006955; P:immune response; NAS.
N. InterPro; IPR00110; Igl.
N. FFam; PF00047; Ig. 1.
N. FFam; PF00047; Ig. 1.
N. SWART; SW00406; IG. 1 IKE; 1.
N. SWART; SW00406; IG. 1 IKE; 1.
N. Bence-Jones protein; Direct protein sequencing;
N. Immunoglobulin V region.
 1 DIQMTQSPSPLSASVGDSVTITCQASQDIRNSLIWYQQKPGKAPKFLIYDAENLEIGVPS 60
 9
 9
 1 DIOMIQSPSSLSASVGDRVIIICQASQDINNYLNWYQQKPGKAPKLLIYDASNLEIGVPS 60
 1 DIQMIQSPSTLSVSVGDRVTITCEASQTVLSYLNWYQQKPGKAPKLLIYAASSLETGVPS
 1 DIQMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLBTGVPS
 Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
"Principle of antibody structure. The primary structure of a monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein Bli). 3. The complete amino acid sequence and the genetic significance of the variability principles for the mechanism of antibody
 0; Gaps
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 ö
 61 RFSGSGSGTDFTFTISGLOPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFRGSGSGTDFALSISSLQPEDFATYYCQQYYNLPYTFGQGTKLEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGQGSGTBFTFTISSVZPZBFATYYCQZYLDLPRTFGQGTKVDLK 107
 Score 453; DB 1; Length 108;
Pred. No. 5.5e-37;
2; Mismatches 17; Indels
 Complementarity-determining-1.
 Length 108;
 Complementarity-determining-2
 Complementarity-determining-3
 11; Indels
 12026 MW; 7A83983986A431E7 CRC64;
81.1%; Score 456; DB 1; 77.6%; Pred. No. 2.8e-37; ive 13; Mismatches 11.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
IG Rappa chain V-I region Bi.
Homo sapiens (Human).
 108 AA
 By similarity.
 Framework-3.
 Framework-1
 PRT;
 SEQUENCE.
MEDLINE=73029807; Pubmed=4563064;
 80.6%;
 Best Local Similarity 77.69
Matches 83; Conservative
 Conservative
 STANDARD;
 108 AA;
 Local Similarity
nes 88; Conserv
 NCBI_TaxID=9606;
```

```
DDT STATE ST
 셤
 셤
 ò
 ò
 TISSUB-Skeletal Muscle;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAUSPERS R.L., Feingold B.A., Grouse L.H., Derge J.G.,

MAISCHIL S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MISCHIL S.F., Jordan H., Moore T., Max S.I., Wang J., Hasheh F.,

Distribution M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

METALOR S.A., McGran P.J., McKernan K.J., Mbramson R.D., Mullahy S.J.,

Montage S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren E.D., Dickson M.C.,

Milalon D.K., Muzny D.M., Garen E.D., Dickson M.C.,

Milakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Moriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Marra M.J., Marra M.J.,

Jones S.J., Marra M.J.,

Marra M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Marra M.J., Marra M.J.,

Mones S.J., Marra M.J.,

Marra M.J., Malalysis of more than 15,000 full-length human
 9
 23 DIQMTQSPSSLSASVGDTVTITCRASQDISNYLAWFQQKPGKAPKSLIYGASSLQSGVQS 82
 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 .;
0
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 80.6%; Score 453; DB 2; Length 236; 80.4%; Pred. No. 1.3e-36; ive 10; Mismatches 11; Indels
 11; Indels
 Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
 25702 MW; 7FBFE4ED23084BC6 CRC64;
 Last sequence update)
Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 236 AA
 InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-set; I.
SMART; SM00406; IGV; I.
PROSITE; PS00290; IG_MHC; UNKNOWN_I.
PROSITE; PS00290; IG_MHC; UNKNOWN_I.
Hypothetical protein.
SEQUENCE 236 AA; 25702 MW; 7FBFE4EI
 Created)
 Query Match
Best Local Similarity 80.4%;
Matches 86; Conservative 1
 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
 EMBL; BC005332; AAH05332.1;
HSSP; P01834; 1HEZ.
 cDNA sequences
 PRELIMINARY;
 rissum=skeletal Muscle;
 Hypothetical protein. Homo sapiens (Human).
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 and mouse
 KV1S HUMAN
ID KV1S H
AC P01611
DT 21-JUL
 Q723Y4
 RESULT 13
Q7Z3Y4
 g
 ઠ
```

108 AA

PRT;

KV1S HUMAN STANDARD;
P01611;
21-JUL-1986 (Rel. 01, Created)

```
1 DIQMIQSPSSVSASVGDRVTITCRASQDISHWLAWYQQKSGKAPKLLIYSASSLENGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Kratzin H., Yang C., Krusche J.U., Hilschmann N.;

"Preparative separation of the tryptic hydrolysate of a protein by high-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes).";

Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).

-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

-!- MISCELLANEOUS: This is a Bence-Jones protein.
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Myosin-reactive autoantibodies in rheumatic carditis and normal
 ..
0
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
 61 RFSGSGSGTEFTLTISSLQPEDFATYFCQQAHSVPLTFGGGTTVDIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Complementarity-determining-1.
 Complementarity-determining-2.
 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
 Complementarity-determining-3.
 Length 108;
 10; Indels
 11608 MW; 782B14A649A60E45 CRC64;
 SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Bence-Jones protein; Direct protein sequencing;
Immunoglobulin V region.
 80.4%; Score 452; DB 1;
80.4%; Pred. No. 6.9e-37;
21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 1g kappa chain V-I region Wes.
 108 AA
 11; Mismatches
 Framework-2.
 Framework-3
 Framework-4
 GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; IG-like.
 01-MAY-2000 (TrEMBLrel. 13, Created)
 PRT;
 MEDLINE=81092279; PubMed=6778806;
 86; Conservative
 PRELIMINARY;
 34
449
88
87
107
108
 ; ig; 1.
 Homo sapiens (Human).
 Homo sapiens (Human).
 PIR; A01877; K1HUWS.
 23
108 1
108 AA;
 P80362; 1WTL.
 Query Match
Best Local Similarity
Matches 86; Conserv
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 Pfam; PF00047
 (Fragment)
 NON TER
SEQUENCE
 SEQUENCE
 fetus.";
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 Q9UL77
 RESULT 15
```

ö 9 9

Search completed: November 16, 2005, 22:01:53 Job time : 60.9908 secs

```
TELEPRATION INCREMENTS SCRI452P
TELEPHONE: 619-554-6312
TELEPHONE: 619-554-6312
TELEPAX: 619-554-6312
TELEPAX: 1019-554-6312
TELEPAX: 1019-554-6312
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: DIOLOGY: linear
WOLECULE TYPE: protein
US-08-276-852-108
 Sequence 108, App
Sequence 6, Appli
Sequence 107, App
 4, Appl
4, Appl
4, Appl
4, Appl
1, Appli
1, Appli
4, Appli
5, Appli
5, Appli
 Sequence 108, App
Sequence 108, App
Sequence 108, App
 November 16, 2005, 21:41:29; Search time 18.1939 Seconds (without alignments) 439.017 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 562
1 DIOMTOSPSSLSASVGDRVT......CQQYDTLPLTFGGGTKVEIK 107
 Sequence 15,
Sequence 15,
Sequence 6,
Sequence 7,
 Sequence 1:
Sequence 1:
Sequence 1:
 Description
 Sequence
Sequence
Sequence
Sequence
 Sequence
Sequence
 Sequence
Sequence
 Sequence
 sued Patents AA:*
/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RDTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*/cgn2_6/ptodata/1/iaa/Packfiles1.pep:*//cgn2_6/ptodata/1/iaa/backfiles1.pep:*//cgn2_6/p
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-08-276-852-108
US-08-899-575-108
US-08-899-575-108
US-08-318-1578-6
US-09-253-1074-6
US-09-253-107
US-08-899-575-107
US-08-899-575-107
US-08-899-575-107
US-09-490-1575-107
US-09-490-153-14
US-09-490-153-14
US-09-157-370-3
US-09-157-370-3
US-09-157-370-3
US-09-157-105
US-09-999-025-15
US-09-999-025-15
US-09-999-025-15
US-09-999-040-15
US-09-999-040-15
US-09-999-040-15
 Total number of hits satisfying chosen parameters:
 513545 seqs, 74649064 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 seq length: 0
seq length: 200000000
 US-10-660-357A-26
 DB
 Length
 Issued
 Query
Match 1
 \begin{array}{c} \mathbf{0} \\ \mathbf{
 Title:
Perfect score:
 Scoring table:
 Score
 \begin{array}{c} 5.25 \\ 5.
 Minimum DB
Maximum DB
 Sequence:
 Database
 .
:
 Result
```

| Sequence 100, Appl Sequence 9, Appl Sequence 67, Appl Sequence 67, Appl Sequence 71, Appl Sequence 11, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 16, Appl Sequence 18, Appl Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Appl Appl Appl Appl Sequence 18, Appl Appl Appl Sequence 18, Appl Appl Appl Appl Appl Appl Appl App |            | OCLONAL ANTIBODIES NCY VIRUS e, Office of Road, Suite 220,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 4 US-08-454-899G-100<br>4 US-09-1348-224-9<br>1 US-08-137-117D-67<br>2 US-08-436-717-67<br>2 US-08-436-717-71<br>2 US-08-436-717-71<br>2 US-08-436-717-71<br>2 US-08-437-642B-39<br>3 US-08-437-642B-39<br>5 US-07-934-373C-39<br>3 US-08-437-642B-34<br>4 US-09-705-686-3<br>4 US-09-705-686-3<br>5 US-08-437-632B-3<br>6 US-09-705-838-3<br>7 US-09-705-838-3<br>8 US-09-705-838-3<br>8 US-09-705-838-3<br>9 US-09-705-838-3<br>9 US-09-705-838-3<br>9 US-09-705-838-3<br>1 US-09-705-838-3<br>1 US-09-705-838-3<br>1 US-09-705-838-3<br>1 US-09-705-838-3<br>1 US-09-705-838-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ALIGNMENTS | plication US/08276852 3108: utcon, Dennis R arbas, Carlos F erner, Richard A MTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES NTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES NTION: TO HUMAN IMMUNODEFICIENCY VIRUS UBNESS: The Scripps Research Institute, Office of Patent Counsel G66 No. 5652138th Torrey Pines Road, Suite 220, olla ABLE FORM: F1 Proppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS SABLE FORM: I PLOPPY disk IEM PC compatible CATION DATA: UNUMBER: US/08/276,852 I B-JUL-1994 IION DATA: NUMBER: US 08/178,302 TION DATA: 30-SEP-1993                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| 86.5<br>86.5<br>86.5<br>86.5<br>86.5<br>86.5<br>86.5<br>86.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |            | pplicatio 138 Burton; Barton; Barbas, C Elerner; ENTION: GUENCES: C ADDRES:  |
| 2 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |            | RESULT 1 US-08-276-852-108 Sequence 108, Applica Patent No. 5652138 GENERAL INFORMATION: APPLICANT: Barbas APPLICANT: Barbas APPLICANT: Barbas APPLICANT: CENTER TITLE OF INVENTION NUMBER OF SEQUENCE CORRESSEE: Pate ADDRESSEE: Pate STREET: Molla STREET: A0666 STREET: A0618 STREET: A0618 STREET: A0618 STREET: BARD COMPRY: USA COUNTRY: USA STREET: PATON APPLICATION PRING APPLICATION PRING APPLICATION APPLICATION PRING APPLICATION APPLICATION PRING APPLICATION APPLICATION PRING APPLICATION |

```
1 ELTGSPSSLSASVGDRVTITCQASQDISNHLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 3 QMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 ó,
 APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN INMUNODEFICIENCY VIRUS
ONUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
 Query Match
93.4%; Score 525; DB 1; Length 107;
Best Local Similarity 94.3%; Pred. No. 2.9e-42;
Matches 99; Conservative 4; Mismatches 2; Indels
 SGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIK 105
 63 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 63 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 sésésérbérérissűgébelatyrogordniketregegrkvelk 10s
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-UUL-1997
 FILING DATE: 24-UUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-UUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
 Sequence 108, Application US/08899575 Patent No. 5804440 GENERAL INFORMATION:
 NAME: Fiting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR14
TELECOMMUNICATION INPORMATION:
TELEPHONE: 619-554-2937
INFORMATION FOR SEG ID NO: 108:
SEQUENCE CHARACTERISTICS:
 : 107 amino acids
amino acid
 MOLECULE TYPE: protein
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 La Jolla
: CA
 USA
 COUNTRY: US
 US-08-899-575-108
 US-08-899-575-108
 TOPOLOGY:
 RESULT
 ద
 ð
 g
 8
 g
 ਨੇ
 1 ELTQSPSSLSASVGDRVTITCQASQDISNHLNWYQQKPGKAPKLLIYDASNLETGVPSRF 60
 3 QMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF 62
 3 QMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 Gaps
 ö
 ö
 Sequence 108, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8 CITY: La Jolla STATE: CA
 93.4%; Score 525; DB 1; Length 107; 94.3%; Pred. No. 2.9e-42; rive 4; Mismatches 2; Indels
Query Match 93.4%; Score 525; DB 1; Length 107; Best Local Similarity 94.3%; Pred. No. 2.9e-42; Matches 99; Conservative 4; Mismatches 2; Indels
 61 SGSGSGTDFTFTISSLQPEDIATYXCQQYDNLPLTFGGGTKVEIK 105
 SGSGSGTDFTFTISGLOPEDIATYYCOOYDTLPLTFGGGTKVEIK 107
 COMPUTER KEADABLE FORM:
MEDIUM TYPE: FILPOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSITCATION NUMBER: US 08/276,852
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1993
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: SCR1452P
TELECOMMULICATION INFORMATION:
NAME: FILING, Thomas
REGISTRATION NUMBER: SCR1452P
TELECOMMULICATION INFORMATION:
TELECOMMULICATION PROPRATION:
TELEC
 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
 107 amino acids
amino acid
 Query Match
Best Local Similarity 94.3
Matches 99; Conservative
 MOLECULE TYPE: protein US-08-899-575-108
 ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 linear
 USA
 RESULT 2
US-08-899-575-108
 COUNTRY:
 63
 ò
 g
 ઠ
```

RESULT 4 PCT-US95-08743-108 ; Sequence 108, Application PC/TUS9508743

```
US-08-318-157B-6
 US-09-253-794-6
 Best Lock
Matches
 RESULT 6
 g
 ò
 Q
 δ
 62
 3 OMTOSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 Gaps
 Sequence 6, Application US/08318157B

Patent No. 5874540

GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
 ö
 HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
 Query Match 93.4%; Score 525; DB 5; Length 107; Best Local Similarity 94.3%; Pred. No. 2.9e-42; Matches 99; Conservative 4; Mismatches 2; Indels
 COFTWART APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08743

FILING DATE: 11-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/276,852

FILING DATE: 18-JUL-1994

INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TYPE: amino acid

MOLECULE TYPE: protein

PCT-US95-08743-108
 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVBIK 107
 61 SGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIK 105
 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/318,157B
FILLING DATE: 05-OCT-1994
CLASSIFICATION: 424
 18733/464
 TITLE OF INVENTION: HUMAN NEUTRALIZI
TITLE OF INVENTION: TO HUMAN IMMUNOI
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 ATTORNEY/AGENT INFORMATION:
NAME: SAXE BETNARD D.
REGISTRATION NIMBER: 28.665
REFERENCE/DOCKET NUMBER: 18
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
 (202) 672-5399
 TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
GENERAL INFORMATION:
 RESULT 5
US-08-318-157B-6
 TELEFAX:
 63
 a
 ઠ
 ò
 셤
```

```
ò
 9
 1 DIQLTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQKPGKAPKLLIYEASNLQAGVPS 60
 1 DIQMIQSPSSLSASVGDRVTITCQASQDINNYLAWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIOMTOSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
 ö
 ö
 61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Length 107;
 Length 107;
 Version #1.30
 Query Match 89.5%; Score 503; DB 2; L. Best Local Similarity 89.7%; Pred. No. 3.4e-40; Matches 96; Conservative 4; Mismatches 7;
 Query Match
89.5%; Score 503; DB 4; L
Best Local Similarity 89.7%; Pred. No. 3.4e-40;
Matches 96; Conservative 4; Mismatches 7;
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
 STATE: D.C.
COUNTRY: USA
ZIP: 2000/TRY: USA
ZIP: 2000/TRY: USA
COMPUTER READABLE FORM:
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
 NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMFUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-199
CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-0CT-1994
ATTORNEY/AGENT INFORMATION:
 MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-253-794-6
 Sequence 6, Application US/09253794
Patent No. 6676924
GENERAL INFORMATION:
 LENGTH: 107 amino acids
 TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
 APPLICANT: HANSEN, Hans J.
 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
 NUMBER OF SEQUENCES:
 TELEX: 904136
```

```
ZIP: 92037
 ð
 US-08-899-575-107
 TOPOLOGY:
 COUNTRY:
 В
 à
 ð
 ö
 1 ELTQSPSSLSASVGDRVTITCQASQDIRNYLNWYQQKPGKAPKLLIYDASNSETGVPSRF 60
1 DIQLTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQKPGKAPKLLIYEASNLQAGVPS 60
 3 OMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 Gaps
 Sequence 107. Application US/08276852
; Sequence 107. Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
 APPLICANT: Burton, Dennis R
 APPLICANT: Bratch (Carlos F
 APPLICANT: Bratch (Carlos F
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
 TITLE OF INVENTION: TO HUMAN INMUNOBERICIENCY VIRUS
 TITLE OF TO HUMAN INMUNOBERICIENCY VIRUS

 ö
 61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Query Match 89.3%; Score 502; DB 1; Length 107; Best Local Similarity 89.5%; Pred. No. 4.3e-40; Matches 94; Conservative 5; Mismatches 6; Indels
 SGSGSGRDFTFTISSLQPEDVATYYCQQHQNVPLTFGGGTKVEIK 105
 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
FILING DATE: 30-SEP-1993
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: FILLING THOMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELECHONE: 619-554-2937
 RESULT 8
US-08-899-575-107
; Sequence 107, Application US/08899575
 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
 Floppy disk
 : 107 amino acids
amino acid
 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-107
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 92037
 ర్
 COUNTRY:
 g
 ò
 8
 유
 셤
 ð
```

```
3 OMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 0; Gaps
 Sequence 107, Application US/08899575

Sequence 107, Application US/08899575

GENERAL INFORMATION:
APPLICANT: Burben, Dennis R
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
 Score 502; DB 1; Length 107;
Pred. No. 4.3e-40;
5; Mismatches 6; Indels
 SGSGSGRDFTFTISSLQPEDVATYYCQQHQNVPLTFGGGTKVEIK 105
 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 COMPUTER RELABBLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 34-JUL-1997
CLASSIFICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
RIOR APPLICATION NUMBER: US 07/954,148
APPLICATION NUMBER: US 07/954,148
ATCHANG DATE: 30-SEP-1992
ATTOMENYAGENT INFORMATION:
ANALE: ACCUPANT OF THE PARAMETRY O
 SCR1452P
 REGISTRATION NUMBER: 34,163
REPERDICE/DOCKET UNBER: SCT
TELECOMMUNICATION:
TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
 Query Match
Best Local Similarity 89.5%;
Matches 94; Conservative
 : 107 amino acids
amino acid
 NAME: Fitting, Thomas REGISTRATION NUMBER:
 ; MOLECULE TYPE: protein US-08-899-575-107
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 La Jolla
```

```
LENGTH: 107 amino acids TYPE: amino acid
 108 amino acids
 (212)596-9090
 Query Match
Best Local Similarity 87.99
Matches 94; Conservative
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 SEQUENCE CHARACTERISTICS
 TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-107
 MOLECULE TYPE: protein
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 TYPE: amino acid STRANDEDNESS:
 linear
 g
 ò
 3 QMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF
 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: TO PC DOS/MS-DOS
SOFTWARE: PAFENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-UUL-1995
PRILING DATE: 18-UUL-1994
FILING DATE: 18-UUL-1994
 ö
 ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: La Jolla
STATE: CA
 ; DB 1; Length 107; 4.3e-40;
 63 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 6; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,402
FILING DATE: 30-SEP-1993
FILING DATE: 30-SEP-1993
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTOMNUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
 5; Mismatches
 89.3%; Score 502;
89.5%; Pred. No. 4
 SCR1452P
 COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
 : 107 amino acids
amino acid
 94; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Best Local Similarity
 RESULT 10
PCT-US95-08743-107
 US-08-899-575-107
 Query Match
 Matches
 ò
```

```
3 QMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPSRF 62
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 Gaps
 ;
0
Length 107;
 COMPUTER: FLOPPY CLIAR
COMPUTER: FLOPPY CLIAR
COMPUTER: BEACHIOR COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY-AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 DB 3; Length 108;
 63 SGSGSGTDFTFISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 SGSGSGRDFTFTISSLQPEDVATYYCQQHQNVPLTFGGGTKVEIK 105
 STREET: James F. Haley, Jr., Esq. c/o Fish & Neave CITY: New York STATE: New York
 Indels
 GENERAL INFORMATION:
APPLICANT: Rnappik, Achim
APPLICANT: 11ag, Vic
APPLICANT: G. Liming
APPLICANT: Moroney, Simon
APPLICANT: Plackthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
Score 502; DB 5;
Pred. No. 4.3e-40;
5; Mismatches 6
 Score 493; DB 3
Pred. No. 3e-39;
6; Mismatches
 Sequence 14, Application US/09025769B Patent No. 6300064
 INFORMATION FOR SEQ ID NO: 14:
 87.7%;
Query Match 89.3%;
Best Local Similarity 89.5%;
Matches 94; Conservative
```

```
RESULT 14
 ઠ
 a
 Š
 셤
 ô
 1 DIOMIQSPSSLSASVGDRVTITCOASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 1 DIQMIQSPSSLSASVGDRVITICRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
Gaps
 MEDIUM TYPE Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONFUTER: IBM PC compatible
CORFWARE: Patentin Release #1.0, Version #1.30 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, ESG.
RECISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHENCE (202) 912-2020
 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
 ö
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLOPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 RESIDENTIAL TRANSPORTATION RESIDENTATION REPORT TO THE TRANSPORT TO THE TR
 87.7%; Score 493; DB 4; Length 108; 87.9%; Pred. No. 3e-39;
 7; Indels
 ilag, vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

CORRESPONDENCE ADDRESS:
 STREET: 1666 K Street, N.W., Suite 300
 Pred. No. 3e-39;
6; Mismatches
 MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-070A-14
 Sequence 14, Application US/09490070A Patent No. 6696248 GENERAL INFORMATION:
 RESULT 13
US-09-490-153-14
; Sequence 14, Application US/09490153
 SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
 INFORMATION FOR SEQ ID NO: 14:
 ZIP: 20006
COMPUTER READABLE FORM:
 CITY: Washington STATE: D.C. COUNTRY: USA
 TOPOLOGY: linear
 94; Conservative
 Best Local Similarity
 US-09-490-070A-14
 61
 Query Match
 Matches
 유
 ð
 g
 셤
 ò
 g
 ò
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLAWYQQKPGKAPKLLIYAASSLQSGVPS 60
 1 DIOMIOSPSSLSASVGDRVIITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLEIGVPS
 0; Gaps
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
 Version #1.30 (EPO)
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 US-09-490-324-14

Sequence 14, Application US/09490324

Fatent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter

11 11 19, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373
 Ouery Match 87.7%; Score 493; DB 4; Length 108; Best Local Similarity 87.9%; Pred. No. 3e-39; Matches 94; Conservative 6; Mismatches 7; Indels
 Ge, Liming
Moroney, Simon
Plueckthuu, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIA Release #1.0, Versi

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-200

PRIOR APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-R04G-1995

ATTORNEY AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/S
 STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
 LENGTH: 108 amino acids
 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
 Pack, Peter
Ilag, Vic
 CITY: New York
STATE: New York
 COUNTRY: USA
 US-09-490-153-14
```

```
1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
 Sequence 3, Application US/09157370A

Patent No. 62623B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STEINBACHER, Stefan

TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
FILE REFERENCE: P814.1-8072

CURRENT APPLICATION NUMBER: US/09/157,370A

CURRENT APPLICATION NUMBER: US/09/157,370A

CURRENT APPLICATION NUMBER: OS/765,179

EARLIER APPLICATION NUMBER: PCT/EP95/02626

EARLIER PILING DATE: 1997-01-14

EARLIER PILING DATE: 1994-07-15

EARLIER PILING DATE: 1994-07-15

SOFTWARE: PATENTING DATE: 1994-07-15
 Gaps
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York COUNTRY: USA ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ö
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPFGGGTKVEIK 107
 Query Match 87.7%; Score 493; DB 4; Length 108; Best Local Similarity 87.9%; Pred. No. 3e-39; Matches 94; Conservative 6; Mismatches 7; Indels
 CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9000
INFORMATION FOR SEQ ID NO: 14:
 STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-490-324-14
 LENGTH: 108 amino acids
TYPE: amino acid
 SEQUENCE CHARACTERISTICS
 RESULT 15
US-09-157-370-3
 g
 ò
 ઠે
```

```
ö
 9
 1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLAWYQQKPGKAPKLLIYDASNLESGVPS 60
 1 DIOMTOSPSSLSASVGDRVTITCQASQDINNYLAWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 ö
 61 RFSGSGSGTDFTFTISGLOPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSLPYTFGQGTKVEIK 107
 DB 3; Length 109;
 8; Indels
 86.8%; Score 488; DB 3;
87.9%; Pred. No. 9e-39;
tive 5; Mismatches
 Search completed: November 16, 2005, 22:07:21 Job time : 19.1939 secs
 Query Match
Best Local Similarity 87.9³
Matches 94; Conservative
US-09-157-370-3
 日
 ò
 ద
 ઠે
```

THIS PAGE BLOOM (GEFTS)

```
TYPE: PRT
CORGANISM: Homo Sapiens
US-10-330-613-26
a
 RESULT
 g
 ò
 November 16, 2005, 22:02:09; Search time 65.6949 Seconds (without alignments) 681.481 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 562
1 DIQMTQSPSSLSASVGDRVT......CQQYDTLPLTFGGGTKVEIK 107
 Sequence
Sequence
Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
 Description
 Sequence
 Sequence
 Sequence
 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
7/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US10B_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US10B_PUB.pep:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-10-330-613-26
US-10-330-530-26
US-10-357-26
US-10-727-155-318
US-10-016-986-108
US-10-364-743-49
US-10-644-277-56
US-10-644-277-56
US-10-644-277-56
US-10-644-277-56
US-10-644-277-56
US-10-644-277-56
US-10-644-277-56
US-10-644-277-56
US-10-679-62-93-21
 Total number of hits satisfying chosen parameters:
 1867879 segs, 418409474 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-10-660-357A-26
 seq length: 0
seq length: 200000000
 DB
 Length
 107
107
107
107
1113
1113
1113
1164
164
 Query
 1000.0
1000.0
994.3
993.1
993.1
993.1
993.1
993.1
993.1
 Title:
Perfect score:
 Scoring table:
 Score
 Minimum DB
Maximum DB
 protein
 Sequence:
 Searched:
 Database
 Run on:
 42645978601
 Result
 Š
```

```
Sequence 6, Appli
Sequence 6, Appli
Sequence 107, App
Sequence 10, Appl
Sequence 49, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 2296, Appl
Sequence 12, Appl
Sequence 15, Appl
 Sequence 64, Appl
Sequence 132, App
Sequence 53, Appl
Sequence 54, Appl
Sequence 24, Appl
Sequence 14, Appl
 ö
 9
 9
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMIQSPSSLSASVGDRVIITCQASQDINNYLAWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Sequence 44,
 Sequence 56,
 Sequence
 ö
 Query Match 100.0%; Score 562; DB 14; Length 107; Best Local Similarity 100.0%; Pred. No. 1.5e-42; Matches 107; Conservative 0; Mismatches 0; Indels 0
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 US-10-330-613-26

Sequence 26, Application US/10330613

Publication No. US20030147809A1

GENERAL HYPROMATION:
APPLICANT: Gudas, Jean
ITILE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REPERENCE: ABGENIX. 0.22A

CURRENT PILING DATE: 2002-12-26

PRIOR PILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE PELLOR NOS: 40

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 107
 4 US-11-132-143-88

4 US-10-444-27-44

US-10-644-27-45

US-10-644-27-43

US-10-364-47-53

S US-10-364-473-53

S US-10-364-743-53

S US-10-364-743-24

6 US-10-452-533-24

US-10-452-533-24

US-10-452-533-24

US-10-452-533-24

US-10-452-533-24

US-10-452-533-24

US-10-452-533-24

US-10-452-533-24

US-10-25-336-130

US-11-01-986-107

US-11-131-648-20

US-11-131-648-40

US-11-131-648-40

US-11-131-648-40

US-11-131-648-40

US-11-131-648-40

US-11-131-648-40

US-11-131-648-40

US-11-131-648-40

US-11-131-648-40

US-10-307-27-155-130

US-10-307-27-155-130

US-10-307-27-155-130

US-10-307-27-155-130

US-10-999-040-155

US-09-999-040-15

US-09-999-041-15

US-09-999-041-15

US-10-364-11-13

US-10-364-11-13

US-10-364-11-13

US-10-364-11-13
 ALIGNMENTS
```

```
APPLICANT:
 APPLICANT:
 ઠે
 셤
 ઠ
 9
 1 DIQMIQSPSSLSASVGDRVIITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 1 DIQMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 1 DIOMIOSPSSLSASVGDRVITITCQASQDINNYLNWYQQKPGKAPKCLIYDASNLETGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 .
0
US-10-330-26; Application US/10330530; Sequence 26, Application US/10330530; Publication No. US20030152514A1; GENERAL INFORMATION:
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES; FILE REFERENCE: ABGRIX.031A; CURRENT APPLICATION NUMBER: US/10/330,530; CURRENT FILING DATE: 2002-12-26; PRIOR APPLICATION NUMBER: US 60/346414; PRIOR FILING DATE: 2001-12-18; NUMBER OF SEQ ID NOS: 40; SOFTWARE: FEASTSEQ for Windows Version 4.0
 Length 107;
 Length 107;
 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Sequence 26, Application US/10660357
Sequence 26, Application US/10660357
Sequence 26, Application US/10660357
Sequence 26, Application No. US20040115205A1
GENERAL INPORMATION:
APPLICANT: Bar-Eli, Menashe
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
CURRENT PEPLICATION NUMBER: 105/030C1
CURRENT PELICATION NUMBER: 105/030C1
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
 Indels
 Indels
 Query Match 100.0%; Score 562; DB 16; Best Local Similarity 100.0%; Pred. No. 1.5e-42; Matches 107; Conservative 0; Mismatches 0;
 Query Match 100.0%; Score 562; DB 14; Best Local Similarity 100.0%; Pred. No. 1.5e-42; Matches 107; Conservative 0; Mismatches 0;
 Sequence 318, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
 ; SEC 1D NO 26
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-530-26
 ORGANISM: Homo Sapiens
 US-10-660-357-26
 JS-10-660-357-26
 엄
 ò
 g
 ò
```

APPLICANT: John S. Babcook

```
1 DIQMIQSPSSLSASVGDRVIITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 ö
 US-IO-OIG-986-108

Publication No. US20030187247A1

GENERAL INFORMATION:

APPLICANT: Barbas, Carlos F

APPLICANT: Lorenter, Nichard A

TITLE OF INVENTION: TO HUMAN IMMUNDEFICIENCY VIRUS

FILE REPREBENCE: 313.2CON1

CURRENT APPLICATION NUMBER: US 09/149, 898

PRIOR FILING DATE: 1994-09-08

PRIOR PRILING DATE: 1994-07-18

PRIOR PRILING DATE: 1994-07-18

PRIOR PRILING DATE: 1994-07-18

PRIOR PRILING DATE: 1994-07-18

PRIOR PRILING DATE: 1994-01-06

PRIOR APPLICATION NUMBER: US 08/178,302

PRIOR APPLICATION NUMBER: US 07/954,148

PRIOR PRILING DATE: 1992-09-30

PRIOR APPLICATION NUMBER: US 07/954,148

PRIOR PRILING DATE: 1992-09-30

PRIOR PRINCE PREASED FOR WINGOWS VERSION 4.0

SEQ ID NO 108

LENGTH 107
 61 RESGSGSGTDFTFTISGLOPEDIATYYCOOYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISSLQPEDIATYXCQQYDNLPITFGGGTRLEIK 107
 Score 530; DB 17; Length 107;
Pred. No. 1e-39;
 3; Indels
 TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS TITLE OF INVENTION: FACTOR AND USES THEREOF FILE REPERENCE: ABGENIX.073A CURRENT APPLICATION NUMBER: US/10/727,155 CURRENT FILING DATE: 2003-12-02 PRIOR FILING DATE: 2002-12-02 NUMBER OF SEQ ID NOS: 320 SSEPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 318 LENGTH: 107
 4; Mismatches
 Scott Kläkamp
Mary Haak-Frendscho
Palaniswami Rathanaswami
 Query Match
Best Local Similarity 93.5%;
Matches 100; Conservative 4
 Kathy Manchulencho
Raffaella Faggioni
Giorgio Senaldi
 TYPE: PRT ORGANISM: Artificial Sequence
 Qiaojuan Jane Su
Jaspal S. Kar
Orit Foord
Larry Green
Xiao Feng
 Craig Pigott
Meina Liang
 TYPE: PRT ORGANISM: Homo sapiens
 Rozanne Lee
 US-10-727-155-318
```

```
; TYPE: PRT
; ORGANISM: human
US-10-452-593-49
 US-10-644-277-56
 US-10-364-743-21
 d
 g
 ò
 ò
 ò
 g
 1 ELTQSPSSLSASVGDRVTITCQASQDISNHLNWYQQKPGKAPKLLIYDASNLETGVPSRF 60
 3 DIQMTQSPSSLSASVGDRVTITTCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS 62
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Gaps
 ö
 ó
 63 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLGVTFGPGTKVDIK 109
 93.1%; Score 523; DB 15; Length 113; 93.5%; Pred. No. 4.7e-39; ive 3; Mismatches 4; Indels
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Length 107;
 61 SGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIK 105
 63 SGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 2; Indels
 Sequence 49, Application US/10364743
Publication No. US20040009178A1
| GENERAL INRORMATION:
| APPLICANT: Boudish, Katherine S. |
| APPLICANT: Mild, Martha A. |
| APPLICANT: Maruyama, Toshiaki |
| APPLICANT: Mar
 Sequence 49, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
 APPLICANT: Bowdish, Katherine S.
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR APPLICATION NUMBER: US 0/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
 Score 525; DB 14;
Pred. No. 2.9e-39;
4; Mismatches 2;
 PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN WERSION 3.2
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-108
 Query Match
Best Local Similarity 94.3%;
Matches 99; Conservative
 Query Match
Best Local Similarity 93.5;
Matches 100; Conservative
 TYPE: PRT
ORGANISM: human
 RESULT 6
US-10-364-743-49
 US-10-364-743-49
 US-10-452-593-49
 셤
 g
 g
 ઠે
 δ
 g
```

```
APPLICANT: Foord, Orit
APPLICANT: Liang, Meina L.
APPLICANT: Liang, Meina L.
APPLICANT: Liang, Meina L.
APPLICANT: Liang, Meina L.
APPLICANT: Alluwalia, Kiran
APPLICANT: Bhakta, Sunil
TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
FILE REFERENCE: AGGENIX. 091-09
CURRENT APPLICATION NUMBER: US/10/644,277
CURRENT FILING DATE: 2003-08-19
PRIOR FILING DATE: 2002-08-19
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO SE
 ö
 3 DIQMIQSPSSLSASVGDRVIITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS 62
 9
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDITTYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 .;
0
 ö
 63 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLGVTFGPGTKVDIK 109
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLPITFGGGTRLEIK 107
 Length 113;
 Length 152;
 4; Indels
 Query Match 93.1%; Score 523; DB 17;
Best Local Similarity 92.5%; Pred. No. 6.3e-39;
Matches 99; Conservative 3; Mismatches 5;
 Query Match 93.1%; Score 523; DB 16; Best Local Similarity 93.5%; Pred. No. 4.7e-39; Matches 100; Conservative 3; Mismatches 4;
 Frederickson, Shana
Wild, Martha A.
Maruyama, Toshiaki
No. US20040009178Alan, Mary Jean
 60/428,807
 Sequence 21, Application US/10364743; Publication No. US20040009178A1; GENERAL INFORMATION: APPLICANT: Bowdish, Katherine S. APPLICANT: Frederickson, Shane; APPLICANT: Maruyama, Toshiaki; APPLICANT: No. US20040009178A1an, Maruyama,
 Sequence 56, Application US/10644277 Publication No. US20050058639A1 GENERAL INFORMATION:
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 49
LENGTH: 113
 APPLICANT: Gudas, Jean M. APPLICANT: Haak-Frendscho, Mary
 ; TYPE: PRT;
; ORGANISM: Homosapien
US-10-644-277-56
```

```
Publication No. US20040110930A1
 RESULT 12
US-11-132-143-88
 TYPE: PRT
 FEATURE:
 a
 ò
 ö
 3 DIOMIQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS 62
 3 DIQMIQSPSSLSASVGDRVIITCQASQDISNYLWWYQQKPGKAPKLLIYDASNLETGVPS 62
 1 DIOMIQSPSSLSASVGDRVTITCOASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIOMIOSPSSLSASVGDRVTITCOASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Gaps
 ;
0
 ;
0
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLFFGGGTKVEIK 107
 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLGVTFGPGTKVDIK 109
 63 RFSGSGSGTDFTFTISSLQPEDIATYXCQQYDNLGVTFGPGTKVDIK 109
 Score 523; DB 15; Length 164;
Pred. No. 6.8e-39;
3; Mismatches 4; Indels
 RFSGSGSGTDFTFTISGLOPEDIATYYCOOYDTLPLTFGGGTKVEIK 107
 Length 164;
 4; Indels
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bridd, Martha A.
APPLICANT: Wild, Martha A.
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
CURRENT APPLICANTON INMBER: US/10/452,593
CURRENT PRILING DATE: 2003-06-02
FRIOR PRILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/356,086
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.2
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR PRILON DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 164
 tch
al Similarity 93.5%; Pred. No. 6.8e-39;
100; Conservative 3; Mismatches 4;
 Sequence 21, Application US/10452593; Publication No. US20040258699A1; GENERAL INFORMATION:
 Query Match
Best Local Similarity 93.5%;
Matches 100; Conservative
 ORGANISM: human
US-10-452-593-21
 TYPE: PRT
ORGANISM: human
 SOFTWARE: Pate
SEQ ID NO 21
LENGTH: 164
 US-10-452-593-21
 US-10-364-743-21
 Query Match
 TYPE: PRT
 Best Local
Matches 10
 염
 ò
 g
 ò
 셤
 g
 8
 ò
```

```
9
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYHQKPGKAPELLIXDASNLETGVPS 82
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 Gaps
 FRATURE:
NAME/KEY: misc_feature
| LOCATION: (232) ... (232) | CTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-132-143-88
 0
 FEATURE:

NAME/KEY: misc feature

LOCATION: (232)...(232)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-679-620-88
 .;
0
 83 RFSGSGYGIDFILISSLQPEDFATYYCQQYDNLPLTFGGGTKVEIK 129
 Query Match
92.7%; Score 521; DB 20; Length 502;
Best Local Similarity 92.5%; Pred. No. 3.3e-38;
Matches 99; Conservative 2; Mismatches 6; Indels
 Query Match 92.7%; Score 521; DB 16; Length 502; Best Local Similarity 92.5%; Pred. No. 3.3e-38; Matches 99; Conservative 2; Mismatches 6; Indels
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCOQYDTLPLTFGGGTKVEIK 107
 Sequence 88 Application US/11132143
Publication No. US2005020797741
GENERAL INFORMATION:
APPLICANT: Large Scale Biology
APPLICANT: Reinl, Stephen J.
APPLICANT: Bedwards, Patricia C.
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/11/132,143
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: US/10/679,620
PRIOR FILING DATE: 2003-10-03
PRIOR FILING DATE: 2002-10-03
GENERAL INFORMATION:

APPLICANT: Large Scale Biology
APPLICANT: Reinl, Stephen J.

APPLICANT: Reinl, Stephen J.

APPLICANT: Reinl, Stephen J.

TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/10/679,620
CURRENT FILING DATE: 2003-10-03
PRIOR PILING DATE: 2003-10-03
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTIN version 3.2
SEQ ID NO 88
LENGTH: 502
 OTHER INFORMATION: Hufab H2 , see Example 2
 OTHER INFORMATION: HufAb H2 , see Example 2
 SOFTWARE: Patentin version 3.2
SEQ ID NO 88
LENGTH: 502
 ORGANISM: Artificial Sequence FEATURE:
 ORGANISM: Artificial Sequence
 ò
```

ö

ö

RESULT 11 US-10-679-620-88 ; Sequence 88, Application US/10679620

```
1 DIQMIQSPSSLSASVGDRVIITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS 60
 1 DIOMIQSPSSLSASVGDRVIIITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLEIGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1 DIQMTQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 1;
 Length 107;
 61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNL-ITFGGGTRLEIK 106
 61 RFSGSGSGTDFTFTISGLOPEDIATYYCOOYDTLPLTFGGGTKVEIK 107
 61 RFSGSGSGTDFTFTINSLQPEDIATYYCQEYNNLPYSFGQGTKLEIK 107
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 Score 512.5; DB 20; Length
Pred. No. 3.8e-38;
4; Mismatches 3; Indels
 90.7%; Pred. No. 4.6e-38;
cive 6; Mismatches 4; Indels
 APPLICANT: PULLEN, NICHOLAS
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MACCAM
FILE REFERENCE: ABX-PF6
CURRENT FALICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR PLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
LENGTH: 107
 Search completed: November 16, 2005, 23:05:44 Job time: 66.6949 secs
 Sequence 132, Application US/11031485 Publication No. US20050232917A1 GENERAL INFORMATION:
 91.2%;
 Best Local Similarity 90.7
Matches 97; Conservative
 Query Match
Best Local Similarity 92.5
Matches 99; Conservative
 TYPE: PRT; ORGANISM: Homo sapiens
US-11-031-485-132
 US-11-031-485-132
 g
 ઠે
 Q
 셤
 d
 6
 APPLICANT: Schering Corporation and Abgenix, Inc.
APPLICANT: Schering Corporation and Abgenix, Inc.
APPLICANT: Greenfeder, Scott
APPLICANT: Corvalan, Jose
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COME
TITLE OF INVENTION: HUMAN MONOCLONAL
TITLE OF INVENTION: HUMBEN SAME
TITLE REFERENCE: L101564MI
CURRENT PAPLICATION NUMBER: US/10/401,344
CURRENT PILING DATE: 2003-03-27
NUMBER OF SEQ 1D NOS: 22
SOFTWARE: Patentin version 3.1
SEQ 1D NO 4
LENGTH: 236
 APPLICANT: Foord, Orit
APPLICANT: Liang, Meina L.
APPLICANT: Liang, Meina L.
APPLICANT: Liang, Meina L.
APPLICANT: Blakta, Suni
TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
TITLE REFERENCE: ABGENIX. 091-19
CURRENT APPLICATION NUMBER: US/10/644,277
CURRENT FILLING DATE: 2003-08-19
PRIOR FILLING DATE: 2002-08-19
PRIOR FILLING DATE: 2002-08-19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
LENGTH: 214
TYPE: PRT
23 DIQMTQSPSSLSASVGDRVIITCQASQDISNYLNWYHQKPGKAPELLIYDASNLETGVPS 82
 23 DIQMTQSPSSLSASVGDRVTITCQASQDIINYLNWYQQKPGKAPKLLIYSASNLETRVPS 82
 1 DIOMIQSPSSLSASVGDRVTITCQASQDINNYLNWYQQKPGKAPKLLIYDASNLETGVPS
 Gaps
 ö
 83 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNHPLIFGGGTKVEIR 129
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 83 RFSGSGYGTDFTLTISSLQPEDFATYYCQQYDNLPLTFGGGTKVEIK 129
 61 RFSGSGSGTDFTFTISGLQPEDIATYYCQQYDTLPLTFGGGTKVEIK 107
 91.6%; Score 515; DB 17; Length 214;
 Query Match 92.2%; Score 518; DB 14; Length 236; Best Local Similarity 93.5%; Pred. No. 2.8e-38; Matches 100; Conservative 1; Mismatches 6; Indels
 US-10-644-277-64
Sequence 64, Application US/10644277
Publication No. US20050058639A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean M.
APPLICANT: Haak-Frendscho, Mary
 Sequence 4, Application US/10401344
Publication No. US20030194404A1
GENERAL INFORMATION:
 NAME/KEY: Signal Peptide;
COCATION: (1)..(22)
CTHER INFORMATION:
US-10-401-344-4
 ORGANISM: Homo sapiens
 ORGANISM: Homosapien
 Query Match
 g
 g
 셤
 ઠ
 ò
 ઠે
 g
```

The main of the corn

```
November 16, 2005, 21:35:48; Search time 6j.3676 Seconds (without alignments) 674.351 Million cell updates/sec
 1 DIQMTQSPSSLSASVGDRVT......CQKFSSPPFTFGPGTKVDIS 107
 2105692
5.1.6
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2105692 seqs, 386760381 residues
GenCore version (c) 1993 - 2005
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-10-660-357A-30
 Copyright
 Perfect score:
Sequence:
 Scoring table:
 Searched:
 Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003as: \* geneseqp2003bs: \* geneseqp2004s: \*

........

A\_Geneseq\_16Dec04:\* 1: geneseqp1980s:\* 2: geneserm1000.

Database :

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\*

| ES        | Description           |          | Add05405 Anti-MUC1 | Adf09843 Human ant | Adp22400 Human ant | Adp46984 Murine li |          | Aau90947 Insulin/i |          | Adk18922 Anti-huma | Adp46980 Murine li | _        |          | Aau90904 Insulin/i | Adk18799 Anti-huma | Adk18833 Anti-huma |          | Adj57622 INFalpha | Human    | Adl25434 Human mAb | Abp44153 Human BLy | Human    |          |          |          |          |
|-----------|-----------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|----------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|----------|-------------------|----------|--------------------|--------------------|----------|----------|----------|----------|----------|
| SUMMARIES | ΙΩ                    | ADC99801 | ADD05405           | ADF09843           | ADP22400           | ADP46984           | AAU90902 | AAU90947           | ADP22358 | ADK18922           | ADP46980           | ADP46982 | AAU90905 | AAU90904           | ADK18799           | ADK18833           | ADK18608 | ADJ57622          | ADJ58753 | ADL25434           | ABP44153           | ABP44250 | ABP44071 | ADG94898 | ADG94980 | ADG95077 |
|           | DB                    | 7        | ۲-                 | 7                  | œ                  | ထ                  | ഹ        | ഗ                  | æ        | 7                  | œ                  | œ        | 2        | Ŋ                  | 7                  | 7                  | 7        | œ                 | œ        | œ                  | Ŋ                  | ß        | ß        | 7        | 7        | 7        |
|           | Query<br>Match Length | 107      | 107                | 107                | 107                | 108                | 242      | 245                | 107      | 107                | 108                | 108      | 239      | 242                | 107                | 107                | 107      | 107               | 107      | 107                | 244                | 244      | 244      | 244      | 244      | 244      |
| ٠         | Query<br>Match        | 100.0    | 100.0              | 100.0              | 93.5               | 93.5               | 93.5     | 93.5               | 91.4     | 8.06               | 90.5               | 90.5     | 90.5     | 90.3               | 90.1               | 90.1               | 90.1     | 90.1              | 90.1     | 90.1               | 90.1               | 90.1     | 1.06     | 90.1     | 90.1     | 90.1     |
|           | Score                 | 556      | 556                | 556                | 520                | 520                | 520      | 520                | 508      | 505                | 503                | 503      | 503      | 502                | 501                | 501                | 501      | 501               | 501      | 501                | 501                | 501      | 501      | 501      | 501      | 501      |
|           | Result<br>No.         | н        | 7                  | 8                  | 4                  | ß                  | 9        | 7                  | 8        | 6                  | 10                 | 11       | 12       | 13                 | 14                 | 15                 | 16       | 17                | 18       | 19                 | 20                 | 21       | 22       | 23       | 24       | 25       |

| Aau90901 Insulin/i<br>Adp6985 Murine li<br>Aaw27568 Anti-TNF-<br>Aao16459 Human ant | M M M E M                                    |                                                          | Ado40410 Single ch<br>Ado40407 Single ch<br>Ado40405 Single ch<br>Ado40409 Single ch<br>Ado40410 Single ch<br>Ado40412 Single ch |
|-------------------------------------------------------------------------------------|----------------------------------------------|----------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------|
| AAU90901<br>ADP46985<br>AAW27568<br>AAO16459                                        | ADK18798<br>ADK18832<br>ADK18615<br>ADJ57614 | ADL25446<br>AD001441<br>AD040413<br>AD040408<br>AD040411 | ADO40410<br>ADO40407<br>ADO40405<br>ADO40409<br>ADO40412                                                                         |
| ω φ 74 Φ                                                                            | rrr 88                                       |                                                          | <b></b>                                                                                                                          |
| 245<br>108<br>107                                                                   | 1001                                         | 107<br>108<br>239<br>247<br>249                          | 250<br>252<br>253<br>253<br>253<br>253                                                                                           |
| 90.1<br>89.9<br>89.7                                                                | 89.7<br>89.7<br>7.68<br>7.68                 | 89.7<br>89.7<br>7.68<br>7.08                             | 899.7<br>7.088<br>7.088<br>7.088<br>7.088                                                                                        |
| 501<br>500<br>499                                                                   | 4 4 4 4 4<br>9 9 9 9 9<br>9 9 9 9 9          | 4 4 4 4 4<br>9 0 0 0 0<br>9 0 0 0 0                      | 4 4 4 4 4<br>0 0 0 0 0 0<br>0 0 0 0 0 0                                                                                          |
| 26<br>23<br>29                                                                      | 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5      | 3333<br>333<br>333<br>333<br>333                         | 4 4 4 4 4 4<br>0 1 2 2 4 4 6                                                                                                     |

## ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 30 ADC99801 standard; protein; 107 AA 01-JAN-2004 (first entry) lung cancer; human. RESULT 1 ADC99801 

WO2003057838-A2. sapiens. Ношо

26-DEC-2002; 2002WO-US041581.

17-JUL-2003.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC.

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99803.

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 30; 78pp; English.

a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody comprising The invention relates to a novel isolated monoclonal antibody

~

ô

Gaps

. 0

Indels

6.2e-32;

Mismatches

9 9

107

ż

SXS

엄 ò

ò

```
1 DIOMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; light chain; human.
 61 RFSGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDIS 107
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDIS
 Human anti-MUC18 monoclonal antibody light chain #8.
 Pred. No.
100.0%; Pre-
 ADF09843 standard; protein; 107
 26-DEC-2002; 2002WO-US041580.
 28-DEC-2001; 2001US-0346414P.
 Best Local Similarity 100.
Matches 107; Conservative
 Best Local Similarity 100.
Matches 107; Conservative
 WPI; 2003-598367/56.
 (ABGE-) ABGENIX INC
 monoclonal antibody
 N-PSDB; ADF09845.
 Sequence 107 AA;
 WO2003057837-A2
 Homo sapiens.
 12-FEB-2004
 17-JUL-2003
 61
 Query Match
 ADF09843;
 Gudas J;
 RESULT 3
 ADF09843
 셤
 셤
 ઠે
 셤
 8
 ò
 ò
 ö
 The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 antibody consists of any one of 10 fully defined sequences of 117-123 binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has oversetted and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting cumour growth (e.g. melanoma, lung tumour or tumour metaetasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metaetatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
 09
 9
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Anti-MUC18 antibody light chain variable region protein, SEQ ID No 30.
 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccin
antigen; tumour metastasis; melanoma; metastatic; human; light chain.
 Gaps
 ö
 Length 107;
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDIS 107
 DB 7; Length 107;
 Indels
 .;
0
 100.0%; Score 556; DB 7; 100.0%; Pred. No. 6.2e-32;
 0; Mismatches
 100.0%; Score 556;
 Claim 3; SEQ ID NO 30; 87pp; English.
 light chain protein of the invention.
 ADD05405 standard; protein; 107 AA
 26-DEC-2002; 2002WO-US041582
 28-DEC-2001; 2001US-0346460P
 (first entry)
 the invention.
 Conservative
 Gudas J, Bar-Eli M;
 WPI; 2003-577496/54.
N-PSDB; ADD05407.
 (ABGE-) ABGENIX INC
 Best Local Similarity
Matches 107; Conser
 metastatic tumor.
 Sequence 107 AA;
 Sequence 107 AA;
 WO2003057006-A2
 Homo sapiens
 01-JAN-2004
 17-JUL-2003
 ADD05405;
 Query Match
 Query Match
```

```
The invention comprises a method for inhibiting cell proliferation associated with expression of MUCIB tumour antigen. The method involves administering anti-MUCIB monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUCIB tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUCIB tumour antigen-specific
 ö
 9
 1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
 1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gарв
 .
0
 RESGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDIS 107
 Length 107;
 Indels
 ö
 100.0%; Score 556; DB 7;
100.0%; Pred. No. 6.2e-32;
ive 0; Mismatches 0;
 Claim 3; SEQ ID NO 30; 83pp; English.
 61
 ВÞ
```

ന

```
anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antibacterial; antiinflammatory; antipsoriatic; antiinflammatory; antipsoriatic; antirheumatic; eating-disorder; immunomodulator; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagoniat; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; pladder cancer; uning cancer; glioblastoma; stomach cancer; endometrial cancer; kidney cancer; colon cancer; pancreatic cancer; prostrate cancer; immuno-mediated inflammatory disease;
 rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis; restenosis; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; anorexia; multiple sclerosis.
 Human anti-TNFa antibody light chain variable region SEQ ID NO:306.
 monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 Example 10; SEQ ID NO 306; 213pp; English.
 ADP22400 standard; protein; 107 AA.
 02-DEC-2003; 2003WO-US038281
 02-DEC-2002; 2002US-0430729P
 (first entry)
 (ABGE-) ABGENIX INC.
 WPI; 2004-480601/45.
 WO2004050683-A2
 Homo sapiens
 09-SEP-2004
 17-JUN-2004.
 ADP22400;
RESULT 4
 ADP22400
```

New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Le Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;

The present invention describes a human monoclonal antibody (1) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region 1 (CDR1) having the two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);

c two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);

c two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);

c and (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying (M1) the level of TNFa in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and TNFa in the sample; (2) a composition comprising the antibody or its functional and a carrier; (3) treating (M2) an animal suffering from a neopolastic, or an immuno-mediated inflammatory disease by selecting an enopolastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (1); and (4) inhibiting (M3) TNFa induced apoptosis by administering the human monoclonal antibody of (1) antiarteriosclerotic, antirheumatic, eating-antiboacterial, antiinflammatory, antisporiatic, antirheumatic, eating-disease and antiapoptotic activities, and can be used as a TNFa antagoniet. The antibody (1) is useful in the preparation of medicament for treating TNF induced apoptosis, neoplastic disease such as premath cancer, ovarian cancer, binder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer,

```
ò
 9
 1 DIOMIQSPSSLSASVGDRVIIICRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
 Murine light chain variable anti-amphetamine antibody protein SeqID 40.
 1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 diseases such as rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and multiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the exemplification of the present invention.
 murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine; PCP; drug addiction; antiaddictive; antibody therapy.
 0; Gaps
 Gunnell MG, Haak-Frendscho M;
 Length 107;
 Query Match 93.5%; Score 520; DB 8; Length 10 Best Local Similarity 94.3%; Pred. No. 2.1e-29; Matches 100; Conservative 2; Mismatches 4; Indels
 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI
 ADP46984 standard; protein; 108 AA
 Carroll FI, Abraham P,
 02-DEC-2003; 2003WO-US038384.
 02-DEC-2002; 2002US-0430717P
 (first entry)
 WPI; 2004-460981/43.
 (ABGE-) ABGENIX INC.
 Sequence 107 AA;
 WO2004050032-A2.
 Mus musculus.
 09-SEP-2004
 17-JUN-2004.
 Owens SM,
 ADP46984;
 61
 Feng X;
 RESULT 5
 ADP46984
 888888888888
 ò
 吕
 ò
 셤
```

This invention relates to novel antibodies, or binding fragments thereof, that bind directly to various drugs of abuse. Specifically, it refers to amman or chimeric monoclonal antibodies that are capable of binding to amphetamine, methamphetamine or phencyclidine (PCP). The present invention describes generating hybridoma cell lines that produce such antibodies and transforming a cell with a gene encoding the antibody, which when conjugated to a therapeut genet, toxin or radiolsotope can be used to treat a patient suffering from a drug addiction. Accordingly, these compositions exhibit antiaddictive activities and can be used for antibody therapy to treat patients suffering from a drug addiction. This polypeptide sequence is a murine light chain variable anti-amphetamine antibody of the invention.

New isolated antibody or its binding fragment that binds specifically to a drug of abuse, useful for treating a patient suffering from addiction to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.

Example 1; SEQ ID NO 40; 88pp; English.

Sequence 108 AA;

ö

Gaps

ö

Indels

4;

2; Mismatches

```
100; Conservative
 Synthetic
 invention
 AAU90947;
 Query Match
Matches
 AAU90947
 RESULT
 셤
 8
 The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site I of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are useful for treating diabetes. Also, peptides that are useful for treating insulin-like growth factor. (IGF-) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or inferior
 ö
 neuropathy.
 9
 DIOMTOSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
 DIOMIOSPSSLSASVGDRVIITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 ö
 Gaps
 Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin insulin-like growth factor receptors.
 Insulin/insulin-like growth factor receptor-binding peptide #2858
 ;
0
 Cytostatic, antidiabetic, neuroprotective, cerebroprotective, ophthalmological, insulin, receptor, gene therapy, diabetes, insulin-like growth factor-1; IGF-1; tumour, prostate, breast, diabetic retinopathy, neurological diseases, stroke, diabetic.
 Pillutla R, Brandt J;
Ostergaard S, Mandecki
 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 Length 108;
 4; Indels
 93.5%; Score 520; DB 8;
94.3%; Pred. No. 2.1e-29;
iive 2; Mismatches 4;
 Schaeffer L,
J, Cheng W,
Hsiao K;
 AAU90902 standard; protein; 242 AA
 Example 5; Fig 36; 390pp; English.
 (DGIB-) DGI BIOTECHNOLOGIES LLC. (NOVO) NOVO NORDISK AS.
 29-MAR-2000; 2000WO-US008528.
 29-MAR-2000; 2000WO-US008528
 (first entry)
 Query Match
Best Local Similarity 94.3
Matches 100; Conservative
 Beasley J, Blume AJ,
Brissette R, Spetzler
Hansen PH, Ravera M,
 WPI; 2002-025774/03
 Sequence 242 AA;
 WO200172771-A2
 18-JUN-2002
 04-OCT-2001
 Synthetic.
 nvention
 61
 AAU90902;
 엄
 ద
 ò
```

Length 242;

Score 520; DB 5; Pred. No. 4.2e-29;

93.5%; 94.3%;

Query Match Best Local Similarity

```
The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor-[IGF-1] receptor are useful for treating insulin-like growth factor (IGF-1) receptor are useful for treating insulin-like growth factor (IGF-1) receptor are receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the
 ö
 136 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 195
 Cytostatic; antidiabetic; neuroprotective; cerebroprotective; obthbalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1; IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
9
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 ö
 Gaps
 Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin insulin-like growth factor receptors.
 Insulin/insulin-like growth factor receptor-binding peptide #2903
 Pillutla R, Brandt J;
Ostergaard S, Mandecki WS;
 o;
 93.5%; Score 520; DB 5; Length 245; 94.3%; Pred. No. 4.3e-29; ive 2; Mismatches 4; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 J, Cheng W, Hsiao K;
 Disclosure; Fig 57; 390pp; English.
 Z
 AAU90947 standard; protein; 245
 DGIB-) DGI BIOTECHNOLOGIES LLC
 29-MAR-2000; 2000WO-US008528.
 29-MAR-2000; 2000WO-US008528.
 (first entry)
 Conservative
 (NOVO) NOVO NORDISK AS
 Spetzler
 Beasley J, Blume --
Brissette R, Spetzler -- PH. Ravera M,
 WPI; 2002-025774/03
 Best Local Similarity
 Sequence 245 AA;
 WO200172771-A2.
 18-JUN-2002
 04-OCT-2001.
 Matches 100;
 ð
```

S

```
The present invention describes a human monoclonal antibody (I) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region 1 (CDI) having the two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421); and (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (S3, ADP22418) or (S4, ADP22442). ABO described: (I) assaying (M1) the level of TNRa in a patient sample, comprising contacting with (I), and detecting the level of binding between the antibody and TNRa in the sample; (2) a composition comprising the antibody or its functional composition.

(Eragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human animal antibody of (I); and (4) inhibiting (M3) TNRa induced apoptosis by administering the human monoclonal antibody of TNRa induced apoptosis by administering the human monoclonal antibody of
 human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; antibody; anabolic; antiarteriosclerotic; antiarthritic; antibacterial; antiinclammatory; antigoritatic; antiarthritic; eating-disorder; immunomodulator; immunosuppressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonist; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer; bladder cancer; lung cancer; glioblastoma; stomach cancer; endometrial cancer; immuno-mediated inflammatory disease; prostrate cancer; immuno-mediated inflammatory disease; protection; stebumatorial cancer; immuno-mediated inflammatory disease; restenosis; autorimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; multiple sclerosis.
New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 Human anti-TNFa antibody light chain variable region SEQ ID NO:264
 Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S, Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee F
Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
 106
 199 RFSGSGSGTDFTLTISSLOPEDVATYYCOKYNSAPFTFGPGTKVDI
 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI
 Example 10; SEQ ID NO 264; 213pp; English.
 ADP22358 standard; protein; 107 AA.
 02-DEC-2003; 2003WO-US038281
 02-DEC-2002; 2002US-0430729P
 (first entry)
 WPI; 2004-480601/45.
N-PSDB; ADP22357.
 (ABGE-) ABGENIX INC
 402004050683-A2
 Homo sapiens,
 17-JUN-2004.
 09-SEP-2004
 61
 ADP22358;
 RESULT 8
ADP22358
 유
 ઠે
```

(I) has anabolic, antiarteriosclerotic, antiarthritic,

```
antibacterial, antinflammatory, antipsoriatic, antirheumatic, eating-
disorders, immunomodulator, immunosuppressive, nephrotropic,
neuroprotective, vasotropic and antiapoptotic activities, and can be used
as a TNFa antagonist. The antiapoptotic activities, and can be used
medicament for treating TNF induced apoptosis, neoplastic disease such as
breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
pancreatic cancer, and prostrate cancer, indney cancer, colon cancer,
pancreatic cancer, and prostrate cancer, or immuno-mediated inflammatory
diseases such as rheumatoid arthritis, glomerulonephritis
atherosclerosis, psoriasis, restenosis, autoimmuno disease, Crohn's
disease, graft-host reactions, septic shock, cachexia, anorexia, and
multiple sclerosis. The present sequence represents a human anti-TNFa
antibody light chain variable region, which is used in the
exemplification of the present invention.
 ö
 The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGP-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGP-D nucleic acids and polypoptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188.0.99 arising in the conditioned medium obtained when
 9
 9
 1 DIOMIOSPSSLSASVGDRVIITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKFLIYAASTLQSGVPS
 Gaps
 ķ
 ö
 New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 antiinflammatory; immunomodulator; cytostatic; gene therapy.
 Length 107;
 Gazit G,
 ch 91.4%; Score 508; DB 8; Length 10 Similarity 91.5%; Pred. No. 1.5e-28; 97; Conservative 3; Mismatches 6; Indels
 Anti-human PDGF-D antibody protein related sequence #148.
 Chen F,
 Disclosure; SEQ ID NO 346; 255pp; English.
 Feng X, Yang X,
 ADK18922 standard; protein; 107 AA
 06-JAN-2003; 2003WO-US000398.
 07-JAN-2002; 2002US-00041860.
 (first entry)
 Jia X,
 WPI; 2003-587119/55.
 (ABGE-) ABGENIX INC.
 Query Match
Best Local Similarity
 Sequence 107 AA;
 WO2003057857-A2.
 Corvalan JRF,
 Homo sapiens.
 06-MAY-2004
 17-JUL-2003.
 Bezabeh B;
 61
 ADK18922;
 ADK18922
 RESULT
 8
 ठ
 셤
 ð
 q
```

9

DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS

88333

셤 ò 셤

8

```
ö
 This invention relates to novel antibodies, or binding fragments thereof, that bind directly to various drugs of abuse. Specifically, it refers to amman or chimeric monoclonal antibodies that are capable of binding to amphetemine, methambhetamine or phencyclidine (PCP). The present invention describes generating hybridoma cell lines that produce such antibodies and transforming a cell with a gene encoding the antibody, which when conjugated to a therapeutic agent, toxin or radioisotope be used to treat a patient suffering from a drug addiction. Accordingly, these compositions exhibit antiaddictive activities and can be used for antibody the reapty to treat patients suffering from a drug addiction. This polypeptide sequence is a murine light chain variable anti-amphetamine antibody of the invention.
 9
 9
 New isolated antibody or its binding fragment that binds specifically to a drug of abuse, useful for treating a patient suffering from addiction to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.
 Murine light chain variable anti-amphetamine antibody protein SeqID 36.
HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 murine, mouse, antibody, amphetamine; methamphetamine, phencyclidine,
PCP, drug addiction, antiaddictive, antibody therapy.
 Gaps
 Haak-Frendscho M;
 ó
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 Length 107;
 Score 505; DB 7; Length 10
Pred. No. 2.4e-28;
2; Mismatches 6; Indels
 Gunnell MG,
 Example 1; SEQ ID NO 36; 88pp; English.
 Ā
 Abraham P,
 ADP46980 standard; protein; 108
 02-DEC-2002; 2002US-0430717P.
 90.8%;
 02-DEC-2003; 2003WO-US038384
 (first entry)
 Similarity 92.5 98; Conservative
 Carroll FI,
 WPI; 2004-460981/43.
 (ABGE-) ABGENIX INC.
 Sequence 108 AA;
 Sequence 107 AA;
 WO2004050032-A2
 Mus musculus
 17-JUN-2004.
 09-SEP-2004
 Owens SM,
 Query Match
Best Local S
 ADP46980,
 Feng X;
 RESULT 10
```

ö

Gaps

. 0

90.5%; Score 503; DB 8; Length 108; 91.5%; Pred. No. 3.3e-28; Indels ive 4; Mismatches 5; Indels

Conservative

Query Match Best Local Similarity Matches 97; Conserva

```
ô
 This invention relates to novel antibodies, or binding fragments thereof, that bind directly to various drugs of abuse. Specifically, it refers to amman or chimeric monoclonal antibodies that are capable of binding to amphetamine, methamphetamine or phencyclidine (PCP). The present invention describes generating hybridoma cell lines that produce such antibodies and transforming a cell with a gene encoding the antibody, which when conjugated to a therapeutic agent, toxin or radioisotope can be used to treat a patient suffering from a drug addiction. Accordingly, these compositions exhibit antiaddictive activities and can be used for antibody to treat patients suffering from a drug addiction. This polypeptide sequence is a murine light chain variable anti-amphetamine antibody of the invention.
 1 DIQMIQSPSSLSASVGDRVIITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
 New isolated antibody or its binding fragment that binds specifically to a drug of abuse, useful for treating a patient suffering from addiction to a drug of abuse, e.g. amphetamine, methamphetamine, or phencyclidine.
 1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 9
1 DIQMIQSPSSISASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS
 murine; mouse; antibody; amphetamine; methamphetamine; phencyclidine; PCP; drug addiction; antiaddictive; antibody therapy.
 Gaps
 Haak-Frendscho M;
 ;
0
 Murine light chain variable anti-amphetamine antibody protein
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPWTFGQGTKVEI 106
 Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI
 90.5%; Score 503; DB 8; L. Lilarity 91.5%; Pred. No. 3.3e-28; Conservative 4; Mismatches 5;
 Gunnell MG,
 Claim 2; SEQ ID NO 38; 88pp; English
 Abraham P,
 ż
 ADP46982 standard; protein; 108
 02-DEC-2003; 2003WO-US038384.
 02-DEC-2002; 2002US-0430717P
 (first entry)
 Carroll FI,
 WPI; 2004-460981/43.
 (ABGE-) ABGENIX INC
 Query Match
Best Local Similarity
 Sequence 108 AA;
 WO2004050032-A2.
 Mus musculus.
 97;
 09-SEP-2004
 17-JUN-2004
 Owens SM,
 ADP46982;
 Feng X;
 Matches
 RESULT 11
 ADP46982
 셤
 ð
 g
 g
 셤
 8
 ò
```

```
Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insullin; receptor; gene therapy; diabetes; insullin-like growth factor-1; IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
 Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin or insulin-like growth factor receptors.
 Insulin/insulin-like growth factor receptor-binding peptide #2861.
 Pillutla R, Brandt J;
Ostergaard S, Mandecki WS;
 90.5%; Score 503; DB 5; Length 239; 91.5%; Pred. No. 6.5e-28; ive 4; Mismatches 5; Indels
 Beasley J, Blume AJ, Schaeffer L,
Brissette R, Spetzler J, Cheng W,
Hansen PH, Ravera M, Hsiao K;
 AAU90905 standard; protein; 239 AA.
 Example 5; Fig 39; 390pp; English.
 (DGIB-) DGI BIOTECHNOLOGIES LLC. (NOVO) NOVO NORDISK AS.
 29-MAR-2000; 2000WO-US008528
 29-MAR-2000; 2000WO-US008528
 (first entry)
 WPI; 2002-025774/03.
 Sequence 239 AA;
 WO200172771-A2.
 18-JUN-2002
 04-OCT-2001
 Synthetic
 AAU90905;
 invention
 Query Match
RESULT 12
ANU90005
XX
AAU900005
XX
AAU900005
DT 18-JU
DE
 Best Loca
Matches
```

```
The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor: I (IGF-1) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. AAU88034-AAU80957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the
```

```
ô
 133 DIQMIQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIXAASTLQSGVPS 192
 9
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 ; 0
Local Similarity 91.5
les 97; Conservative
 ð
 임
```

```
61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 RFSGSGSGTDFTLTISSLOPEDVATYYCOXYNSAPWTFGOGTKVEI
```

ઠે g ADK18799 standard; protein; 107 AA

ADK18799

SKKH

196

요.

RESULT 14 ADK18799

RESULT 13 AAU90904 ID AAU90

```
AAU90904 standard; protein; 242 AA.
```

```
The invention relates to a method of modulating insulin activity in receptor (IR). A composition containing a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor-1 (IGF-1) receptor are useful for treating insulin-like growth factor (IGF) sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in the peptides are also useful in the peptides are also useful in the peptides and research reagents. AAU88034-AAU80957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the
 ö
 Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1; IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
 136 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 195
 9
 Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin or insulin-like growth factor receptors.
 DIQMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 0; Gaps
 Insulin/insulin-like growth factor receptor-binding peptide #2860
 Pillutla R, Brandt J;
Ostergaard S, Mandecki WS;
 RESCSCIPETLISSLOPEDVATYZCOKESSPETFGPGTKVDI 106
 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPYIFGQGTKLEI 241
 Length 242;
 / Match 90.3%; Score 502; DB 5; Length 24:
Local Similarity 90.6%; Pred. No. 7.8e-28;
nes 96; Conservative 5; Mismatches 5; Indels
 Schaeffer L,
J, Cheng W,
Hsiao K;
 Example 5; Fig 38; 390pp; English
 BIOTECHNOLOGIES LLC
 29-MAR-2000; 2000WO-US008528.
 29-MAR-2000; 2000WO-US008528.
 18-JUN-2002 (first entry)
 (DGIB-) DGI BIOTECHNOLOK (NOVO) NOVO NORDISK AS
 Beasley J, Blume AJ,
Brissette R, Spetzler
Hansen PH, Ravera M,
 WPI; 2002-025774/03
 Sequence 242 AA;
 WO200172771-A2.
 04-OCT-2001.
 Synthetic.
 nvention
 AAU90904;
 Н
 61
 Query Match
ò
 셤
 ò
```

Weber R;

Gazit G,

Chen F,

Yang X,

Feng X,

Jia X,

Corvalan JRF, Bezabeh B;

(ABGE-) ABGENIX INC

WPI; 2003-587119/55.

06-JAN-2003; 2003WO-US000398. 07-JAN-2002; 2002US-00041860 New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.

Disclosure; SEQ ID NO 257; 255pp; English

```
The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188 to 99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEPA/Sec-30664188. This sequence corresponds to a protein used in the invention.
 Weber R;
 New human monoclonal antibody that binds to platelet-derived factor-D (PDGF-D), useful for treating chronic and recurrent diseases, such as inflammation, autoimmunity and cancer.
 90.1%; Score 501; DB 7; Length 107; 91.5%; Pred. No. 4.5e-28; ive 3; Mismatches 6; Indels
 antiinflammatory; immunomodulator; cytostatic; gene therapy
 Gazit G,
 PDGF-D antibody protein related sequence #25.
 Chen F,
 Disclosure; SEQ ID NO 223; 255pp; English
 Yang X,
 Feng X,
 06-JAN-2003; 2003WO-US000398
 07-JAN-2002; 2002US-00041860
06-MAY-2004 (first entry)
 Corvalan JRF, Jia X,
 (ABGE-) ABGENIX INC
 WPI; 2003-587119/55
 Query Match
Best Local Similarity
 Sequence 107 AA;
 WO2003057857-A2
 Homo sapiens
 17-JUL-2003
 Bezabeh B;
```

The invention relates to a human monoclonal antibody that binds to platelet-derived growth factor-D (PDGF-D). The antibodies are useful for treating chronic and recurrent human diseases, such as inflammation, autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are useful for modulating collagen formation, and for staging various cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were generated using an active protein fragment of the gene product from the clone 30664188 to 99 arising in the conditioned medium obtained when HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This sequence corresponds to a protein used in the invention.

```
ö
 9
 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS
 1 DIOMIOSPSSISASVGDRVIITCRASOGIRNYLAWYQQNPGKVPKILIYGASTLQSGVPS
 Gaps
 ö
 61 RESGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 Length 107;
 6; Indels
 Match 90.1%; Score 501; DB 7; Local Similarity 91.5%; Pred. No. 4.5e-28; les 97; Conservative 3; Mismatches 6
 Search completed: November 16, 2005, 21:51:42 Job time : 62.3676 secs
Sequence 107 AA;
 Query Match
 Best Loc
Matches
 g
 ò
 셤
 ð
```

ö

Gaps

ö

97; Conservative

Matches

9 9

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS

RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106 

61 61

g ð 8

ઠે

antiinflammatory; immunomodulator; cytostatic; gene therapy

WO2003057857-A2

17-JUL-2003

Homo sapiens

Anti-human PDGF-D antibody protein related sequence #59

(first entry)

06-MAY-2004

ADK18833;

¥

ADK18833 standard; protein; 107

RESULT 15

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

November 16, 2005, 21:37:48; Search time 12.7849 Seconds (without alignments) 805.260 Million cell updates/sec Run on:

US-10-660-357A-30

556 1 DIQMTQSPSSLSASVGDRVT......CQKFSSPPFTFGPGTKVDIS 107 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Score Match Length DB Result No. 

| 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ALIGNMENTS  on 26-May-1995 #text_che H.G. lin chi genes and their 180891; PMID:8258341  ot shown og44392; PIDN:CAA51130. on; immunoglobulin homolobulin                                                                                                                                                                                                                                                                                                                                                                                                                                                | ### 87.9%; Score 489; DB 2; Length 131;  imilarity 89.6%; Pred. No. 38-35;  Conservative 5; Mismatches 6; Indels 0; Gaps 0;  DIOMTOSPSSLASSOBNYITCRASOGIRNYLAWYQNPGKVPKLLIYGASTLQSGVPS 60  DIOMTOSPSSLASSUGNRVITTCRASOGISNYLAWYQNPGKVPKLLIYAASTLQSGVPS 80  RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFFGPGTKVDI 106 |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 80.0<br>79.9<br>79.9<br>79.9<br>79.9<br>79.9<br>79.1<br>105<br>79.1<br>105<br>79.1<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>108<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0<br>79.0 | RESULT 1 S40352 19 kappa chain V-J-C region - human C.Species: Homo sapiens (man) C.Dates: 19-May-1994 #sequence_revisi C.R.Cession: S40352 R.K.lein, R.; Jaenichen, R.; Zachau, R.; Tile: Expressed human immunoglobu A.Title: Expressed human immunoglobu A.Feference number: S40312; MUID:940 A.Reference; preliminary; translation n.A.Molecule type: mRNA A.Residues: 1-131 «KLE» A.Residues: 1-131 «KLE» A.Residues: 1-131 «KLE» A.Residues: In-131 «KLE» A.Residues: In-131 «KLE» A.Residues: In-131 «KLE» C.Superfamily: immunoglobulin V regiC: Keywords: heterotetramer; immunoglobulin homo | larity 87.5 Conservative MTQSPSSLSASV MTQSPSSLSASV GSGSGTDFTLTIE                                                                                                                                                                                                                                             |
| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | RESULT 1 S40352 19 Kappa chain V-J-C reg C;Species: Howo sapiens C;Accession: 840352 R;Klein, R.; Jaenichen, Eur. J. Immunoll. 23, 32, 34 A;Title: Expressed humar A;Reference number: 8403 A;Accession: 84035 A;Acatus: prelliminary; th A;Molecule type: mRNA A;References: EWBI C;Superfamily: immunoglc C;Reywords: heterotetram F;36-110/Domain: immunog                                                                                                                                                                                                                                          | atch cal S 95 21 21 81                                                                                                                                                                                                                                                                                       |
| U U W U U U U U U U U U U U U U U U U U                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | RESULT 1 S40352 19 Kappa C,Species C,Date C,Date C,Accesi R,Klein, B,K.Till: A,Referen A,Referen A,Roccesi A,Molecul A,Residu C,Superfa C,Keyword F,36-110/F                                                                                                                                                                                                                                                                                                                                                                                                                                           | Query M Best Lo Matches Qy Db Qy Oy                                                                                                                                                                                                                                                                          |

| :  |       |      | ,   | ! |          |                    |                        |                                                                                            |
|----|-------|------|-----|---|----------|--------------------|------------------------|--------------------------------------------------------------------------------------------|
| 7  | 489   | 87.9 | 131 | 7 | 840352   | Ig kappa chain V-J | ò                      | 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60                          |
| ~  | 479.5 | 86.2 | 107 | 7 | S36275   | Ig lambda chain V  |                        |                                                                                            |
| m  | 470   | 84.5 | 132 | 7 | 840334   | Ig kappa chain - h | qq                     | 21 DIQMTQSPSSLSASVGNRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 80                         |
| 4  | 463   | 83.3 | 129 | 0 | S52792   | Ig kappa chain V r |                        |                                                                                            |
| S  | 462   | 83.1 | 107 | 7 | S36269   | Ig lambda chain v  | ò                      | 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106                                      |
| 9  | 460   | 82.7 | 95  | 7 | PH0863   | Ig kappa chain V r |                        |                                                                                            |
| 7  | 460   | 82.7 | 107 | 7 | S40366   | Ig kappa chain V-J | a<br>a                 | 81 RFSGSGSGTDFSLTISSLQPEDVATYYCQKYNSVPRTFGQGTKVEI 126                                      |
| 80 | 459.5 | 82.6 | 124 | 7 | S40336   | Ig kappa chain V-J |                        |                                                                                            |
| σ  | 459   | 82.6 | 108 | 7 | B49047   | Ig kappa chain V r |                        |                                                                                            |
| 0  | 459   | 82.6 | 127 | 7 | S40367   | Ig kappa chain V-J | RESULT 2               |                                                                                            |
| _  | 457   | 82.2 | 123 | 7 | S40331   | chain              | S36275                 |                                                                                            |
| ~  | 455   | 81.8 | 107 | 7 | S36264   | chair              | Ig lambda              | Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)                          |
| ۳  | 455   | 81.8 | 125 | 7 | S40349   | chain              | C;Species:             | C; Species: Homo sapiens (man)                                                             |
| 4  | 454.5 | 81.7 | 108 | 7 | S30521   | chain              | C; Date: 03            | C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000                |
| Ŋ  | 454   | 81.7 | 108 | - | K1HUWE   | chain              | C;Accession: S36275    | : S36275                                                                                   |
| 9  | 453   | 81.5 | 125 | 7 | S40333   | Ig kappa chain V-J | R,Griffith             | R; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.; |
| 7  | 452   | 81.3 | 117 | 7 | S46376   | chain              | EMBO J. 12             | EMBO J. 12, 725-734, 1993                                                                  |
| œ  | 451   | 81.1 | 108 | ~ | 836279   | Ig lambda chain V  | A; Title: H            | A, Title: Human anti-self antibodies with high specificity from phage display libraries.   |
| σ  | 451   | 81.1 | 127 | 7 | S11240   | Ig kappa chain V r | A;Reference            | A;Reference number: 836256; MUID:93178448; PMID:7679990                                    |
| 0  | 450   | 80.9 | 117 | 0 | S46371 · | Ig kappa chain V-J | A; Accession: S36275   | : \$36275                                                                                  |
| 7  | 449   | 80.8 | 108 | Н | KIHUBN   | hain 1             | A;Status: ]            | A;Status: preliminary; nucleic acid sequence not shown                                     |
| ~  | 449   | 80.8 | 110 | ~ | S44118   | Ig kappa chain V-J | A; Molecule type: mRNA | type: mRNA                                                                                 |
| m  | 448   | 80.6 | 107 | 7 | 836262   | Ig lambda chain V  | A;Residues             | A;Residues: 1-107 <gri></gri>                                                              |
| 4  | 448   | 90.6 | 108 | 7 | 840330   | Ig kappa chain V-J | A;Cross-re             | A;Cross-references: EMBL:Z18827; NID:g33416; PIDN:CAA79279.1; PID:g939909                  |
| S  | 448   | 90.6 | 108 | 7 | S19674   | Ig kappa chain V r | C;Superfam             | C;Superfamily: immunoglobulin V region; immunoglobulin homology                            |
| 9  | 448   | 90.6 | 129 | 7 | S40317   | Ig kappa chain - h | C; Keywords            | C;Keywords: heterotetramer; immunoglobulin                                                 |
| 7  | 447   | 80.4 | 108 | 7 | K1HURE   | Ig kappa chain V-I | F;16-90/Do             | F;16-90/Domain: immunoglobulin homology <1MM>                                              |
| ۵  | 447   | 80.4 | 129 | 0 | S40369   | Ig kappa chain - h |                        |                                                                                            |
| σ  | 446   | 80.2 | 109 | 7 | S31981   | Ig kappa chain - h | Query Match            | ch 86.2%; Score 479.5; DB 2; Length 107;                                                   |
|    |       |      |     |   |          |                    |                        |                                                                                            |

```
A; Accession: PH0863
 F;89-95/Region:
 F;24-34/Region:
 F;35-49/Region:
 F;50-56/Region:
 F;57-88/Region:
 Query Match
 PH0863
 Вp
 В
 Š
 g
 δ
 셤
 à
 ò
 ö
 23 DIQMTQSPSSLSASVGDRVTITCRASQSIAGYLNWYQQRPGRAPELLIYAASTLRSGVPS 82
 9
 9
 9
 9
 81
 Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
 1 DIQMIQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS
 22 DIQLIQSPSFLSASIGDRVIITCRASQGINSYLAWYQQKPGKAPKLLIYVASTLQSGVPS
 ;Cross-references: EMBL:X85996; NID:g758598; PIDN:CAA59988.1; PID:g758599; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin homology; 38-112/Domain: immunoglobulin homology <IMM>
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIOMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 DIQMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40334
 Gaps
 Gaps
 ij
 ;
 ;
0
 61 RFSGSGSGTDFTLTISSLQPEDVAVYYCQQYYSTP-TFGQGTKVEI 105
 82 RFSGSGSGTEFTLTISSLQPEDFASYYCQQFNSYPFTFGGGTKVEI 127
 Score 463; DB 2; Length 129;
Pred. No. 5e-33;
3; Mismatches 13; Indels
 61 RESGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 Length 132;
 A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
Pred. No. 1.6e-34; Indels
 8; Indels
 Score 470; DB 2;
Pred. No. 1.3e-33;
 3; Mismatches
 3; Mismatches
 8; Mismatches
 A;Status: preliminary; translation not shown A;Molecule type: mRNA
 84.5%;
 ch 83.3%;
1 Similarity 84.9%;
90; Conservative
 89.68;
 Query Match
Best Local Similarity 84.9
Matches 90; Conservative
 95; Conservative
 Query Match
Best Local Similarity
 Best Local Similarity
 A; Residues: 1-132 < KLE>
 A; Molecule type: mRNA
A; Residues: 1-129 <ROC>
 A;Accession: S52792
A;Status: preliminary
 Matches
 유
 ઠે
 g
 ò
 셤
 ઠે
 g
 ò
 d
```

```
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Fitle: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MuID:93178448; PMID:7679990
A;Reference number: S36256; MuID:93178448; PMID:7679990
A;Reference number: S36269
A;Reference number: CSACS6; MuID:93178448; PMID:7679990
A;Reference number: S36269
A;Reference number: CSACS6; MuID:93178448; PMID:7679990
A;Reference number: CSACS6; MuID:93178489; PMID:7679990
A;Reference number
 C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: PH0863
R;Manheimer-Lorry, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
R;Manheimer-Lorry, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.
A;Reference number: PH0862; MUID:92078875; PMID:1660528
 A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPROT:Q9UL70
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
 ö
 ö
 9
 9
 9
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 DIOMIGSPSSLSASVGDRVIITCRESQGIRNDLGWYQQKPGKAPKLLIYGTSSLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 A,Cross-references: EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID:g939915
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F,16-90/Domain: immunoglobulin homology <IMM>
 Gaps
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 83 RFSGSGSGADFTLTISSLQPEDSATYYCQQSYGTPFTFGPGTKVDI 128
 Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
 Length 107;
 Length 95;
 4; Indels
 Ig kappa chain V region (anti-DNA, III-2R) - human (fragment)
 83.1%; Score 462; DB 2;
84.9%; Pred. No. 5.1e-33;
ive 5; Mismatches 11;
 #82.7%; Score 460; DB 2; illarity 93.7%; Pred. No. 6.7e-33; Conservative 2; Mismatches 4
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPP 95
 complementarity-determining 3
 immunoglobulin homology <IMM>
complementarity-determining 1
 complementarity-determining
framework 3
 Best Local Similarity 84.9
Matches 90; Conservative
 framework 2
 1-23/Region: framework
 Query Match
Best Local Similarity
Matches 89; Conserv
```

ö

9

```
Query Match
Best Local Similarity 84.99
....hes 90; Conservative
 89; Conservative
 Local Similarity
 A; Residues: 1-123 < KLE>
 Ig kappa chain - human
 78
 Query Match
Best Local
 Матсрев
 RESULT 11
 S40367
 g
 ઠે
 g
 ò
 셤
 ò
 셤
 ઠ
 Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #semmence vonition to the contractions
 C; Accession: B49047
R; Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
 C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C; Accession: 840366
R; Klein, R.; Jaanichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: 840312; MUID:94080891; PMID:8258341
A; Accession: S4036
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-107 < KLE>
A; Cross-references: RMBL:X72476; NID:9441420; PIDN:CAA51144.1; PID:9441421
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 28-102/Domain: immunoglobulin homology < IMM>
 ö
 9
 75
 9
 72
 Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Ciscession: $40336
Riklein, R.; Jaenichen, R.; Zachau, H.G.
Riklein, R.; Jaenichen, R.; Zachau, H.G.
A; Title: Expressed human immunoglobulin chi genes and their hypermutation.
A; Reference number: $40312; MulD: 94080891; PMID: 8258341
A; Reference number: $40312; MulD: 94080891; PMID: 8258341
A; Reference number: Remainary; translation not shown
A; Residues: 1-124 <KLE>
 Species: Homo sapiens (man)
Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS
 16 DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 A;Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PID:g441361
(S.Usperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
 Gaps
 Gaps
 1;
 ö
 Score 459.5; DB 2; Length 124; Pred. No. 9.6e-33; 9; Mismatches 8; Indels 1
 Score 460; DB 2; Length 107;
Pred. No. 7.5e-33;
 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSS-PPFTFGPGTKVDI
 4; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPP 95
 2; Mismatches
 9; Mismatches
Ig kappa chain V-J region - human
 Ig kappa chain V-J region - human
 ch 82.7%;
1 Similarity 93.7%;
89; Conservative
 ch 82.6%;
1 Similarity 83.2%;
89; Conservative
 Query Match
Best Local Similarity
 Local Similarity
 61
 13
 73
 Query Match
 Matches
 RESULT 9
B49047
```

유 ઠે d

ઠે 셤 ò a

```
Sylosy,
Skappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: 540367
C;Accession: 23, 3248-3271, 1993
A;Itile: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: 840312; MUID:94080891; PMID:8258341
A;Scatus: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>F;33-107/Domain: immunoglobulin homology <IMM>
 1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60
 18 DIOMIOSPSSLSASVGDRVIIICRASOSISNYLNWYORKPGKAPKLLIYAASSLOSGVPS 77
 C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $4031.
Ey,Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40331
A;Accession: S40331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
 1 DIQMIQSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
A,Reference number: A49047; MUD:92387224; PMID:1516616
A;Accession: B49047
A;Atatus: preliminary
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Residues: 1-108 «VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C;Superfamily: immunoglobulin v region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.L; PID:g441351
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
 Gaps
 Gaps
 ö
 ö
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 RPSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 Length 127;
 Length 108
 12; Indels
 11; Indels
 Score 459; DB 2;
Pred. No. 1.1e-32;
 82.6%; Score 459; DB 2;
84.9%; Pred. No. 9.3e-33;
iive 4; Mismatches 12
 82.6%; bcc. No. 1...
84.0%; Pred. No. 1...
6; Mismatches
```

ö

```
62 FSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI
 Query Match 81.7%;
Best Local Similarity 82.1%;
Matches 87; Conservative
 Query Match
Best Local Similarity 80,55
Best Local 87; Conservative
 A;Cross-references: GDB:136264
 C; Keywords: heterotetramer
 A; Gene: GDB: IGKV1
 C; Accession: S
R; Mariette, X.
 C;Genetics:
 RESULT 15
 83052
 g
 g
 ð
 셤
 ò
 ò
 g
 ઠ
 Iglambda chain V region (clone alpha-CEA4-8A) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 03.Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C;Accession: 836264

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. BMBO J. 12, 725-734, 1993

A;Tile: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: 83626; MUD:93178448; PMID:7679990

A;Accession: 836264

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-107 <GRI>
 0;
 ö
 ö
 9
 61
 9
 9
 19 IQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVPSR 78
 92
 RESULT 13
S40349
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S4034
R;Klein, R., Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3348-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
 17 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIQMTQSPSSLSASVGDRVT1TCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 2 IQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSR
 A,Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
 Gaps
 A;Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g939919 C.S. Superfeamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;16-90/Domain: immunoglobulin homology <IMM>
 Gaps
 Gaps
 ;
0
 ö
 ö
 77 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPRTFGQGTKVBI 122
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYSNYPLTFGGGTKVDI 106
 Length 125;
 61 RESGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 81.8%; Score 455; DB 2; Length 107; 83.0%; Pred. No. 2e-32; ive 7; Mismatches 11; Indels
 Length 123;
 Indels
 12; Indels
 82.2%; Score 457; DB 2; 84.9%; Pred. No. 1.6e-32;
 81.8%; Score 455; DB 2;
83.8%; Pred. No. 2.4e-32;
iive 8; Mismatches 9;
 4; Mismatches
7;32-106/Domain: immunoglobulin homology <IMM>
 A;Accession: S40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
 Local Similarity 83.8%;
nes 88; Conservative
 Local Similarity 84.9
nes 90; Conservative
 Best Local Similarity 83.0
Matches 88; Conservative
 1-125 <KLE>
 Query Match
 Query Match
 Query Match
 A; Residues:
 Best Loca
Matches
 RESULT 12
S36264
 Matches
 g
 В
 ò
 엄
 ò
 원
 ò
 ò
```

```
C;Accession: A01676
R;Goni, F.; Frangione, B.
Proc. Natl. Acad. Sci. U.S.A. 80, 4837-4841, 1983
A;Title: Amino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) wit A;Reference number: A93964; MUID:83273707; PMID:6410398
 A;Molecule type: protein
A;Residues: 1-108 <CGON-
A;Cross-reserences: UNIPROT:P01610
C;Comment: This chain was obtained from a monoclonal antibody against 3,4-pyruvylated gal
 A;Map position: 2p12-2p12
C.Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into las
C;Superfamily: immunoglobulin V region; immunoglobulin homology
 ö
 ä
 9
 9
 9
 9
 numenta kappa chain V-I region (WEA) - human
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
 Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S30521
 1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNDLTWYQQKRGTAPKRLIYGATSLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gape
 Gaps
 .
0
 1;
 61 RFSGSGSGTEFTLTISSLOPEDFATYYCOOLNSYPPYTFGGGTKLEIN 108
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSS-PPFTFGPGTKVDIS 107
 Length 108;
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 Length 108;
 A,Reference number: $30520
A,Accession: $30521
A,Sactus: prefaininary
A,Rolecule type: mRNA
A,Residues: 1-108 «MAR»
A,Cross-references: UNIPROT:09UL79; EMBL:218327
A;Cross-references: UNIPROT:immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin bomology
C;Keywords: heterocteramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
79 FSGSGSGTDFTLTISSLOPEDFATYYCQQFNTYPLTFGGGTKVEI 123
 10; Indels
 Indels
 DB 2;
 Score 454; DB 1;
Pred. No. 2.5e-32;
9; Mismatches 10
 81.7%; Score 454.5; DB 2
80.6%; Pred. No. 2.3e-32;
 submitted to the EMBL Data Library, October 1992
 10; Mismatches
 F;16-90/Domain: immunoglobulin homology <IMM>F;23-88/Disulfide bonds: #status predicted
```

61 RFSGSGSGTEFTLTINSLQPEDFATYYCLQYSSFPWTFGQGTKVEV 106

Search completed: November 16, 2005, 22:04:09 Job time : 12.7849 secs

CONTRACTOR OF THE CUSPTON

```
SEQUENCE FROM N.A.
NCBI_TaxID=9606;
 09UL70;
01-MAY-2000 (
01-MAY-2000 (
01-OCT-2003 (
 (Fragment)
424
4119
4117
4117
4113
4113
4113
407
507
399
399
399
 NON TER
NON TER
SEQUENCE
 fetus.";
 Q6GMX8
 Q9UL70
 RESULT 2
OGGMX8
 RESULT 1
Q9UL70
 셤
 ò
 g
 SETTT
 sapien
sapien
sapien
sapien
sapien
sapien
sapien
sapien
 sapien
sapien
sapien
sapien
sapien
sapien
 sapien
sapien
 sapien
 sapien
 sapien
 sapien
 sapien
 November 16, 2005, 21:36:13; Search time 59.9908 Seconds (without alignments) 913.348 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 DIQMTQSPSSLSASVGDRVT......CQKFSSPPFTFGPGTKVDIS 107
 homod
 уошоц
 homod
 рошо
 homo
 homo
 homod
 homo
 homo
 homo
 рошо
 homo
 homo
 homo
 рошо
 Description
 P01610
P0362
P04430
P04430
P04430
P01607
P01608
P01608
P01608
P01608
P01608
P01608
P01608
P01608
P01609
P01594
P01594
P01599
P01599
P01599
P01599
P01599
P01599
P01599
P01610
 Q6pit5
P01604
P01598
Q7z473
 Q6gmx8
Q6pih7
 051n6C
 Q6gmx9
 1612378
 5.1.6
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1612378 segs, 512079187 residues
 version 5
- 2005 (
 SUMMARIES
 Q6GMX8
Q6FIH7
KV1R_HUMAN
KV1Y_HUMAN
Q7Z3¥4
KV1V_HUMAN
Q9UL77
Q9UL77
Q6GMWI
 096889
0652C8
KVIP HUMAN
KVIP HUMAN
KVIO HUMAN
0652C9
KVID HUMAN
066MX0
KVIE HUMAN
KVIB HUMAN
KVIB HUMAN
KVIB HUMAN
KVIB HUMAN
 QGGMX9
QGPIT5
KV1L_HUMAN
KV1F_HUMAN
Q7Z473
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop'10.0 , Gapext 0.5
 Q9UL70
 GenCore (c) 1993
 UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
 US-10-660-357A-30
556
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 Query
Match Length DB
 Copyright
 88800

68800

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900

6900
 Title:
Perfect score:
 Scoring table:
 Score
 445
443.5
442.5
442
 437
436.5
436.5
436.5
433
433
433
433
431
431
427
427
425
 Sequence:
 Searched:
 Database
 Run on:
 Result
```

```
ö
 sapien
sapien
sapien
sapien
sapien
 9
 9
sapien
 homo sapien
homo sapien
 synthetic c
 mus musculu
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIQMIQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS
 Gaps
 homo
homo
homo
homo
homo
homo
homo
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 MEDLINE-88277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
 ö
 Q6pih4 | P01595 | P01595 | P01606 | Q96pf6 | P01601 | P01612 | P01612 | P01612 | P01612 | P01625 | P06314 | P01625 | Q94yf0 | P01625 | P01
 61 RFSGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 Length 108;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
 89.6%; Score 498; DB 2; Length 10
90.6%; Pred. No. 2.8e-43;
ive 4; Mismatches 6; Indels
 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
 Created)
Last sequence update)
Last annotation update)
 EMBL, AF015044, AAD56280.1; -. PRIN, PROBS.1, PROBS.1, PROBS.3, PHO863, PHO863, PHO863, PHO863, PHO863, PHO863, PHO863, PHO863, PHO863, PROPORTO, IRROPOSISO, INCEPTO, IRROPOSITE, PS50835, IG_LIKE; 1.
 108 AA
 236 AA
 ALIGNMENTS
 HUMAN
 KV1C HUMAN
KV1N HUMAN
 Q96PF6
KV11_HUMAN
KV11_HUMAN
KV11_HUMAN
 KV4C HUMAN
 (TrEMBLrel. 13, Created)
 PRT;
 PRT;
 Q9QYE0
 GGGMX8;
05-JUJ-2004 (TrEMBLrel. 27, C.
05-JUJ-2004 (TrEMBLrel. 27, L.
05-JUJ-2004 (TrEMBLrel. 27, L.
Hypothetical protein.
Homo sapiens (Human).
 Ouery Match
Best Local Similarity 90.67
Matches 96; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Homo sapiens (Human)
```

```
[1]
SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 'ISSUE=Lung;
 KV1R HUMAN
P01610;
 Query Match
 SEQUENCE
 RESULT 4
KV1R_HUMAN
 8
 Š
 g
 TISSUB-Primary B-Cells,

WEDLINE-22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

Astraubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIJUBRER R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Distribution L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brahleton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rahla S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEban P.J., McKernan K.J., Malek J.A., Guarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Medicon and initial analysis of more than 15,000 full-length human
 ö
 1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 82
 23 DIQMIQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
 Gaps
 GFIH7;
0.5-JUL-2004 (TrEMBLrel. 27, Created)
0.5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
0.5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=9606;
Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
 ö
 Score 480; DB 2; Length 236;
Pred. No. 4.8e-41;
5; Mismatches 8; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 RFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSFPFTFGPGTKVDI
 Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 Hypothetical protein.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
 Sci. U.S.A. 99:16899-16903(2002).
 236 AA.
 EMBL, BC07764; AAH73764 I.

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003597; Ig_cl.

InterPro; IPR003596; Ig_W.

Pfam; PF07654; Cl.-8et; I.

Pfam; PF07654; Cl.-8et; I.

SMART; SM00407; Ig; 2.

SMART; SM00409; IG; 2.

SMART; SM00406; IGW: I.

PROSITE; PS00835; IG_LIKE; 2.

HOSITE; PS00835; IG_LIKE; 1.
 86.3%;
 93; Conservative
 cDNA sequences.
 PRELIMINARY;
 SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
 Best Local Similarity
 Eukaryota; Metazoa;
Mammalia; Eutheria;
 NCBI_TaxID=9606;
 and mouse
 SEQUENCE
 Query Match
 Q6PIH7
 RESULT 3
Q6PIH7
ID Q6PIH
AC Q6PIH
DT 05-U
DT 05-U
DE HYPO
OC Mamm
OX NCBL
 셤
 à
8
```

```
RA Strausberg K.D., Feingold E.A., Grouse L.H., Derge J.G.,
Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Bloomstein M.J., Usdan B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
R. Brownstein M.J., Usdan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchehko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevcheko Y., Bouffard G.G.,
Rotriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
M. Jones S.J., Marra M.A.,
Warra M.A.,
Warra M.A.,
Warra M.A.,
Wanra M.A.,
Wannes C.D.,
Wannes C.D., Smailus D.E., Schnerch A., Schein J.E.,
Rand Mouse CDM. Sequences ";
 ò
 9
 82
 23 DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 0; Gaps
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RFSGSGSGTEFTLTISSLOPEDFATYYCQQLNSSPPTFGGGTKVEI 128
 61 RESCSGSGTDFTLTISSLOPEDVATYYCOKESSPPFTFGPGTKVDI 106
 Length 236;
 11; Indels
 Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034141; AAH34141.1; -.
 Hypothetical protein.
SEOUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Match B2.4%; Score 458; DB 2; Local Similarity 84.0%; Pred. No. 8.7e-39; les 89; Conservative 6; Mismatches 11;
 21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region WEA.
 108 AA
 PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN_1.
 MEDLINE=83273707; PubMed=6410398;
 InterPro; IPR003199; IG.
InterPro; IPR00310; Ig-like.
InterPro; IPR00310; Ig_C1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_WHC.
Pfam; PF07654; C1-8et; I.
SMART; SM00407; IGC1; I.
SMART; SM00407; IGC1; I.
 STANDARD;
 Homo sapiens (Human)
 HSSP; P01607; 1AR2.
 SEQUENCE FROM N.A.
```

```
-!- MISCELLANEOUS: This is a Bence-Jones protein.
 STRAND
 TURN
 TURN
 TURN
 TURN
 TURN
 RESULT 6
 2723Y
 셤
 8
 1 DIQMIQSPSSLSASVGDRVIITCRASQGIRNDLIWYQQKRGTAPKRLIYGATSLQSGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated galactose
in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S., 80:4837-4841(1983).
-!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
against 3,4-pyruvylated galactose and isolated from a patient with
PIR; A01876; K1HUWE.
HSSP; P80362; 1WTL.
 Gaps
 SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=95086080; PubMed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Scolomon A., Stevensn F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
 Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.; (Caracterization and preliminary crystallographic data on the VL-related fragment of the buman kI Bence Jones protein Wat.", J. Mol. Biol. 147:185-193(1981).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 ÷
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTEFTLTINSLQPEDFATYYCLQYSSFPWTFGQGTKVEV 106
 Score 454; DB 1; Length 108; Pred. No. 9e-39;
 Complementarity-determining-1.
 Complementarity-determining-2.
 Complementarity-determining-3
 10; Indels
 11840 MW; 9249B61F0945618C CRC64;
 Immunoglobulin V region,
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
02-OCT-2004 (Rel. 45, Last annotation update)
1G Kappa chain V-I region WAT.
Homo sapiens (Human)
 108 AA
 9; Mismatches
 Framework-4.
By similarity.
 Framework-3
 Framework-1
 Framework-2
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
 Biochemistry 33:14848-14857(1994)
 SEQUENCE OF 1-35.
MEDLINE=81267384; PubMed=6167731;
 PERM; PF00047; ig; 1.
SWART; SW00406; IGv; 1.
PROSITE; PS0815; IG_LIKE; 1.
Direct protein sequencing; Im
 81.7%;
82.1%;
 Query Match
Best Local Similarity 82.1
Matches 87; Conservative
 STANDARD;
 49
56
88
97
107
88
 108 AA;
 NCBI_TaxID=9606;
 HUMAN
 DOMAIN
DISULFID
 SEQUENCE
 KV1Y HUN
P80362;
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 ઠે
 셤
 ઠે
 셤
```

```
1 DIGMTGSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 0; Gaps
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
 SEQUENCE FROM N.A.
TISSUE=Skeleten Muscle;
MEDIINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
3D-etructure; Bence-Jones protein, Direct protein sequencing;
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 RESGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDI 106
 Framework-2.
Complementarity-determining-2.
 Length 108;
 Complementarity-determining-1.
 Complementarity-determining-3.
 11; Indels
 11737 MW; D9D941B3F0FAE697 CRC64;
 Last sequence update)
Last annotation update)
 By similarity.
TN -> SD (in Ref. 2)
 81.5%; Score 453; DB 1;
80.2%; Pred. No. 1.1e-38;
 236 AA.
 10; Mismatches
 Framework-3.
 Framework-1
PDB; 1WTL; X-ray; A/B=1-108.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
INTERPRO; IPR007110; IG-11ke.
 Created)
 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
 Conservative
 PRELIMINARY;
 Immunoglobulin V region
 (Human)
 108 1
108 AA;
 Local Similarity
les 85; Conserv
 NCBI_TaxID=9606;
 Homo sapiens
 DOMAIN
DOMAIN
DOMAIN
DISULFID
 NON TER
SEQÜENCE
 Query Match
 CONFLICT
 DOMAIN
DOMAIN
DOMAIN
 STRAND
 STRAND
 DOMAIN
 STRAND
 STRAND
 STRAND
 STRAND
 STRAND
 Q7Z3Y4
 STRAND
```

ô 9 9 ô

Gaps

; 0

12; Indels

Length 108;

Complementarity-determining-1. Framework-2.

Complementarity-determining-2.

Framework-3.

Complementarity-determining-3. Framework-4.

By similarity.

```
1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIQLTQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60
 PEam; PF00047; ig; 1.
SMART; SM00466; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Amyloid; Direct protein sequencing; Immunoglobulin V region.
DOMAIN
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 11840 MW; CD3FD944FE96FD37 CRC64;
 80.2%; Score 449; DB 1;
80.2%; Pred. No. 2.9e-38;
iive 9; Mismatches 12
 interPro; IPR007110; Ig-like.
 85; Conservative
 56
88
97
107
108
 Homo sapiens (Human).
 108 AA;
 108 AA;
 Local Similarity
 NCBI_TaxID=9606;
 (Fragment)
 NON TER
SEQUENCE
 SEQUENCE
 DISULFID
 Query Match
 NON TER
NON TER
 DOMAIN
DOMAIN
DOMAIN
DOMAIN
 Q9UL77
 DOMAIN
 RESULT 8
Q9UL77
 임
 SOC CONTRACT SET THE PORT OF THE PORT OF THE PRICE OF THE
 ઠ
 ò
 셤
 셤
 ò
Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Depking R.F., Jordan H., Moore T., Max S.I., Wang J., Haite F., Diatchenko L., Marusina K.P., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guiba R.A., Arichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murny D.M., Sodergran R.J., Lu X., Gibbs R.A., Abrey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mrzywinski M.I., Skalska U., Samilus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 9
 82
 1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2; Dwulet F.E., O'Connor T.P., Benson M.D.; Propriation in Akappa I primary (AL) amyloid protein (BAN)."; Mol. Immunol. 23.73-78(1986).
PIR; A01878; KIHUBN.
HSSP; P80362; 1WTL.
GO; GO:0005576; C:artracellular; NAS.
GO; GO:0005576; C:artracellular; NAS.
GO; GO:0005576; P:immune response; NAS.
 13.AUG-1987 (Rel. 05, Created)
13.AUG-1987 (Rel. 05, Last sequence update)
05.JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-I region BAN.
Homo sapiens (Human).
Exkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ö
 KFSGSGSGTDFTLTISSLQPEDFATYYCQQYKSYPVTFGGGTKLEI 128
 80.9%; Score 450; DB 2; Length 236; 82.1%; Pred. No. 5.8e-38; ive 7; Mismatches 12; Indels
 61 RFSGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 SEQUENCE FROM N.A.
TISSUESKeletal Muscle;
Strausberg R.,
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
 108 AA
 PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 PRT;
 InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003066; Ig WHC.
InterPro; IPR003596; Ig V.
Pfam; PF07654; C1-set; I.
 EMBL; BC005332; AAH05332.1;
HSSP; P01834; 1HEZ.
 87; Conservative
 KV1V HUMAN STANDARD;
P04430;
 IGV; 1
 Hypothetical protein
 Local Similarity
 SMART; SM00406;
 SEQUENCE.
 SEQUENCE
 Query Match
 KVIV HUMAN

TO KVIV HUMAN

AC PO4430,

DT 13-AUG-

DT 05-AUG-

DE IG RAPE

OC MAMMA 10

OX NUBL TR

RN NUBL TR

RN MEDLINI

RR MADL TR

RR
 Matches
 a
 ò
 ò
```

```
ö
 9
 9
 1 DIQMIQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKRGKAPNLLIYAASSLQSGVPS
 1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 0; Gaps
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 SEQUENCE FROM N.A.
MEDLINE=98277139; Pubmed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
 61 RPSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 Query Match
80.6%; Score 448; DB 2; Length 108;
Best Local Similarity 83.0%; Pred. No. 3.7e-38;
Matches 88; Conservative 5; Mismatches 13; Indels
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
 11738 MW; C06681716C4D16F3 CRC64;
 fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AR035037; AAD56273.1; -.
108 AA
 PIR; B49047; B49047.
PIR; S34083; S34083.
HSSP; P01607; IBWW.
InterPro; IPR007110; Ig-like.
InterPro; IPR03596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 PRELIMINARY;
```

```
MEDLINE=76023758; PubMed=809329;
MEDLINE=76023758; PubMed=809329;
Palm W., Hilschmann N.;
The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their
 MEDLINE=76039968; PubMed=1182131;
Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
"The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein REI refined at 2.0-A resolution.";
Blochemistry 14:4943-4952[1975].
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
 PIR, A91663, KIHURE.

R PDB; 1AR2; X-ray; 0=1-107.

R PDB; 1RR1; X-ray; A/B=1-107.

R PDB; 1RR1; X-ray; A/B=1-107.

R GO; GO:0005576; C:extracellular; NAS.

R GO; GO:0005957; F:antigen binding; NAS.

R GO; GO:0005957; P:immune response; NAS.

R InterPro; IPR007110; 1g-1ike.

R InterPro; IPR0047; 1g; 1.

R SWART; SW00406; IGy. 1.

R PROSITE; PS50835; IG_LIKE; 1.

R PROSITE; PS50835; IG_LIKE; 1.

R PD = structure; Bence-Jones protein; Direct protein sequencing; Immune the structure; Bence-Jones protein; Direct protein sequencing;
 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEI 106
 Complementarity-determining-1.
Framework-2.
 Complementarity-determining-3.
Framework-4.
 Complementarity-determining-2.
 combining site.";
Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
 .! - MISCELLANEOUS: This is a Bence-Jones protein
 Last sequence update)
Last annotation update)
 Framework-1
 Framework-3
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
25-OCT-2004 (Rel. 45, Last anno
1g kappa chain V-I region Rel.
 STANDARD;
 Immunoglobulin V region
 34
49
56
88
97
107
88
 Homo sapiens (Human)
 24
35
50
57
89
89
23
 11104
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
11100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
1100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
100
10
 KV10 HUMAN
P01607;
 DOMAIN
DOMAIN
DISULFID
STRAND
STRAND
 STRAND
TURN
STRAND
TURN
 DOMAIN
 TURN
STRAND
TURN
 DOMAIN
 STRAND
TURN
STRAND
 STRAND
 KWINTY 9

KVIO LHUMAN

AC PO1667

DT 21-JUL

DE ENKARY

COC ENKARY

COC ENKARY

RR MEDLIN W

RR MED
 DOMAIN
g
```

```
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
An stapleron M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Widnin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.J.,
A Brokat S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pakey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Nones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
 ö
 9
 9
 1 DIOMTOSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS
 1 DIOMIGSPSSLSASVGDRVIITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ö
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDIS 107
 61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQIT 107
 Length 108;
 13; Indels
 Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
82
90
98 .
106
11902 MW, 9E8143E1188BCEZA CRC64;
 (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
/"remBlrel. 27, Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 80.4%; Score 447; DB 1;
ilarity 79.4%; Pred. No. 4.7e-38;
Conservative 9; Mismatches 13
 236 AA
 EMBL, BC073/91, AA473791.1; ...
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003596; Ig.
Pfam; PF00647; Ig. 2.
SWART; SM00407; IG. 2.
SWART; SM00407; IG.; I.
SWART; SM00407; IG.; I.
SWART; SM00406; IG.; I.
PROSITE; PS50835; IG_LIKE; 2.
 and mouse cDNA sequences.
 PRELIMINARY;
 05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
Hypothetical protein.
 Homo sapiens (Human)
 Local Similarity
nes 85; Conserv
 SEQUENCE FROM N.A.
TISSUE=Spleen;
 FROM N.A.
 NCBI_TaxID=9606;
 05-JUL-2004
 STRAND
NON TER
SEQUENCE
 SEQUENCE
 Query Match
 OGGMW1;
 HELIX
STRAND
STRAND
 O6GMW1
 Best Loc
Matches
 RESULT 10
Q6GMW1
 SHHHH
 ò
 셤
 ò
 셤
 HE CONTROL OF THE CON
```

```
PRELIMINARY;
 Pfam; PF00047; 19; 2.
 Homo sapiens (Human).
NCBI_TaxID=9606;
 NON TER
NON TER
SEQUENCE
 Name=scFv;
 NON TER
NON TER
SEQUENCE
 Query Match
 065ZC8
 Best Loca
Matches
 RESULT 13
Q652C8
 셤
 ò
 9
 9
 61
 24 IQMTQSPSSLSASVGDRVTITCRASQGISNDLGWYQQKPGKAPKLLIYAASSLQSGVPSR 83
 1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS
 2 IQMIQSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSR
 1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 Gaps
 variable region (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 26, Last annotation update)
Anti-etreptococcal/anti-myosin immunoglobulin kappa light chain
 1;
 ;
0
 Query Match 79.8%; Score 443.5; DB 2; Length 107; Best Local Similarity 84.0%; Pred. No. 1.1e-37; Matches 89; Conservative 2; Mismatches 14; Indels 1;
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 61 RESCSCSCTOFTLTISSLQPEDVATYYCOKESSPPFTFGPGTKVDI 106
 RFSGSGSGTDFTLTISGLOAEDFATYYCOO-SYSALTFGPGTKVDI 105
 ch 80.0%; Score 445; DB 2; Length 236; 1 Similarity 83.8%; Pred. No. 1.9e-37; 88; Conservative 5; Mismatches 12; Indels
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
 62 FSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 FSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYPWTFGQGTKVEI 128
 107 AA; 11501 MW; 070549FDE0754748 CRC64;
 Hypothetical protein. SEPE6A087APAC437 CRC64; SEQUENCE 236 AA; 25751 MW; 5BFE6A087APAC437 CRC64;
 Ciin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035033; AAD56269.1; -.
HSSP; P01607; 1BWW.
InterPro; IPR007110; Ig-like.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 Best Local Similarity
 SEQUENCE
 Query Match
 fetus.";
 096SA9;
 096SA9
 Q9UL81
 RESULT 11
090L8
1D 090L8
AC 090L8
DT 01-MA
DE MYOSE
RESULE
RA WU X.
RA WU X
 RESULT 12
Q96SA9
 Matches
 셤
 à
 OCCORRE
 g
 ò
```

```
ö
 7
 9
 9
 1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gape
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 1;
 ô
MEDIJNE=98375893; PubWed=9712075; MEDIJNE=98375893; PubWed=9712075; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.; molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody V region genes."; J. Immunol. 161:2020-2031 (1998).

EMBL; U96396; AAB68785.1; -.
 Query Match 79.6%; Score 442.5; DB 2; Length 107; Best Local Similarity 84.0%; Pred. No. 1.4e-37; Matches 89; Conservative 4; Mismatches 12; Indels 1
 / Match 79.5%; Score 442; DB 2; Length 244; Local Similarity 78.3%; Pred. No. 4e-37; nes 83; Conservative 12; Mismatches 11; Indels
 61 RESGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQ-SYSTLTFGGGTKVEI 105
 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
 26127 MW; 4B1F17868338F2BF CRC64;
 MEDLINE=97362799; PubMed=9219263;
MEDLINE=97362799; PubMed=9219263;
Rontermann R.E., Wing M.G., Winter G.;
Rontermann Recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
EMBL; Y13057; CAA713600.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig.V.
 Last sequence update)
Last annotation update)
 Created)
 PRT;
 PIR; P49047; B49047.
PIR; P4867; P40867.
PIR; S19640; S116840.
PIR; S34083; S34083.
PIR; S34086; S34086.
HSSP; P01607; 1BWW.
INTERPRO; IPRO07110; IG-like.
INTERPRO; IPRO07110; IG-like.
INTERPRO; IPRO07110; IG-like.
 SMART; SM00409; ĬG; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
 PROSITE, PS50835; IG_LIKE; 1.
 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
 Single-chain Fv (Fragment).
```

```
Hilschmann N.;
 KV1P HUMAN
P01608;
 Gamma globu
York (1969)
 DISULFID
NON TER
SEQUENCE
 SEQUENCE
 Query Match
Best Local
 DOMAIN
DOMAIN
DOMAIN
 DOMAIN
 DOMAIN
 RESULT 15
KV1P HUMAN
 Cum.)
 DUTTO
 ଚ
 셤
 ò
 셤
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ö
9
 23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVTS 82
 1 DIQMIQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 SEQUENCE FROM N.A.
MEDLINE=85014148; PubMed=6091049;
Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
 Eukamo agrema (Aradmam).
Eukamo agrema (Aradmam).
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 ö
 Ig kappa chain V-I region Walker.
Framework-1,
 242
 61 RFSGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 83 RFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGGGTRLEI 128
 Complementarity-determining-1.
 Score 440; DB 1; Length 129;
Pred. No. 3e-37;
 Complementarity-determining-2.
 Complementarity-determining-3.
 14; Indels
 197 RFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLEI
 RESGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI
 14069 MW; F941FA07D4AFC2F9 CRC64;
 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
12-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Walker precursor.
 5; Mismatches
 A
 By similarity.
 PIR; A01883; K.HUWK.
HSSP, P01607; 1BWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
 Framework-2
 EMBL; X00965; CAA25477.1; ALT_TERM.
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Tmmunoqlobulin V region; Signal.
 82.1%;
 Query Match
Best Local Similarity 82.1:
 STANDARD;
 129
45
45
71
71
78
110
119
129
 Homo sapiens (Human)
 120
45
129
129 AA;
 NCBI_TaxID=9606;
 KV1W HUMAN
 DISULFID
NON_TER
 61
 SEQUENCE
 DOMAIN
 SIGNAL
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 ઠે
 g
 ò
 g
 ò
 음
 ò
 ద
```

```
ö
 9
 9
 Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.; (In) Franck F., Shugar D. (eds.); Gamma globulins: structure and function, pp.57-74, Academic Press, New
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 ö
 Complementarity-determining-1.
 Complementarity-determining-2.
 Complementarity-determining-3.
 Length 108;
 61 RPSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVD 105
 61 RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVD 105
 "Chemical structure of 2 kappa-type Bence Jones proteins
 13; Indels
 11782 MW; F5ACEDE5A313DF3A CRC64;
 Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967)
 marker.
-1- MISCELLANEOUS: This is a Bence-Jones protein.
 79.0%; Score 439; DB 1;
80.0%; Pred. No. 3.1e-37;
ive 8; Mismatches 13;
 SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-JUL-2004 (Rel. 44, Last annotation update)
19 kappa chain V-I region Roy.
108 AA.
 By similarity.
 Framework-1.
 Framework-3
 PIR; A91638; KIHURY.
HSSP; PO1607; 1BWW.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
 MEDLINE=68362076; PubMed=5595110;
 84; Conservative
 34
24
88
88
107
108
 .mmunoglobulin V region
 REVISIONS TO 39 AND 41.
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1
 Homo sapiens (Human)
 108 AA;
 Similarity
 NCBI_TaxID=9606;
```

Search completed: November 16, 2005, 22:01:54 Job time : 60.9908 secs

The project of the corre

Н

us-10-660-357a-30.rai

```
MOLECULE TYPE:
FRAGMENT TYPE:
 Sequence 9, Appli
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 84, Appli
Sequence 84, Appli
Sequence 84, Appli
Sequence 84, Appli
Sequence 81, Appli
Sequence 83, Appli
Sequence 83, Appli
Sequence 83, Appli
Sequence 83, Appli
Sequence 82, Appli
Sequence 18, Appli
 November 16, 2005, 21:41:29; Search time 18.1939 Seconds (without alignments) 439.017 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 DIQMTQSPSSLSASVGDRVT......CQKFSSPPFTFGPGTKVDIS 107
 Description
 Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/ReCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5.1.6
Compugen Ltd.
 US-08-559-226-9
US-09-125-098-9
US-09-125-098-9
US-08-559-226-1
US-08-125-098-1
US-08-899-575-84
US-08-899-575-84
US-08-899-575-84
US-08-899-575-84
US-08-899-575-83
US-08-899-575-83
US-08-899-575-83
US-08-899-575-83
US-08-899-575-83
US-08-899-575-83
US-08-899-575-82
 Total number of hits satisfying chosen parameters:
 513545 seqs, 74649064 residues
version :
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 GenCore (c) 1993
 US-10-660-357A-30
556
 seq length: 0
seq length: 200000000
 В
 1006
1006
1007
1007
1007
1007
1007
1007
 Length
 Copyright
 Query
 12646
 Scoring table:
 Score
 Title:
Perfect score:
 OM protein -
 Minimum DB Maximum DB 0
 Searched:
 Sequence:
 Database
 Run on:
 Result
```

| US-08-974-899-3 US-09-755-798-3 US-09-755-798-3 US-09-240-241-177 US-07-934-373C-3 US-08-417-642B-3 US-08-146-206C-3 US-08-146-206C-3 US-09-705-686-3 US-09-705-392A-3 US-09-705-392A-3 US-09-705-392A-3 US-09-705-398-3 US-08-276-85-85 US-08-25-85 US-08-899-575-85 US-08-899-575-85 US-08-899-575-85 US-08-899-575-85 US-08-90-575-85 US-09-90-90-90-90-90-90-90-90-90-90-90-90-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Lhat Bind Human TNFa ergion #1.25                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 88-974-<br>9-795-<br>9-795-<br>9340-<br>9340-<br>99-705-<br>99-705-<br>99-705-<br>99-705-<br>88-899-<br>88-899-<br>10595-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1059-<br>1 | IGNM R.J. 226 V 226                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | n US/08599226  n US/08599226 Deborah J. Oom, Hendricus R. Andrew J. Andrew J. Andrew J. Andrew J. Human Antibodi. Tristan J. Trista                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| м 4 м М м 4 4 4 4 4 11 11 11 11 11 11 11 11 11 11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | CCOC COC COC COC COC CCC CCC CCC CCC CC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 110000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | lfeld, Joc) [len, Deborian on the property of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 4 4 6 10 10 10 10 10 10 10 10 10 10 10 10 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | pplication marginal salfeld salfeld Allen, labkovsi hadele salfeld kaymakc, kaymakc, labkovsi mankovin mankovin modula, vaughan white, wilton, wilton, wilton, wilton, wilton, wilton, schoente                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | -9 Application 6090382 T: Salfeld, T: Allen, DT T: Hogenbo T: Kaymakca T: Markovic T: Markovic T: Markovic T: Markovic T: Roberts, T: Roberts, T: Schoenban, T: White, T: Schoenban, T: White, T: White, T: White, T: White, T: Woldban, T: Wo                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 44<br>44<br>77<br>77<br>77<br>77<br>77<br>77<br>77<br>77<br>77<br>77<br>77<br>7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 22.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7.6<br>2.7 |
| 20000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | RESULT 1 US-08-599- Sequence Patent APPLI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 64                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

```
1 DIQMIQSPSSLSASIGDRVIITCRASQGIRNYLAWYQQKPGKAPKLLIXAASTLQSGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 DIOMTOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIQMIQSPSSLSASIGDRVTITCRASQGIRNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 60
 APPLICANT:
APPLICANT:
APPLICANT: Mankovic.
APPLICANT: Macovic.
APPLICANT: Moduinness, b..
APPLICANT: Sakorafas, Paul
APPLICANT: Sakorafas, Paul
APPLICANT: Scheenhaut, David
APPLICANT: Scheenhaut, David
APPLICANT: White, Michael
APPLICANT: Wiscant
APPLICANT
APPLIC
 90.1%; Score 501; DB 4; Length 107; 89.6%; Pred. No. 5.9e-37;
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/540,018 FILING DATE: 31-MARCH-2000 CLASSIPICATION:
 5; Mismatches
 Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
Kaymakcalan, Zehra
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 9, Application US/09540018 Patent No. 6509015
 Salfeld, Jochen G.
 : 107 amino acids
amino acid
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
 Query Match
Best Local Similarity 89.6
Matches 95; Conservative
 SEQUENCE CHARACTERISTICS
 linear
 MOLECULE TYPE:
FRAGMENT TYPE:
 TOPOLOGY:
 RESULT 3
US-09-540-018-9
 LENGTH:
 US-09-540-018-9
 ò
 g
 ď
 셤
 ઠે
 ö
 ö
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIQMIQSPSSLSASIGDRVIITCRASQGIRNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 60
 Gaps
 Gaps
 ö
 ö
 90.1%; Score 501; DB 3; Length 107; 89.6%; Pred. No. 5.9e-37; ive 5; Mismatches 6; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPYAFGQGTKVEI 106
 90.1%; Score 501; DB 3; Length 107; 89.6%; Pred. No. 5.9e-37;
 61 RFSGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human INFa
NUMBER OF SEQUENCES: 37
 6; Indels
 COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
 89.6%; Pred. w.
 Salfeld, Jochen G.
Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
Kaymakcalan, Zehra
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DECORT, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/OCKET NUMBER: BBI-043
TELECOMMUNICATION INFORMATION:
TELECPHONE: (617)227-7400
 E: LAHIVE & COCKFIELD
60 State Street, suite 510
 Sequence 9, Application US/09125098
Patent No. 6258562
GENERAL INFORMATION:
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus R
APPLICANT: Hoogenboom, Pendricus R
APPLICANT: Mankovich, John A.
APPLICANT: Mankovich, John A.
APPLICANT: Raymakcalan, Zehra
APPLICANT: Mankovich, John A.
APPLICANT: Schoenbaut, David
APPLICANT: Vaughan, Tristan J.
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
 Schoenhaut, David
Vaughan, Tristan J.
White, Michael
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
 : 107 amino acids
amino acid
 Query Match
Best Local Similarity 89.6
Matches 95; Conservative
 Best Local Similarity 89.6
Matches 95, Conservative
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
 CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE &
 Massachusetts
 linear
 Boston
 FILING DATE:
 US-09-125-098-9
 RESULT 2
US-09-125-098-9
 LENGTH:
US-08-599-226-9
 STREET:
 CITY: 1
STATE:
 Query Match
 셤
 ò
```

```
g
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 60
 1 DIOMIOSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 0; Gaps
 APPLICANT: Salfeld, Jochen G.
APPLICANT: Allen, Deborah J.
APPLICANT: Allen, Deborah J.
APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Kaymakcalan, Zehra
APPLICANT: Labkovsky, Boris
APPLICANT: Mankovich, John A.
APPLICANT: McGuinness, Brian T.
APPLICANT: Roberts, Andrew J.
APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Tristan J.
APPLICANT: Wilton, Andrew J.
TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS: 37
61 RESCSGSGTDFILITSSLOPEDVATYYCOKESSPPFTFGPGTKVDI 106
 RFSGSGSGTDFTLTISSLOPEDVATYYCQRYNRAPYTFGGGTKVEI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPYAFGQGTKVEI 106
 Score 499; DB 3; Length 107;
Pred. No. 8.8e-37;
 6; Indels
 ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,226
FILING DATE: 08-FEB-1996
 5; Mismatches
 ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
 ATTORNEY/AGENT INPORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
 Sequence 1, Application US/08599226
Patent No. 6090382
 89.7%;
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
 : 107 amino acids
amino acid
 Query Match
Best Local Similarity 89.6'
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
 Massachusetts
 linear
 CLASSIFICATION:
 Boston
 USA
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 TOPOLOGY:
 COUNTRY:
 RESULT 5
US-09-125-098-1
 US-08-599-226-1
 g
 ઠે
Š
 a
 ઠે
```

; Sequence 1, Application US/09125098

```
1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 ö
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQRYNRAPYTFGQGTKVEI 106
 Length 107;
 APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Vaughan, Trietan J.
APPLICANT: White, Michael
APPLICANT: White, Andrew J.
APPLICANT: Witch, Andrew J.
 89.7%; Score 499; DB 3; Length 10
89.6%; Pred. No. 8.8e-37;
ive 5; Mismatches 6; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,098
 Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
Kaymakcalan, Zehra
 Allen, Deborah J.
Hoogenboom, Hendricus R.J.M.
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,226
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: BII-043
TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
 Sequence 1, Application US/09540018; Patent No. 6509015; GENERAL INFORMATION: APPLICANT: Salfeld, Jochen G. APPLICANT: Hoogenboom, Hendricue; APPLICANT: Hoogenboom, Hendricue
 Labkovsky, Boris
Mankovich, John A.
McGuinness, Brian T
Roberts, Andrew J.
 ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
Salfeld, Jochen G.
 107 amino acids
 Query Match
Best Local Similarity 89.07
Each of 95, Conservative
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQUENCES: 37
 MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
 Massachusetts
 TYPE: amino acid
 Boston
 USA
 TELEPHONE:
 COUNTRY:
 STREET:
CITY: Bo
 US-09-125-098-1
 US-09-540-018-1
```

```
INFORMATION FOR SEQ ID NO: 84: SEQUENCE CHARACTERISTICS: LENGHT: 107 amino acids TYPE: amino acid TOPOLOGY: linear
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 Query Match
Best Local Similarity 89.4%;
Matches 93; Conservative
 ADDRESSEE: Patent Counsel
 STREET: 10666 No. 5652:
STREET: Mail Drop TPC8
CITY: La Jolla
 , MOLECULE TYPE: protein US-08-276-852-84
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 STATE: CA
COUNTRY: USA
 92037
 92037
 US-08-899-575-84
 COUNTRY:
 RESULT 8
 셤
 ò
 임
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIQWIQSPSSLSASVGDRVIIITGRASQGIRNYLAWYQQKPGKAPKLLIYAASTLQSGVPS 60
 Gaps
 .;
0
 Sequence 84, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQRYNRAPYTFGQGTKVEI 106
 Score 499; DB 4; Length 107;
Pred. No. 8.8e-37;
5; Mismatches 6; Indels
 APPLICANT: Labkovsky, Boris
APPLICANT: Mankovich, John A.
APPLICANT: McGuinness, Brian T.
APPLICANT: Roberts, Andrew J.
APPLICANT: Sakorafas, Paul
APPLICANT: Schoenhaut, David
APPLICANT: Schoenhaut, David
APPLICANT: White, Michael
APPLICANT: Wilton, Andrew J.
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IMP PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

SUSTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/540,018

FILING DATE: 31-MARCH-2000

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/599,226

FILING DATE: 08-FEB-1996

ATORNEY/AGENT INFORMATION:

NAME: Deconti, Giulio A., Jr.

REGISTRATION NUMBER: BBI-043

TELEPHONE: (617)227-7400

TELEPHONE: (617)227-5941

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: AMINO acid
 STREET: 60 State Street, suite 510 CITY: Boston
Kaymakcalan, Zehra
 89.78;
 Query Match
Best Local Similarity 89.65
 MOLECULE TYPE: peptide FRAGMENT TYPE: internal
 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & C
 Massachusetts
 linear
 USA
 RESULT 7
US-08-276-852-84
 COUNTRY:
 US-09-540-018-1
 g
 ò
```

```
3 OMTOSPSSLSASVGDRVTITCRASOGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSRF
 Gaps
 Sequence 84, Application US/08899575;
Sequence 84, Application US/08899575;
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Burton, Dennis R
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBFLICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
 ;
0
5652138th Torrey Pines Road, Suite 220,
 Length 107;
 63 SGSGSGIDFILTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 SGSGSGTDFTLTISSLOPEDVATYYCOKYNSAPRTFGQGTKVEI 104
 6; Indels
 COMPUTER: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FLING DATE: 18-JUL-1994
PRIOR APPLICATION NUMBER: US/08/276,852
FLING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTONNEY/AGENT INPORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: SCR1452P
TELECOMMULICATION INPORMATION:
TELEPHONE: 619-554-2937
 Score 483; DB 1;
Pred. No. 2.2e-35;
5; Mismatches 6
```

```
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERIFICS:
LENGTH: 107 amino acids
TYPE: amino acid
 FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
 86.9%;
 86.9%;
ilarity 89.4%;
Conservative
 LENGTH: 107 amino acids TYPE: amino acid
 Query Match
Best Local Similarity 89.4°
Matches 93; Conservative
 MOLECULE TYPE: protein US-08-899-575-84
 ; MOLECULE TYPE: protein PCT-US95-08743-84
 Local Similarity
nes 93; Conserv
 PCT-US95-08743-84
 TOPOLOGY:
 TOPOLOGY:
 Query Match
 Matches
 RESULT 10
 셤
 ð
 셤
 ઠે
 셤
 ò
 3 OMTOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSRF 62
 1 ELTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRF 60
 Gaps
 GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lener, Richard A
TITLE OF INVENTION: TO HUMAN INMUNODEFICIENCY VIRUS
INVENTION: TO HUMAN INMUNODEFICIENCY VIRUS
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
 ö
 Score 483; DB 1; Length 107;
Pred. No. 2.2e-35;
 63 SGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 SGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGGGTKVEI 104
 6; Indels
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-UUL-1997
YYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
 5; Mismatches
 CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,163
FILING DATE: 10-SEP-1992
ATTORNEY AGENT INFORMATION:
NAME: FILLING THOMASER: 34,163
REGERENCE/DOCKET NUMBER: 34,163
FELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
 Sequence 84, Application US/08899575 Patent No. 5804440
 Query Match
Best Local Similarity 89.4%;
Matches 93; Conservative
 LENGTH: 107 amino acids TYPE: amino acid
 , MOLECULE TYPE: protein US-08-899-575-84
 linear
 CLASSIFICATION:
 USA
 COUNTRY:
 쉽
 ò
 원
```

```
9
 1 ELTÓSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRP
 3 QMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSRF
 0; Gaps
 ö
 HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TO HUMAN IMMUNODEFICIENCY VIRUS
170
 Length 107;
 Length 107;
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBOD TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Pateintn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
 63 SGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 SGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGQGTKVEI 104
 Score 483; DB 5; Length 10
Pred. No. 2.2e-35;
5; Mismatches 6; Indels
 63 SGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 SGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGQGTKVEI 104
 Indels
Score 483; DB 1;
Pred. No. 2.2e-35;
 5; Mismatches
 Sequence 84, Application PC/TUS9508743 GENERAL INFORMATION:
```

```
APPLICATION NUMBER:
 USA
 ð
 92037
 JS-08-899-575-83
 COUNTRY:
 ò
 g
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLLIYGASTLQSGVPS 60
 1 DIQMIQSPSSLSASVGDRVTITCRASQSINSYLDWYQQKPGKAPKLLIYAASSLQSGVPS 60
 Gaps
 Sequence 33, Application US/08276852
; Sequence 83, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
 APPLICANT: Burton, Dennis R
 APPLICANT: Burton, Carlos F
 APPLICANT: Lerner, Richard A
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN INFUNOBERCIENCY VIRUS
 NUMBER OF SEQUENCES: 170
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Patent Counsel
 STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
 STREET: Mail Drop TPC8
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ö
 Query Match

86.3%; Score 480; DB 4; Length 214;
Best Local Similarity 86.8%; Pred. No. 8.1e-35;
Matches 92; Conservative 5; Mismatches 9; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPFTFGPGTKVBI 106
 GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: MUELLEN, BILLEN E.
APPLICANT: MUELLEN, BILLEN E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GOVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABS-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
 SOFTWARE: Patentin release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 71, Application US/09472087
Patent No. 6682736
 NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
 PRIOR APPLICATION DATA
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-71
 92037
 US-08-276-852-83
 US-09-472-087-71
 SEQ ID NO 71
LENGTH: 214
 셤
 ò
```

```
9
 3 QMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSRF
 0; Gaps
 ### Sequence 83 Application US/08899575
Sequence 83 Application US/08899575
Sequence 83 Application US/08899575
Sequence 83 Application US/08899575
Septicant: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Counsel
STREET: ADDRESSEE: Patent Counsel
STREET: ADDRESSEE: Patent Counsel
STREET: Anil Drop TPC8
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
STREET: Anil Drop TPC8
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
STREET: Anil Drop TPC8
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
TITLE OF INVENTION:
 Length 106;
 63 SGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 SGSGSGTDFTLTISSLQPEDVATYYCQKYNSVPRTFGGGTKVEI 104
 6; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER:
COMPUTER: TEM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: A35
PRIOR APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATPORNEY/AGENT INPORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: SCR1452P
TELEPHONE: 619-554-2937
 Score 475; DB 1;
Pred. No. 1.1e-34;
 8; Mismatches
 SCR1452P
 NAME: Fitting, Thomas
REGISTATION NUMBER: 34,163
REPERENCE/DOCKET NUMBER: SCR1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTER ISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
 Query Match
Best Local Similarity 86.5%;
Matches 90; Conservative
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-276-852-83
```

```
Search completed: November 16, 2005, 22:07:21 Job time : 18.1939 secs
 PCT-US95-08743-83
 TOPOLOGY:
 LENGTH:
 g
 à
 셤
 à
 3 QMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSRF 62
 1 ELTQSPSSLSASIGDRVTITCRASQGINNYLAWYQQRPGKVPRLLIYAASTLQSGVPTRF 60
 Gaps
 Sequence 83, Application US/08899575
Fatent No. 580440
GENERAL INFORMATION.
GENERAL INFORMATION.
THICHORY BUTTON, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
NUMBER OF EXQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
 ö
 Query Match 85.4%; Score 475; DB 1; Length 106; Best Local Similarity 86.5%; Pred. No. 1.1e-34; Matches 90; Conservative 8; Mismatches 6; Indels
 63 SGSGSGTDFTLTISSLOPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 61 SGSGSGTDFTLTISSLQPEDVATYYCQKYNSVPRTFGGGTKVEI 104
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FLING DATE: 24-JUL-1997
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FLING DATE: 30-SEP-1994
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34.163
REGISTRATION NUMBER: SCR1452P
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
 LENGTH: 106 amino acids; TYPE: amino acid TOPOLOGY: linear; MOLECULE TYPE: protein US-08-899-575-83
 : 106 amino acids amino acid
 TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 106 amino acid
 619-554-6312
 , MOLECULE TYPE: protein US-08-899-575-83
 ZIP: 92037
COMPUTER READABLE FORM:
 linear
 ð
 RESULT 14
US-08-899-575-83
 COUNTRY:
 셤
 ò
```

```
9
 1 ELTQSPSSLSASIGDRVTITCRASQGINNYLAWYQQRPGKVPRLLIYAASTLQSGVPTRF
 3 QMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSRF
 3 QMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPSRF
 0; Gaps
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNBER: PCT/US95/08743
FILING DATE: 11-701-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 11-00-1995
BRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLI
 ö
 Length 106;
 Query Match

85.4%; Score 475; DB 5; Length 106;

Best Local Similarity 86.5%; Pred. No. 1.1e-34;

Matches 90; Conservative 8; Mismatches 6; Indels
 63 SGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTXVDI 106
 61 SGSGSGTDFTLTISSLQPEDVATYYCQKYNSVPRTFGGGTKVEI 104
 Score 475; DB 1; Length 10
Pred. No. 1.1e-34;
8; Mismatches 6; Indels
 63 SGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 SGSGSGTDFTLTISSLQPEDVATYYCOKYNSVPRTFGGGTKVEI 104
 PCT-US95-08743-83
; Sequence 83, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
 FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
 85.4%;
 106 amino acids
amino acid
Query Match
Best Local Similarity 86.5'
Matches 90; Conservative
 MOLECULE TYPE: protein
```

7110 2001 B 1177 (1277)

Sequence

Sequence Sequence

Н

```
DIOMIOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 US-10-330-613-30

Sequence 30, Application US/10330613

Sequence 30, Application US/10330613

Publication No. US20030147809A1

GENERAL INFORMATION:
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUCL8 ANTIGEN

TITLE OF INVENTION ANTIBODIES AGAINST THE MUCL8 ANTIGEN

FILE REFERENCE: AGENIX.022A

CURRENT APPLICATION NUMBER: US/10/330,613

CURRENT PILING DATE: 2002-12-26

PRIOR PILING DATE: 2001-12-18

NUMBER: OF SEQ ID NOS: 40

SOFTHARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 107
 100.0%; Score 556; DB 14;
100.0%; Pred. No. 3.7e-39;
ive 0; Mismatches 0;
US-10-041-860-323

US-10-041-860-223

US-10-133-715-9

US-10-133-715-9

US-10-133-715-9

US-10-133-715-9

US-10-623-05-9

US-10-623-076-9

US-10-623-076-9

US-10-623-076-9

US-10-623-076-9

US-10-623-076-9

US-10-623-076-9

US-10-623-076-9

US-10-623-08-9

US-10-623-08-9

US-10-622-928-9

US-10-622-928-9

US-10-622-962-9

US-10-293-418-261

US-10-293-418-261

US-10-293-418-261

US-10-293-418-261

US-10-293-418-261

US-10-041-860-39

US-10-041-860-256

US-10-041-860-256

US-10-133-715-1

US-10-133-715-1

US-10-133-715-1
 US-10-622-932-1
US-10-623-065-1
US-10-623-076-1
 ALIGNMENTS
 Query Match
Best Local Similarity 100.
Matches 107; Conservative
 244
1007
1007
1007
1007
1007
 TYPE: PRT
ORGANISM: Homo Sapiens
 US-10-330-613-30
 -
 RESULT
 8
 g
 ò
 d
 Sequence 36, Appl
Sequence 38, Appl
Sequence 9, Appli
 November 16, 2005, 22:02:09; Search time 65.6949 Seconds (without alignments) 681.481 Million cell updates/sec
 Sequence 30, A
Sequence 30, A
Sequence 306,
Sequence 40, Al
Sequence 264,
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 30,
 556
1 DIQMTQSPSSLSASVGDRVT......CQKFSSPPFTFGFGTKVDIS 107
 Sequence Sequence S
 Description
 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/NSO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MBW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/USO0B_PUBCOMB.pep:*
 5.1.6
Compugen Ltd
 US-10-330-613-30
US-10-310-530-30
US-10-660-357-30
US-10-727-155-306
US-10-727-155-366
US-10-041-860-346
US-10-041-860-346
US-10-725-962-38
US-10-725-962-38
US-10-725-962-38
US-10-725-962-38
 Total number of hits satisfying chosen parameters:
 1867879 seqs, 418409474 residues
 GenCore version (c) 1993 - 2005
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 ü
 US-10-660-357A-30
 seq length: 0
seq length: 200000000
 B
 Length
 107
107
107
107
107
107
108
108
 Copyright
 Query
Match
 100.0
 100.0
 93.5
90.5
90.5
90.5
1.0
90.5
 Perfect score:
 Scoring table:
 556
520
520
520
520
503
503
503
 Score
 .
 0B
0B
 OM protein
 Sequence:
 Searched:
 Minimum |
Maximum |
 Database
 Run on:
```

ö

Gaps

; 0

Indels

Length 107;

Result Š. 9 9

> 107 107

Sequence 261, App Sequence 41, Appl Sequence 1, Appli Sequence 39, Appl Sequence 222, App

Sequence Sequence

Sequence

Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence Sequence

Sequence

9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 4, Appli 4, Appli 9, Appli 82, Appli 82, Appli

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

```
Larry Green
Xiao Feng
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Mus musculus
 Jaspal S. F
Orit Foord
 US-10-727-155-306
 RESULT 5
US-10-725-962-40
 US-10-725-962-40
 APPLICANT:
APPLICANT:
APPLICANT:
 TYPE: PRT
 APPLICANT:
 APPLICANT:
APPLICANT:
 APPLICANT:
 ò
 g
 1 DIOMIOSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIOMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIOMIOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 Gaps
 0
 ;
US-10-330-530-30

Sequence 30, Application US/10330530

Publication Vo. US20030152514A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

TITLE OF INVENDING: METHODS FOR USING ANTI-MUC18 ANTIBODIES

FILE REFRENCE: ABGENIX.031A

CURRENT FILING DATE: 2002-12-26

PRIOR FILING DATE: 2001-12-18

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 107
 Length 107;
 Length 107;
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDIS 107
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDIS 107
 Sequence 30, Application US/10660357
; Sequence 30, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INPORMATION:
 APPLICANT: Bar-Eli, Menashe
; APPLICANT: Bar-Eli, Menashe
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: WATIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
 Indels
 Indels
 100.0%; Score 556; DB 16;
100.0%; Pred. No. 3.7e-39;
tive 0; Mismatches 0;
 100.0%; Score 556; DB 14;
100.0%; Pred. No. 3.7e-39;
tive 0; Mismatches 0;
 Sequence 306, Application US/10727155 Publication No. US20050049402A1 GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.
Matches 107; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 107; Conservative
 TYPE: PRT
ORGANISM: Homo Sapiens
 TYPE: PRT
ORGANISM: Homo Sapiens
 US-10-727-155-306
 RESULT 3
US-10-660-357-30
 US-10-330-530-30
 US-10-660-357-30
 g
 g
 ò
 ઠે
```

```
1 DIOMIQSPSSLSASVGDRVIITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 9
 1 DIOMIDENE SELSASVGDRVIITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLOSGVPS
 1 DIOMTOSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 .
0
 .
0
 Score 520; DB 17; Length 108; Pred. No. 3.9e-36; 2; Mismatches 4; Indels
 Query Match
93.5%; Score 520; DB 17; Length 107;
Best Local Similarity 94.3%; Pred. No. 3.9e-36;
Matches 100; Conservative 2; Mismatches 4; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPFTFGPGTKVDI 106
 APPLICANT: Qiagjuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
PRIOR FILING DATE: 2002-12-02
SOFTWARE: FastEEQ for Windows Version 4.0
 APPLICANT: Frank I. Carroll
APPLICANT: Philip Abraham
APPLICANT: Philip Abraham
APPLICANT: Mellinda G. Gunnell
APPLICANT: Mary Haak Frendscho
APPLICANT: Xiao Feng
ITTLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
FILE REFERENCE: AGGENIX: 071A
CURRENT APPLICATION NUMBER: US/10/725,962
CURRENT APPLICATION NUMBER: 60/430717
PRIOR FILING DATE: 2002-12-02
PRIOR PLING DATE: 2002-12-02
PRIOR FILING DATE: 2002-13-02
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 108
 Mary Haak-Frendscho
Palaniswami Rathanaswami
 Sequence 40, Application US/10725962
Publication No. US20050013809A1
GENERAL INFORMATION:
APPLICANT: Samuel M. Owens
APPLICANT: Frank I. Carroll
 Kathy Manchulencho
Raffaella Faggioni
Giorgio Senaldi
 Query Match 93.5%;
Best Local Similarity 94.3%;
Matches 100; Conservative
Scott Klakamp
 Craig Pigott
Meina Liang
Rozanne Lee
```

ö

, APPLICANT: John S. Babcook

```
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 346
LENGTH: 107
 ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-346
 TYPE: PRT
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
 US-10-309-762-86
 US-10-725-962-36
 US-10-309-762-86
 APPLICANT: APPLICANT: APPLICANT: N
 Matches
 셤
 à
 g
 g
 ઠે
DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
 1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKFLIYAASTLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 ö
 91.4%; Score 508; DB 17; Length 107; 91.5%; Pred. No. 3.9e-35;
 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 APPLICANT: Giorgio Senaldi.
APPLICANT: Giorgio Senaldi.
APPLICANT: Giorgio Antibolis DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: PACYOR AND USES THEREOF
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR APPLICATION NUMBER: 60/430729
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FaatSEQ for Windows Version 4.0
SOFTWARE: FaatSEQ for Windows Version 2002-12-02
 APPLICANT: Ford, Xiao
APPLICANT: Ford, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazit, Gadit
APPLICANT: Gazit, Gadit
APPLICANT: Bezabeh, Birpan
APPLICANT: Bezabeh, Birpan
APPLICANT: BEZABH, Birpan
APPLICANT: ANTHODIES DIRECTED TO PDGFD AND USES
TITLE OF INVENTION: THEREOF
FULE REFERENCE: ABGENIX.05.1A
CURRENT APPLICANTON WHORER: US/10/041,860 .
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI
 9
 Mismatches
 Sequence 346, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION: APPLICANT: Corvalan, Jose R.F.
 Sequence 264, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
 Palaniswami Rathanaswami
 Mary Haak-Frendscho
 Kathy Manchulencho
Raffaella Faggioni
 APPLICANT: John S. Babcook
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
 97; Conservative
 Jia, Xiao-Chi
 Craig Pigott
 TYPE: PRT
ORGANISM: Homo sapiens
 Meina Liang
 Rozanne Lee
 Best Local Similarity
 RESULT 7
US-10-041-860-346
 US-10-727-155-264
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 Query Match
 APPLICANT
 Matches
음
 ò
 a
 ઠે
 유
 ò
 셤
```

```
ö
 ö
 1 DIQMTQSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
 9
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIOMIQSPSSLSASVGDRVIIICRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS
 Gaps
 Gaps
 ;
0
 ;
0
 Sequence 86, Application US/10309762

Sequence 86, Application US/10309762

Publication No. US20040018198A1

GENERAL INFORMATION:

APPLICANT: Gudas, Jean

APPLICANT: Foltz, Ian

APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: ANTIBODIES

TITLE OF INVENTION: ANTIBODIES

CURRENT FILING DATE: 2002-12-02

PRIOR PLLING DATE: 2002-12-02

PRIOR PLLING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 246

SOFTWARE: FastSEQ for Windows Version 4.0
 DB 15; Length 107;
 Length 107,
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 6; Indels
 Indels
 APPLICANT: Philip Abraham
APPLICANT: Melinda G. Gunnell
APPLICANT: Mary Haak-Frendscho
APPLICANT: Xiao Feng
TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
FILE REFERENCE: ABGRAY, 071A
CURRENT APPLICATION NUMBER: US/10/725,962
CURRENT FILING DATE: 2003-12-02
 5;
DB 14;
Score 505; DB 14
Pred. No. 7e-35;
2; Mismatches
 Score 503; DB 15
Pred. No. 1e-34;
 4; Mismatches
 Sequence 36, Application US/10725962
Publication No. US20050013809A1
GENERAL INFORMATION: OWERS
APPLICANT: Samuel M. OWERS
APPLICANT: Frank I. Carroll
 90.5%;
 90.8%;
Query Match 90.8
Best Local Similarity 92.5
Matches 98; Conservative
 97; Conservative
```

```
ORGANISM: homo sapiens
 ò
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIOMTOSPSSLSASVGDRVTITCRASOGISNYLAWYOOKPGKVPKLLIYAASTLOSGVPS 60
 1 DIOMIQSPSSLSASVGDRVIITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS
 Gaps
 Gaps
 ·
0
 ö
 Score 503; DB 17; Length 108;
Pred. No. 1e-34;
4; Mismatches 5; Indels
 Score 503; DB 17; Length 108; Pred. No. 1e-34; 4; Mismatches 5; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 Sequence 38, Application US/10725962
; Publication No. US20050013809A1
; Publication No. US20050013809A1
; Publication No. US20050013809A1
; Publication No. US20050013809A1
; APPLICANT: Samuel M. Owens
; APPLICANT: Philip Abraham
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Xiao Feng
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; TITLE OF INVENTION: ANTIBODIES AGAINST DRUGS OF ABUSE
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430717
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
PRIOR APPLICATION NUMBER: 60/430717
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 141
SEQTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 108
 Query Match 90.5%;
Best Local Similarity 91.5%;
Matches 97; Conservative
 Query Match
Best Local Similarity 91.5%;
Matches 97; Conservative
 CITY: Boston
 ; LENCTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-725-962-38
 ; ORGANISM: Mus musculus US-10-725-962-36
 RESULT 11
US-09-801-185A-9
 RESULT 10
US-10-725-962-38
 g
 ò
 셤
 ò
 ઠ
```

```
9
 1 DIOMIOSPSSLSASVGDRVIIITCRASOGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIOMTOSPSSLSASIGDRVTITCRASOGIRNYLAWYOOKPGKAPKLLIYAASTLOSGVPS
 Gaps
 .;
0
 Length 107;
 61 RESCSGSGTDFTLTISSLQPEDVATYYCQKESSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLFISSLOPEDVATYYCQKYNSAPYAFGQGTKVEI 106
 COMPUTER: ISEN PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/801,185A
FILING DATE: 07-MARCOWN>
PRIOR PRIORITION NUMBER: US 08/599,226
APPLICATION NUMBER: US 08/59,226
APPLICATION NUMBER: US 06/031,476
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: US 09/125,098
FILING DATE: 07-AUG-1998
 Indels
 APPLICANT: Corvalan, Jose R.F.
APPLICANT: Corvalan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao-Dong
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
 Query Match
90.1%; Score 501; DB 10;
Best Local Similarity 89.6%; Pred. No. 1.5e-34;
Matches 95; Conservative 5; Mismatches 6;
 ATTORNEY AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-043CPUSCN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
 CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 107
TYPE: PRT
 ;
**MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-801-185A-9
 Sequence 32, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
STATE: Massachusetts
 ZIP: 02109
COMPUTER READABLE FORM:
 TYPE: amino acid
```

```
US-10-133-715-9
 Query Match
 FEATURE:
 g
 ò
 셤
 ò
 δ
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS 60
 1 DIQMIQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
 1 DIQMIQSPSSLSASVGDRVIITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
 1 DIOMTOSPSSLSASVGDRVTITCRASOGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 Gaps
 ö
 ö
 90.1%; Score 501; DB 14; Length 107; 91.5%; Pred. No. 1.5e-34; tive 3; Mismatches 6; Indels
 Query Match 90.1%; Score 501; DB 14; Length 107; Best Local Similarity 91.5%; Pred. No. 1.5e-34; Matches 97; Conservative 3; Mismatches 6; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPLTFGGGTKVEI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPLTFGGGTKVBI 106
 APPLICANT: Peng, Xiao
APPLICANT: Vang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Cazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: WITHEROF
FILLE OF INVENTION: THRREOF
FILE REFERENCE: ABGENIX.051A
CURRENT PILLOATION NUMBER: US/10/041,860
CURRENT FILLOATION NUMBER: US/10/041,860
CURRENT FILLOATION NOS: 377
NUMBER OF SEQ ID NOS: 377
 APPLICANT: Gazit, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezabeh, Binyam
AITLE OF INVENTION: ATHEREOF
TITLE OF INVENTION: THEREOF
 FILE REFERENCE: ABGENIX.051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
 Sequence 223, Application US/10041860 Publication No. US20030157109A1 GENERAL INFORMATION:
APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
 Sequence 257, Application US/10041860; Publication No. US20030157109A1
GENERAL INFORMATION: APPLICANT: Corvalan, Jose R.F. APPLICANT: Jia, Xiao-Chi
 Ouery Match
Best Local Similarity 91.57
 Feng, Xiao
Yang, Xiao-Dong
Chen, Francine
 ORGANISM: homo sapiens
 RESULT 13
US-10-041-860-223
 US-10-041-860-223
 RESULT 14
US-10-041-860-257
US-10-041-860-32
 SEQ ID NO 223
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 g
 쉽
 ò
 ò
```

```
1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPS 60
 1 DIQMIQSPSSLSASIGDRVIITCRASQGIRNYLAWYQQKPGKAPKILIYAASTLQSGVPS
 1 DIOMIQSPSSLSASVGDRVIIICRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNYLAWYQQNPGKVPKLLIYGASTLQSGVPS
 Gaps
 ö
 Sequence 9. Application US/10133715

Publication No. US2003026898A1

GENERAL INFORMATION:

APPLICANT: Pischkoff, Steven

APPLICANT: Pischkoff, Steven

TITLE OF INVENTION: Use of TNF-a Antibodies and Another Drug

FILE REFERENCE: BB1-186

CURRENT APPLICATION NUBER: US/10/133,715

CURRENT FILING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 107
 Score 501; DB 14; Length 107;
Pred. No. 1.5e-34;
3; Mismatches 6; Indels (
 90.1%; Score 501; DB 15; Length 107;
89.6%; Pred. No. 1.5e-34;
tive 5; Mismatches 6; Indels
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPLTFGGGTKVEI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPYAFGQGTKVEI 106
 61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKFSSPPFTFGPGTKVDI 106
 ; OTHER INFORMATION: 2SD4 light chain variable region US-10-133-715-9
; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 257
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-257
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 91.5%;
Matches 97; Conservative
 Best Local Similarity 89.6
Matches 95; Conservative
```

Search completed: November 16, 2005, 23:05:44 Job time : 65.6949 secs

```
November 16, 2005, 21:35:48; Search time 61.3676 Seconds (without alignments) 674.351 Million cell updates/sec
 1 EIVMTQSPATLSVSPGERAT........CQQYNNWPRTFGQGTKVEIK 107
 2105692
5.1.6
Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2105692 seqs, 386760381 residues
 version :
- 2005 (
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 GenCore (c) 1993 .
 US-10-660-357A-34
 Copyright
 Perfect score:
 Scoring table:
```

Sequence:

Run on:

Searched:

## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2003as:\*geneseqp2003bs:\*geneseqp2004s:\* Geneseq 16Dec04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*geneseqp2002s:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

length: 0 length: 2000000000

sed

8 1 1 1 1 1 1 1

Minimum I Maximum I

| Description         | Adc99805 Anti-huma Add05409 Anti-huma Add05412 Anti-MUC1 Adf09847 Human ant Adc99777 Anti-huma Add05381 Anti-huma Adf09819 Human ant Abr54896 Light cha Abr54896 Light cha Abr54891 Light cha Abr54891 Light cha Adp22407 Human ant Adp22407 Human ant Adp22408 Light cha Adr3402 Light cha Adr3402 Light cha Adr54891 Light cha Abr54891 Light cha | Abr42858 Tumour-sp |
|---------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|
| SUMMARIES<br>B ID   | 7 ADC99805<br>7 ADD05409<br>7 ADD05442<br>7 ADD05442<br>7 ADD05481<br>7 ADC9977<br>7 ADC9977<br>7 ADC9977<br>7 ADC9977<br>6 ABK54896<br>6 ABK54890<br>6 ABK54891<br>8 ADP22404<br>8 ADP22404<br>8 ADP22404<br>8 ADP2406<br>6 ABK54891<br>6 ABK54891<br>7 ADG96768<br>8 ABK54893<br>8 ABK54893<br>8 ABK54893<br>8 ABK54893<br>8 ABK54893<br>8 ABK54893<br>8 ABK54893<br>8 ABK54893                                                                                                                                                                                                                                                                                                                                            | 6 ABR42858         |
| Length DB           | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 117                |
| %<br>Query<br>Match |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 93.6               |
| Score               | N N N N A A A W W W W W W W W W W W W W                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 520.5              |
| Result<br>No.       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 25                 |

| 26 | 520.5 | 93.6 |    | 117 |     | ABR42860     | Abr42860 | Tumour-sp |  |
|----|-------|------|----|-----|-----|--------------|----------|-----------|--|
| 28 | 520.5 | 9 6  |    | 11  |     | ABW02446     | Abw02446 | Human mon |  |
| 29 | 520.5 | 93   |    | 11  | _   | ABW02466     | Abw02466 |           |  |
| 30 | 520.5 | 93.  |    | 17  |     | ABW02465     | Abw02465 | Human mon |  |
| 31 | 520   | 93.  |    | 46  | 'n  | ABP45257     | Abp45257 | Human BLy |  |
| 32 | 520   | 93.  |    | 46  |     | ADG96084     | Adg96084 | Single ch |  |
| 33 | 517   | 93.  |    | 07  |     | ADJ80364     | Ad 30364 |           |  |
| 34 | 516   | 92.  |    | 07  | 60  | ADP22240     | Adp22240 | Human ant |  |
| 35 | 516   | 92.  |    | 07  | 60  | ADP22278     | Adp22278 | Human ant |  |
| 36 | 516   | 92.  |    | 27  | 7   | ADC61110     | Adc61110 | Human     |  |
| 37 | 515.5 | 92.  |    | 90  | . ` | ADP22371     | Adp22371 | Human ant |  |
| 38 | 515   | 92.  |    | 54  | 80  | ADL25472     | Ad125472 | Human     |  |
| 39 | 513.5 | 92.  |    | 17  | 9   | ABR42850     | Abr42850 | Tumour-sp |  |
| 40 | 513.5 | 92.4 |    | 17  | 9   | ABR42851     | Abr42851 | Tumour-sp |  |
| 41 | •     |      |    | 17  | 9   | ABR42849     | Abr42849 | Tumour-sp |  |
| 42 | 513.5 |      | .4 | 17  | 9   | ABR42853     | Abr42853 | Tumour-sp |  |
| 43 | 513.5 | 92.4 |    | 17  | _   | ABW02460     | Abw02460 | Human mon |  |
| 44 | 513.5 | 92.4 |    | 17  | _   | ABW02462     | Abw02462 | Human mon |  |
| 45 | 513.5 | 92.  | 4  | 17  | 7   | ABW02459     | Abw02459 | Human mon |  |
|    |       |      |    |     |     | AL. TGNMENTS |          |           |  |

## ALIGNMENTS

anti-human MUC18 monoclonal antibody, heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 34. ADC99805 standard; protein; 107 AA (first entry) lung cancer; human Homo sapiens 01-JAN-2004 

WO2003057838-A2

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P.

(ABGE-) ABGENIX INC.

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99807.

disease New human anti-MUC18 monoclonal antibodies, useful for treating a dor condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 34; 78pp; English,

The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WIC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of WIC18 on the cell surface such as tumours, specifically melanoma, ossophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung canneer, as well as other malignancies. The current sequence is that of the anti-human WIC18 monoclonal antibody

õ

Gaps

ö

Indels

9 9

61

셤 ò

a

ò

ADD05409;

Query Match

SXS

```
The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 anino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and creating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an animal having a metastatic tumour. This protein of the invention.
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; light chain.
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
 1 BIVMTQSPATLSVSPGBRATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Anti-MUC18 antibody light chain variable region L2 protein, SEQ ID 67.
 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
100.0%; Pred. No. 3.1e-34; tive 0; Mismatches 0;
 Disclosure; SEQ ID NO 67; 87pp; English.
 Ŕ
 ADD05442 standard; protein; 107
 28-DEC-2001; 2001US-0346460P.
 26-DEC-2002; 2002WO-US041582
 (first entry)
 107; Conservative
 Bar-Eli M;
 WPI; 2003-577496/54.
 (ABGE-) ABGENIX INC
 Best Local Similarity
 metastatic tumor.
 Sequence 107 AA;
 WO2003057006-A2
 Unidentified.
 01-JAN-2004
 17-JUL-2003
 ADD05442;
 Gudas J,
 Query Match
 Matches
 ADD05442
 RESULT
 g
 ð
 셤
 ð
 ö
 The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds WUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the WUC18 antigen are useful for diagnosing and
 treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis, inhibiting cell invasion associated with melanoma, or increasing survival of an animal with a metastatic tumour. This sequence represents an anti-MCL8 antibody light chain, variable region,
 9
 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPQQAPRLLIFGASTRATGIPA 60
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; light chain.
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Anti-MUC18 antibody light chain variable region protein, SEQ ID No 34.
 Gaps
 ÷
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Length 107;
 Indels
 100.0%; Score 556; DB 7;
100.0%; Pred. No. 3.1e-34;
ive 0; Mismatches 0;
 Claim 3; SEQ ID NO 34; 87pp; English.
 light chain protein of the invention.
 ADD05409 standard; protein; 107 AA.
 26-DEC-2002; 2002WO-US041582.
 28-DEC-2001; 2001US-0346460P.
 (first entry)
 protein of the invention.
 Matches 107; Conservative
 Gudas J, Bar-Eli M;
 WPI; 2003-577496/54.
 (ABGE-) ABGENIX INC
 Local Similarity
 N-PSDB; ADD05411
 metastatic tumor
 Seguence 107 AA;
 WO2003057006-A2
 Homo sapiens
 17-JUL-2003.
 01-JAN-2004
```

```
1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 Gape
 ,
0
100.0%; Score 556; DB 7; Length 107; 100.0%; Pred. No. 3.1e-34; ive 0; Mismatches 0; Indels (
 Conservative
 Local Similarity
les 107; Conserv
 Best Loca
Matches
 g
 ò
```

DB 7; Length 107;

100.0%; Score 556;

Sequence 107 AA;

Query Match

ö

ઠ

```
The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to NUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the call surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody light chain protein of the invention.
 New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
 anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; light chain.
 1 EIVWTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Anti-MUC18 antibody light chain variable region protein, SEQ ID No
 cytostatic, melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 6.
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTXVEIK 107
 Query Match

98.2%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.7e-33;
Matches 104; Conservative 2; Mismatches 1: Indels
 Claim 3; SEQ ID NO 6; 78pp; English.
 ADD05381 standard; protein; 107 AA
 26-DEC-2002; 2002WO-US041581.
 28-DEC-2001; 2001US-0346299P.
 (first entry)
 WPI; 2003-587113/55.
N-PSDB; ADC99779.
 (ABGE-) ABGENIX INC
 lung cancer; human.
 Sequence 107 AA;
 WO2003057838-A2
 Homo sapiens.
 01-JAN-2004
 01-JAN-2004
 ADC99777;
 Gudas J;
 ADD05381
ID ADD
XX
XX
XX
DT 01-
XX
XX
DB Ant
XX
KW MOD
KW ADD
ò
 ઠે
 g
 The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNPAWYQQKPGQAPRLLIFGASTRATGIPA 60
 9
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; light chain; human.
 Inhibiting cell proliferation associated with expression of MUC18 antigen, involves incubating and inhibiting cell by administering MUC18 monoclonal antibody.
 ö
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 100.0%; Score 556; DB 7; Length 107; 100.0%; Pred. No. 3.1e-34; ive 0; Mismatches 0; Indels
 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 RFSGSGSGTEFTLTISSLOSEDFAVYYCQOYNNWPRTFGGGTKVEIK
 Human anti-MUC18 monoclonal antibody light chain #9.
 Claim 3; SEQ ID NO 34; 83pp; English
 ADC99777 standard; protein; 107 AA.
 ADF09847 standard; protein; 107
 26-DEC-2002; 2002WO-US041580
 28-DEC-2001; 2001US-0346414P
 12-FEB-2004 (first entry)
 Best Local Similarity 100.
Matches 107, Conservative
 WPI; 2003-598367/56.
 (ABGE-) ABGENIX INC
 monoclonal antibody
 N-PSDB; ADF09849
 Sequence 107 AA;
 WO2003057837-A2
 Homo sapiens.
 17-JUL-2003
 61
 61
 ADF09847;
 Query Match
 Gudas J;
```

ADRO9847

ADRO98

ö

Gaps

.. 0

9 9

RESULT 5 ADC99777 ID ADC9 XX

셤 ò

```
The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting cell proliferation in patients with tumours, carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific
 Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody.
 1 EIVMTGSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Engineered template; single primer amplification; antibody library; nucleic acid amplification.
 Renshaw M;
 RFSGSGGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Query Match

98.2%; Score 546; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 1.7e-33;
Matches 104; Conservative 2; Mismatches 1; Indels
 Maruyama T, Lin Y,
 Light chain clone HBPAXK2d 3A9 SEQ ID NO:122
 Claim 3; SEQ ID NO 6; 83pp; English.
 Æ
 ABR54896 standard; protein; 107
 Bowdish KS, Frederickson S,
 28-DEC-2001; 2001US-0346414P.
 19-SEP-2001; 2001US-0323455P.
 19-SEP-2002; 2002WO-US029889
 26-DEC-2002; 2002WO-US041580
 (first entry)
 (ALEX-) ALEXION PHARM INC
 WPI; 2003-598367/56.
 (ABGE-) ABGENIX INC
 monoclonal antibody
 N-PSDB; ADF09821.
 Sequence 107 AA;
 #02003025202-A2.
 sapiens
 30-JUN-2003
 17-JUL-2003
 27-MAR-2003
 Synthetic
 61
 ABR54896;
 Gudas J;
 ABR54896
 RESULT
 8
 음
 δ
 The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and conteacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metasteasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
 ö
 9
 EIVWTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a
 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
carcinoma; cancer; malignancy; light chain; human.
 Gaps
 .;
0
 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGGGTKVEIK 107
 Length 107;
 1; Indels
 Human anti-MUC18 monoclonal antibody light chain #2.
 Query Match

98.2%; Score 546; DB 7;
Best Local Similarity 97.2%; Pred. No. 1.7e-33;
Matches 104; Conservative 2; Mismatches 1;
 Claim 3; SEQ ID NO 6; 87pp; English.
 ADF09819 standard; protein; 107 AA
 26-DEC-2002; 2002WO-US041582
 28-DEC-2001; 2001US-0346460P
 (first entry)
 protein of the invention.
 Gudas J, Bar-Eli M;
 WPI; 2003-577496/54
 (ABGE-) ABGENIX INC
 metastatic tumor.
 Sequence 107 AA;
 N-PSDB; ADD05383
 WO2003057837-A2
 WO2003057006-A2
 Homo sapiens
 Homo sapiens
 12-FEB-2004
 17-JUL-2003
```

ADF09819

g

8

g

à

ö

0; Сарв

9 9 ß

```
19-SEP-2002; 2002WO-US029889
 19-SEP-2001; 2001US-0323455P.
 (ALEX-) ALEXION PHARM INC.
 Homo sapiens,
 27-MAR-2003.
 Synthetic.
 invention
 н
 Query Match
 sequence
 유
 8
 g
 ઠ
```

```
Bowdish KS, Frederickson S,
 ABR54897;
 sequence.
 Query Match
 Local
 Best Loca
Matches
 RESULT 10
 ABR54897
엄
 ò
 The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other, and contacting (S) with a primer having the predetermined sequence in the presence of a polymers and nucleotides under conditions suitable for polymerisation of the nucleotides and a sequence at one end and a sequence complementary to the predetermined sequence at the other end. M1 is useful for amplifying a mucleic acid. M1 can be used for products that can be used ilbrary. M1 is useful for preparing amplified products that can be used to transform an appropriate host organism to product the polypeptide or protein encoded by the target sequence. M1 is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of antibody library uncleic acid sequence, but also for amplifying simultaneously more than one different target nucleic acid sequence located on the same or different nucleic acid molecules. ACC62635 to ACC62753 and ABRS4841 to han an antibody library sequence used in the exemplification of the present sequence used in the exemplification of the present
 9
 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPQQAPRLLIYGASTRATGIPA 60
 Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 Engineered template; single primer amplification; antibody library; nucleic acid amplification.
 ;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPTFGQGTKVEIK 107
 Score 534; DB 6; Length 107; Pred. No. 1.4e-32;
 Light chain clone HBPAXK2d 3D12 SEQ ID NO:126.
 3; Mismatches
 Example 3; Fig 8b-c; 68pp; English.
 ABR54900 standard; protein; 107 AA
 96.0%;
 30-JUN-2003 (first entry)
 Jest Local Similarity 95.3
Matches 102; Conservative
 Local Similarity
 Sequence 107. AA;
 WO2003025202-A2.
```

```
The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered mucleic acid strand (S) acid strand. M1 comprises providing an engineered mucleic acid strand (S) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence in the other, and contacting (S) with a primer having the predetermined sequence in the presence of a polymers and nucleotides. Also described is an engineered nucleic acid strand (I) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other end. M1 is useful for amplifying a nucleic acid. M1 can be used for producing an antibody library. M1 is useful for preparing amplified products that can be used to transform an appropriate host organism to produce the polypeptide or protein encoded by the target sequence. M1 is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of the target nucleic acid sequence, but also for amplifying similtaneously
 ö
 more than one different target nucleic acid sequence located on the same or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to ABR54998 represent sequence used in the exemplification of the present
 9
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGTSTRATGIPA
 Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
 Gaps
 Engineered template, single primer amplification; antibody library; nucleic acid amplification.
 ö
Renshaw M;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPGTFGQGTKVEIK 107
 Length 107;
Lin Y,
 95.3%; Score 530; DB 6; 94.4%; Pred. No. 2.7e-32; ive 3; Mismatches 3;
 Light chain clone HBPAXK2d 3A12 SEQ ID NO:123.
Maruyama T,
 Example 3; Fig 8b-c; 68pp; English.
 ABR54897 standard; protein; 107 AA
 19-SEP-2002; 2002WO-US029889.
 19-SEP-2001; 2001US-0323455P
 (first entry)
 Conservative
 WPI; 2003-313359/30.
 Similarity
 Sequence 107 AA;
 WO2003025202-A2.
 Homo sapiens
 30-JUN-2003
 101;
 27-MAR-2003.
 Synthetic.
```

(ALEX-) ALEXION PHARM INC.

```
The present invention describes a method (M1) for amplifying a nucleic caid strand. MI comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other, and contacting (S) with a primer having the predetermined sequence in the presence of a polymers and nucleotides under conditions suitable for polymerisation of the nucleotides. Also described is an engineered nucleic acid strand (I)
 or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to ABR54998 represent sequence used in the exemplification of the present
 having a predetermined sequence at one end and a sequence complementary to the predetermined sequence at the other end. M. is useful for amplifying a nucleic acid. M. can be used for producing an antibody library. M. is useful for preparing amplified products that can be used to transform an appropriate host organism to produce the vector can be used to transform an appropriate host organism to produce the polypeptide or protein encoded by the target sequence. M. is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. M. is useful not only for producing large amounts of one target nucleic acid sequence, but also for amplifying simultaneously more than one different target nucleic acid sequence located on the same
 Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined
 Maruyama T, Lin Y,
 Example 3; Fig 8b-c; 68pp; English.
 Frederickson S,
 Bowdish KS,
 invention
 seguence
```

Sequence 107 AA;

ö 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60 Gaps ö 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPNTFGPGTKVDIK 107 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107 , DB 6; Length 107; 4.5e-32; 3; Indels 4; Mismatches 94.8%; Score 527; 93.5%; Pred. No. 4 Matches 100; Conservative Best Local Similarity Query Match 쉽 ò

ABR54883 standard; protein; 107 AA. 

30-JUN-2003 (first entry)

Light chain clone HBPAXKIb 3A2 SEQ ID NO:109.

Engineered template; single primer amplification; antibody library; nucleic acid amplification.

Homo sapiens Synthetic. WO2003025202-A2.

27-MAR-2003

19-SEP-2002; 2002WO-US029889

19-SEP-2001; 2001US-0323455P

(ALEX-) ALEXION PHARM INC.

Renshaw M;

Renshaw M; Lin Y, Maruyama T, Frederickson S, Bowdish KS,

Amplifying nucleic acid by contacting engineered nucleic acid strand having predetermined sequence at one end and sequence complementary to predetermined sequence at other end, with primer having predetermined sequence

Example 3; Fig 8b-c; 68pp; English.

The present invention describes a method (M1) for amplifying a nucleic acid strand. M1 comprises providing an engineered nucleic acid strand (S) acid strand. M1 comprises providing an engineered nucleic acid strand (S) having a predetermined sequence at one end and a sequence complementary to the predetermined sequence in the presence of a polymers or primer having the predetermined sequence in the presence of a polymers and nucleotides. Mas described is an engineered mucleic acid strand (I) and nucleotides. Mas described is an engineered and a sequence complementary to the predetermined sequence at the other end. M1 is useful for to the predetermined sequence at the other end. M1 is useful for to the predetermined sequence at the other end. M1 is useful for library. M1 is useful for preparing amplified products that can be used to transform an appropriate host organism to product the product a family content encoded by the target sequence. M1 is useful to amplify a family of related sequences to build a complex library such as, for example an antibody library. M1 is useful not only for producing large amounts of antibody library. M1 is useful not only for producing large amounts of antibody library uncleic acid sequence, but also for amplifying simultaneously core than one different target nucleic acid sequence located on the same or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54811 to increase.

Sequence 107 AA;

ö Gaps ö Length 107; 94.8%; Score 527; DB 6; Length 10 93.5%; Pred. No. 4.5e-32; ive 5; Mismatches 2; Indels Local Similarity 93.5 ses 100; Conservative Query Match Best Loca Matches

1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 셤

61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107 61 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPITFGQGTRLEIK 107 ò

RESULT 12 ADP22404

ADP22404 standard; protein; 107 AA ADP22404:

(first entry)

09-SEP-2004

Human anti-TNFa antibody light chain variable region SEQ ID NO:310.

ovarian cancer; human; monoclonal antibody; tumour necrosis factor-alpha; TNFa; anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic; antiarchritic; antincheumatic; eating-disorder; immunomodulator; immunomoupressive; nephrotropic; neuroprotective; vasotropic; antiapoptotic; TNFa antagonist; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancel bladder cancer; lung cancer; glioblastoma; stomach cancer; prostrate cancer; immuno-mediated inflammatory disease; prostrate cancer; immuno-mediated inflammatory disease; restences; prostrate cancer; immuno-mediated inflammatory disease; restences; restences; supportant inflammatory disease; restences; settle inflammatory disease; psoriasis; restences; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; multiple sclerosis. 

```
New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 Green L, Feng X, Klakamp S;
 Qiaojuan JS;
 Haak-Frendscho M, Rathanaswami P, Pigott C,
Manchulencho K, Faggioni R, Senaldi G, Qiao
 Example 10; SEQ ID NO 310; 213pp; English.
 Babcook JS, Kang JS, Foord O,
 02-DEC-2003; 2003WO-US038281.
 02-DEC-2002; 2002US-0430729P
 WPI; 2004-480601/45.
 (ABGE-) ABGENIX INC.
 WO2004050683-A2
Homo sapiens.
 17-JUN-2004
 arthritis.
```

The present invention describes a human monoclonal antibody (1) that

CC (a) a heavy complementarity determining region 1 (DRN1) having the

two fully defined 5 amino acid sequence (51, ADP22417) or (52, ADP22421);

CC and (b) a light chain CDR1 having the two fully defined 11 amino acid

sequence (53, ADP22418) or (54, ADP22424). ADB0 described: (1) assaying

(M1) the level of TNFa in a patient sample, comprising contacting with

(I), and detecting the level of binding between the antibody and TNFa in

the sample; (2) a composition comprising the antibody or its functional

fragment and a carrier; (3) treating (M2) an animal suffering the human

cc animal in need of treatment for the disease by administering the human

monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced

apoptosis in an animal by selecting an animal in need of treatment for

cr TNFa induced apoptosis by administering the human monoclonal antibody of

(1). (1) has anabolic, antiarteriosolerotic, antiarthritic,

antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating
disorders, immunomodulator, immunosuppressive, nephrotropic,

contracted apoptosis by administering the human monoclonal antibody of

(1). (1) has anabolic, antiarteriosolerotic, antiarthritics, and can be used

as a TNFa antagonist. The antibody (1) is useful in the preparation of

medicament for treating TNF induced apoptosis, neoplastic disease such as

comment cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,

conference ancer, ovarian cancer, bladder cancer, or immuno-mediated inflammatory

alberosclerosis, psorianis, restencesis, one mediated inflammatory

alberosclerosis, psorianis, restencesis, one mediated inflammatory

diseases such as rheumatoid arthritis, glomerulonephritis,

antibody light chain variable region, which is used in the

control of the present invention.

Sequence 107 AA;

```
9
 1 EIVWTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 ö
Query Match 94.8%; Score 527; DB 8; Length 107; Best Local Similarity 93.5%; Pred. No. 4.5e-32; Matches 100; Conservative 5; Mismatches 2; Indels
```

> a ઠે

ADP22407 standard; protein; 107 AA 

(first entry) 09-SEP-2004 Human anti-TNFa antibody light chain variable region SEQ ID NO:313.

ovarian cancer; freumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis; restenosis; autoimmune disease; Crohn's disease; graft-host reaction; septic shock; cachexia; anorexia; multiple sclerosis. anti-TNFa antibody; anabolic, antiarteriosclerotic; antiarthritic; antibacerial; antiinflammatory; antipsoriatic; antirheumatic; eating-disorder; immunomodulator; immunosuppressive; nethrotropic; neuroprotective; vasotropic; antiapoptocic; TNFa antagonist; TNF induced apoptosis; neoplastic disease; breast cancer; ovarian calledar cancer; glioblastoma; stomach cancer; endometrial cancer; kidney cancer; colon cancer; pancreatic cancer; prostrate cancer; immuno-mediated inflammatory disease; tumour necrosis factor-alpha; TNFa; human; monoclonal antibody;

Liang ML, Lee R;

Homo sapiens.

WO2004050683-A2.

17-JUN-2004.

02-DEC-2003; 2003WO-US038281.

02-DEC-2002; 2002US-0430729P.

(ABGE-) ABGENIX INC.

Feng X, Klakamp t t C, Liang ML, Le Qiaojuan JS; Haak-Frendscho M, Rathanaswami P, Pigott Manchulencho K, Faggioni R, Senaldi G, C Green L, Foord O, Kang JS, Babcook JS,

WPI; 2004-480601/45.

New recombinant human monoclonal antibody that specifically binds to Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such as cancers, or immuno-mediated inflammatory diseases such as rheumatoid arthritis.

Example 10; SEQ ID NO 313; 213pp; English.

The present invention describes a human monoclonal antibody (I) that specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:

(a) a heavy chain complementarity determining region I (CDR1) having the two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421); and (b) a light chain CDR1 having the two fully defined 11 amino acid sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying (M) and detecting the level of binding between the antibody and TNRa in the sample; (2) a composition comprising the antibody or its functional fragment and a carrier; (3) treating (M2) an animal suffering from a neoplastic, or an immuno-mediated inflammatory disease by selecting an animal in need of treatment for the disease by administering the human concolonal antibody of (I); and (4) inhibiting (M3) TNRa induced apoptosis by administering the human monoclonal antibody of (I); and (4) inhibiting (M3) TNRa induced apoptosis by administering the human monoclonal antibody of (I); and induced apoptosis by administering the human monoclonal antibody of (I); (I) has anabolic, antiarteriosclerotic, antirheumatic, eating-clisotherial, antiinflammatory, antipoptotic activities, and can be used as a TNRa antegoniar. He antiabody (I) is useful in the preparation of medicament for treating TNF induced apoptosis, neoplastic disease such as a TNRa and prostrate cancer, lung cancer, colon cancer, pancreatic cancer, ovarian cancer, kidney cancer, colon cancer, pancreatic cancer, and prostrate cancer, or immuno-mediated inflammatory diseases such as theumatoid arthritis, glomerulonephritis, pancreatic and arthritis, glomerulonephritis, antendence of the cancer, or immuno-mediated inflammatory antender cancer, or immuno-mediated inflammatory attribution antender cancer, and prostrate cancer, or immuno-mediated inflammatory attribution antender cancer, and prostrate cancer, or immuno-mediated inflammatory attribution antender cancer antender cancer antender cancer antender cancer antender cancer antende atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's disease, graft-host reactions, septic shock, cachexia, anorexia, and

RESULT 13 ADP22407

```
Search completed: November 16, 2005, 21:51:43
 02-FEB-2004; 2004WO-US002892
 01-FEB-2003; 2003US-0444229P.
 Ä
 /note=
 /note=
 WPI; 2004-604432/58.
 Foster C,
 (TANO-) TANOX INC.
 Sequence 107 AA;
 WO2004070010-A2
 Homo sapiens.
 04-NOV-2004
 19-AUG-2004
 61
 Singh S,
 ADR31547;
 Query Match
 made
 Region
 Region
 Region
 Best Loca
Matches
 RESULT 15
 ADR31547
 셤
 ò
 ద
 8
 원
 ठ
 ö
 ö
 The present invention relates to an antibody comprising a variable light chain region or a variable heavy chain region. The antibody and methods are useful for treating a disorder associated with an abnormally high IgE level, e.g. asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a food allergy. The present sequence represents human anti-IgE antibody light chain combined L16 and JK4.
 9
 EIVWTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
 9
 9
 for
 New high affinity human monoclonal antibodies, particularly those directed against isotypic determinants of immunoglobulin E, useful for asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a food allergy.
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 EIVWTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
multiple sclerosis. The present sequence represents a human anti-TNFa antibody light chain variable region, which is used in the exemplification of the present invention.
 Gaps
 antibody; variable light chain; variable heavy chain; Antiallergic; Dermatological; Immunosuppressive; IgE; asthma; allergic rhinitis; eczema; urticaria; atopic dermatitis; food allergy; CDR.
 ö
 ;
0
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIK 107
 RFSGSGSGTEFILTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 94.8%; Score 527; DB 8; Length 107; 94.4%; Pred. No. 4.5e-32; ive 3; Mismatches 3; Indels
 Length 107;
 Score 527; DB 8; Length 10 Pred. No. 4.5e-32; 3; Mismatches 3; Indels
 Human anti-IgE antibody light chain L16 and JK4.
 Disclosure; SEQ ID NO 2; 101pp; English.
 ADR43402 standard; protein; 107 AA
 02-FEB-2004; 2004WO-US002894.
 01-FEB-2003; 2003US-0444229P.
 Match 94.8%; Local Similarity 94.4%; les 101; Conservative
 Ξ
 (first entry)
 Query Match
Best Local Similarity 94.4
Matches 101; Conservative
 뎚
 Singh S, Foster C,
 WPI; 2004-604433/58
 (TANO-) TANOX INC
 Sequence 107 AA;
 Sequence 107 AA;
 WO2004070011-A2
 Homo sapiens
 19-AUG-2004.
 04-NOV-2004
 н
 61
 Query Match
 ADR43402;
 RESULT 1.
ADR43402
 g
 ð
 8 x 3 3 3
 g
 ò
 ò
```

```
ö
 The invention relates to a method for generating a humanised high affinity antibody from an antibody of interest. The method involves selecting a suitable human template as the framework for the H (heavy) and L (light) chain variable (V) domains of the high affinity antibody to be made. The method is useful for generating high affinity antibodies useful in diagnostics, prophylaxis and treatment of diseases. The present sequence is Li6/JK4 human light chain consensus sequence template. This sequence is used in the exemplification of the invention.
 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
 Generating a humanized, high affinity antibody from an antibody of interest comprises selecting a suitable human template as the framework for the H and L chain variable domains of the high affinity antibody to
 1 EIVWTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 ,
0
 RESGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVBIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIK 107
 Length 107;
 'Match 94.8%; Score 527; DB 8; Length 10
Local Similarity 94.4%; Pred. No. 4.5e-32;
les 101; Conservative 3; Mismatches 3; Indels
61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK
 L16/JK4 human light chain consensus sequence template.
 Antibody; diagnostic; prophylaxis; therapy; human
 Example 1; SEQ ID NO 2; 100pp; English.
 Location/Qualifiers
 ż
 "Kabat CDR"
 "Kabat CDR"
 /note= "Kabat CDR"
 ADR31547 standard; protein; 107
```

Job time : 62.3676 secs

THE PLANT DEPTO

```
Query Match
 g kappa chain v r y kappa chain v r kappa chain v l kappa chain v l kappa chain v l kappa chain v r kappa chain v r kappa chain v r kappa chain prekapa chain prekapa chain preappa chain preappa chain v l ppa chain v r a chain v r a chain v r
 November 16, 2005, 21:37:48; Search time 12.7849 Seconds (without alignments) 805.260 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 EIVMTQSPATLSVSPGERAT......CQQYNNWPRIFGQGTKVEIK 107
 Description
 version 5.1.6
- 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 283416 segs, 96216763 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 840343
8240343
8240328
826525
826522
8203424
834001
834001
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
83601
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 S34005
S40362
 GenCore
Copyright (c) 1993
 US-10-660-357A-34
556
 seq length: 0 seq length: 2000000000
 %
Query
Match Length DB
 PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 Perfect score:
 Scoring table:
 473
466.5
466.5
464.5
464
464
464
463.5
 462
461.5
460.5
460.5
459.5
459
459
 Score
 535
527
524
504.5
486.5
486.5
481.5
475
 Minimum DB Maximum DB
 Database :
 Searched:
 Sequence:
 Run on:
 Result
No.
```

| S20635                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Kappa chain V region - human Species: How sapiens (man) Species: How sapiens (man) Species: How sapiens (man) Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 Accession: S14005; S10524 Mariette, X.; Tsapis, A.; Brouet, J.C. r. J. Immunol. 23, 846-881, 1993 Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal Reference number: S14001; MUID: 93209281; PMID: 7681398 Accession: S14005 Status: preliminary Molecule type: mRNA Residues: 1-107 < MAR> Cross-references: EMBL: Z18330 Superfamily: immunoglobulin v region; immunoglobulin homology Keywords: heterotetramer; immunoglobulin 16-90/Domain: immunoglobulin homology < INM>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 96.2%; Score 535; DB 2; Length 107; imilarity 95.3%; Pred. No. 3.3e-39; Conservative 3; Mismatches 2; Indels 0; Gaps 0; EIVWIQSPAILSVSPGERAILSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | RESULT 2 840362 Ig kappa chain - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: 840362 R;Klein, R.; Jaenichen, R.; Zachau, H.G. R;Klein, R.; Jaenichen, R.; Zachau, H.G. Bur. J. Immunol. 23, 3246-3271, 1995 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: 840312; MUID:94080891; PMID:8258341 A;Accession: 840362 A;Status: preliminary; translation not shown A;Accession: BMBL:X72472; NID:9444412; PID:9441413 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;26-100/Domain: immunoglobulin homology <imm></imm>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | n<br>revision<br>ouet, J.C<br>1993<br>analysis<br>ID:932092<br>v region;<br>v v region;<br>homology                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SRATLS STATLS STATLS SLOSEI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | revis: chau, 1993 0,1994 ID:940 ID:94                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | human<br>an)<br>nce_r<br>4 4<br>i Bro<br>51, 1<br>51, 1<br>i MUI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 96.2%<br>195.3%<br>196.3%<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100.00<br>100 | Zac                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000<br>100                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | on - hu<br>18 (mar<br>19 (2004)<br>19 (                                                                                                                                                                                                                                                                                                                            | 11arity 95.3%; Pr<br>Conservative 3;<br>VMTQSPATLSVSPGERATLS<br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | is (mar<br>sequenc<br>1, R.;<br>1248-32<br>1248-32<br>10312;<br>125<br>135<br>136<br>136<br>136<br>136<br>137<br>138<br>138<br>138<br>138<br>138<br>138<br>138<br>138<br>138<br>138                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | region<br>napiens<br>993 #sec<br>993 #sec<br>995; S3<br>805; S3<br>915; S34<br>915; S34<br>915; S34<br>918; EMBRA<br>MRNA<br>MRNA<br>MRNA<br>MRNA<br>MRNA<br>MRNA<br>MRNA<br>MR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | rit<br>nse<br>OSF<br>GSG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | mar.<br>ien<br>her<br>hur<br>NA<br>KLE<br>EN<br>EN<br>EN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 800000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | V reg o sapp - 1993 34005; TGa; TGa; TGa; 34005; Juina e: mR e: mR 1100; Juina immer: jumu: terot: immu: immu:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ch<br>102; Conser<br>1 ElWTOSPA<br>1 ElWTOSPA<br>1 ELWTOSPA<br>61 RFSGSGGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | - hu<br>-1994<br>-1994<br>40362<br>aenic<br>1. 23<br>8886<br>mber:<br>40362<br>imina<br>e: mina<br>e: nces:<br>immu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 4458.5<br>444458.5<br>44557.5<br>44557.5<br>44557.5<br>4457.5<br>4457.5<br>4457.5<br>4447.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448.5<br>4448 | chain: Home Specific Home Spec                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Mar<br>Mar<br>Mar<br>Mar<br>Muno<br>pre-<br>pre-<br>rel<br>1-<br>typ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | pa cha<br>ies: P<br>: 02-r<br>stsion:<br>estsion:<br>estsion:<br>es: Nuc<br>rence<br>es: Nuc<br>rence<br>ssion:<br>us: jon:<br>us: jon:<br>us | Mat                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | pa chi<br>ies: 1<br>: 06-h<br>ssion: N. R. n. n. R. n. r. n. r. n. r. n. r. n.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | RESULT 1 S14005 19 kappa chain V region - human C;Species: Homo sapiens (man) C;Date: 02-Dec-1933 #sequence revision C;Accession: S34005; S30524 R;Mariette, X.; Trapis, A.; Brouet, J Eur. J. Immunol. 23, 846-851, 1993 A;Title: Nucleotidic sequence analysis A;Accession: S34005 A;Accession: S34005 A;Accession: S34005 A;Essidues: 1-107 *MARA A;Residues: 1-107 *MARA A;Cross-references: EWBL:Z18330 C;Superfamily: immunoglobulin V region C;Keywords: heterotetramer; immunoglof F;16-90/Domain: immunoglobulin homolog                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Query M<br>Best Lo<br>Matches<br>Qy<br>Db<br>Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | RESULT<br>1g kap<br>1g kap<br>1g kap<br>C'Spec<br>C'Acte<br>C'Acte<br>R'Klei<br>Bur<br>A'Tti<br>J A'Tti<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>C'Super<br>C'Super<br>C'Super<br>C'Super<br>C'Super<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>C'Super<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster<br>A'Ster |

Length 117;

DB 2;

94.8%; Score 527;

g ò g

```
ij
 ä
 1 EIVWITOSPATLSVSPGERATLSCRASOSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 9
 79
 59
 1 EIVMTQSPVTLSVSPGERATLSCRASQSISNSYLAWYQQKPSGSPRLLIYGASTRATGIP 60
 C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
 C.Species: Homo sapiens (man)
C.Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 20 EVVMTQSPATLSVSPGERATISCRASQSVIHNLAWYQQKPGQAPRILIYGAYTRATGVPA
 EIVWTOSPATLSVSPGERATLSCRASOSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 A;Cross-references: EMBL:X72438; NID:g441344; PIDN:CAA51106.1; PID:g441345 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;35-109/Domain: immunoglobulin homology <IMM>
 C;Accession: S40328
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
 Gapa
 Gaps
 C;Accession: B26555
R;Middaugh, C.R.; Litman, G.W.
J:Biol. CAPPAICAL 3671-3673, 1987
A;Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A;Reference number: A92630; MUID:87137666; PMID:3102493
A;Accession: B26555
A;Molecule type: protein
A;Residues: 1-116 <MID>
 1;
 1,
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPR-TFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPR-TFGQGTKVEIK 107
 80 RFSGSGSGTEFTLTISGLQSEDLATYYCQQYNDWPPWTFGQGTKVEIK 127
 60 ARFSGSGSGTEFTLTISSLOSEDFAVYYCOOYNNWPRIFGOGTKVEIK 107
 61 ARFSGSGSGTEFTLTISSLQSEDFAVYCQQYNNWPPTFGGGTRVEIK 108
 Length 131;
 Length 116;
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin P;16-90/Domain: immunoglobulin homology <IMM>
 Indels
 Indels
 Score 490.5; DB 2;
Pred. No. 2.6e-35;
6; Mismatches 7;
 DB 2;
 Score 486.5; DB 2
Pred. No. 5.1e-35;
 7; Mismatches
 A, Accession: S40328
A, Status: preliminary; translation not shown
 Ig kappa chain V-III region (Ger) - human
 87.5%;
88.0%;
 88.28;
 87.0%;
 Local Similarity 88.0
les 95; Conservative
 Best Local Similarity 87.0
Matches 94; Conservative
 A; Residues: 1-131 < KLE>
 Ig kappa chain - human
 A; Molecule type: mRNA
 Query Match
 Query Match
 Best Loc
Matches
 RESULT 6
 RESULT
 셤
 à
 g
 8
 ò
 ద
 g
 Š
 d
 ð
 Ig Kappa chain V-III region (Pom) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01897
R;Klapper, D.G.; Capra, J.D.
R;Klapper, D.G.; Capra, J.D.
R,Klapper, D.G.; Capra, J.D.
A;Rifapper, D.G.; Capra, J.D.
A;Reference number: A01897
A;Accession: A01897
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer F;16-91/Domain: immunoglobulin homology <IMM>
 A;Cross-references: UNIPROT:P01624
C;Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
 ä
 ö
 o;
 9
 80
 9
 11 EIVMTÓSPATLSVSPGERATLSCRASÓSVSSNLAWYÓGKÞGÓAPRLLIYGASTRATGIPA 70
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 21 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPTVLIYGASTRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 Gaps
 Gaps
 1;
 ;
0
 ;
0
 DB 1; Length 109;
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPYTFGQGTKLEIK 127
 71 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPLTFGGGTKVEIK 117
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Length 128;
 Indels
 3; Indels
 Indels
 ch 90.7%; Score 504.5; DB 1;
1 Similarity 90.7%; Pred. No. 1.4e-36;
98; Conservative 5; Mismatches 4;
 Pred. No. 1.7e-38;
3; Mismatches 3;
 93.9%; Score 522; DB 2;
92.5%; Pred. No. 5.1e-38;
iive 5; Mismatches 3;
 F;16-91/Domain: immunoglobulin homology <IMM>F;23-89/Disulfide bonds: #status predicted
 94.48;
 A,Gene: GDB:IGKV3
A,Cross-references: GDB:136266
A,Map position: 2p12-2p11
il Similarity 94.4
101; Conservative
 Local Similarity 92.5
nes 99; Conservative
 A; Molecule type: protein A; Residues: 1-109 < KLA>
 Query Match
Best Local S
Matches 98
 61
Best Local &
Matches 101
 Query Match
 C, Genetics:
 RESULT 4
```

g ઠે 요

ò

```
C; Accession: A30553
 Query Match
 RESULT 10
 RESULT 11
 셤
 ઠે
 d
 셤
 ò
 g
A56701

Ig kappa chain V region precursor (HuA) - human (fragment)

C;Species Humo sapiens (man)

C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000

C;Accession: A56701

R;Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.

J. Biol. Chem. 270, 12457-12465, 1995

A;Title: Human and mouse monoclonal antibodies to blood group A substance, which are neathernorm number: A56701; MUID:95279371; PMID:7759488
 RjAlim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Tabbaited to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy A;Reference number: JE0243
 RESULT 8
523628
19 Aspa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: 823628
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
J. Exp. Med. 175, 831-842, 1992
A;Fitle: analysis of self-associating immunoglobulin G rheumatoid factors from the A;Reference number: 823623; MUID:92156804; PMID:1740665
 ö
 ô
 9
 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80
 9
 Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 A;Cross-references: EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID:g1335190 C.S. Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology MM>
 Gaps
 Gaps
 A;Cross-references: GB:L41174; NID:g762823; FIDN:AAA64877.1; PID:g762824 (S.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;36-110/Domain: immunoglobulin homology <IMM>
 ö
 ö
 81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPRSFGQGTKVBIK 127
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Score 486; DB 2; Length 128;
Pred. No. 6.1e-35;
9; Mismatches 6; Indels
 Length 111;
 Score 482; DB 2; Length LL. Pred. No. 1.2e-34;
 9; Mismatches
 8; Mismatches
 86.0%;
 86.7%;
86.0%;
 Query Match
Best Local Similarity 86.0
Marches 92, Conservative
 Best Local Similarity 86.0
Matches 92; Conservative
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <NIC>
 A; Molecule type: DNA
A; Residues: 1-111 <OLE>
 A;Status: preliminary
 Accession: JE0244
 A; Accession: A56701
 Query Match
 RESULT 9
 a
 ઠે
 ò
 a
 셤
 ò
 유
```

```
C;Accession: A01898
R;Jirik, F.R.; Sorge, J.; Fong, S.; Heitzmann, J.G.; Curd, J.G.; Chen, P.P.; Goldfien, R Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A;Title: Cloning and sequence determination of a human rheumatoid factor light-chain gene A;Reference number: A01898; MUID:86177570; PMID:3083417
 Cicomplex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lan CiSuperfamily: immunoglobulin V region; immunoglobulin homology CiReywords: autoantibody, chronic lymphocytic leukemia; heterotetramer; immunoglobulin F;1-20/Domain: signal sequence #status predicted <SIG> F;21-115/Product: rheumatoid factor, Ig kappa chain V-III region (CLL) #status predicted F;21-43/Region: framework 1
 ö
 9
 9
 9
 80
 N;Alternate names: rheumatoid factor
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
 21 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQPPRLLIYGASTRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 EVVLTQSPATLSVSPGERATLSCRASQSVHSNLAWYQQKPGQAPRLLIYRASTRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 ö
 1,
 61 RFSGSGSGTDFILTISSLQSEDFALYYCQQYNTWPPLTFGGGTKVBIK 108
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNW-PRTFGQGTKVEIK 107
 Length 215;
 Length 115;
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-212 <ALL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
 Indels
 Indels
 A;Molecule type: DNA
A;Residues: 1-115 <JTR>
A;Note: the sequence was determined from the germline gene
C;Genetics:
 Score 475; DB 1; Le
Pred. No. 4.9e-34;
2; Mismatches 3;
 Query Match 86.6%; Score 481.5; DB 2; Best Local Similarity 86.1%; Pred. No. 2.4e-34; Matches 93; Conservative 7; Mismatches 7;
 RFSGSGGTEFTLTISRLQSEDFAVYYCQQYNNWP 115
 61 RESGSGGTEFILTISSLOSEDFAVYYCOOXNNWP 95
 region (CLL) - human
 F;77-108/Region: framework 3
F;109-115/Region: complementarity-determining 3
F;43-108/Disulfide bonds: #status predicted
 70-76/Region: complementarity-determining 2
 F;36-110/Domain: immunoglobulin homology <IM
F;44-54/Region: complementarity-determining
F;55-69/Region: framework 2
 Query Match
Best Local Similarity 94.7%;
Matches 90; Conservative
 Ig kappa chain precursor V-III
 GDB:136266
 A,Gene: GDB:IGKV3
A,Cross-references: GDB:1:
A,Map position: 2p12-2p11
A;Introns: 17/1
```

à d ò 셤

```
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantl A;Reference number: A30601; MUID:89215279; PMID:2496160
 C;Accession: PL0022
R;Kipps, T.J; Tomhave, B.; Chen, P.P.; Carson, D.A.
N. Exp. Med. 167, 840-852, 1988
A;Title: Autoantibody-associated kappa light chain variable region gene expressed in chrons. A;Reference number: PL0021; MUID:88171307; PMID:3127527
 A,Cross-references: UNIPROT:P18135
C,Comment: The protein is one of the surface immunoglobulin M autoantibodies expressed ir
 A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp for a fisulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lan C;Superfamily: immunoglobulin V region; immunoglobulin homology
 ô
 ij
 29
 9
 C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: D30601
 C.Species: Homo sapiens (man)
C.Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
 1 BIVWTOSPATLSVSPGERATLSCRASOSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 21 BIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQRPGQAPRLLIYDASNRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP
 1; Gaps
 ö
 60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Length 109;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQOYNNWPRTFGQGTKVEIK 107
 81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPLTFGGGTKVEIK 127
 Length 144;
 A;Cross-references: UNIPROT:09UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;IG-91/Domain: immunoglobulin homology <IMM>
 Indels
 8; Indels
 DB 2;
 9
 Score 473; DB 2;
Pred. No. 8.9e-34;
 Ig kappa chain V-III region (Cur) - human (fragment)
 Ig kappa chain precursor V-III region (Hah) - human
 ch 84.1%; Score 467.5; DB 11 Similarity 83.3%; Pred. No. 2e-33; 90; Conservative 11; Mismatches
 Query Match 85.1%; Score 473; DE Best Local Similarity 84.1%; Pred. No. 8.9e Matches 90; Conservative 9; Mismatches
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining F;116-127/Domain: J region <JRG>
F;128-144/Domain: C region (fragment) <JRG>
 A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
 Query Match
Best Local Similarity
 A;Accession: PL0022
A;Molecule type: mRNA
A;Residues: 1-129 <KIP>
 A; Accession: D30601
 A; Gene: GDB: IGKV3
 C, Genetics:
 RESULT 15
K3HUHA
 g
 ò
 ò
 유
 ઠે
 g
 A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy A; Reference number: JE0243
A; Accession: JE0243
 RESULT 13
PLO106
PLO106
PLO106
PLO106
PLO106
PLO106
PLO106
PLO106
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Ao-Unn-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PLO106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma secx
A;Reference number: PLO106; MUID:89235583; PMID:2541221
 J. Immunol. 142, 688-694, 1989
A,Title: Characterization of four homologous L chain variable region genes that are rela A,Reference number: A30553; MUID:89093959; PMID:2492051
A,Accession: A30553
 R;Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson,
 ö
 ô
 9
 9
 21 EIVWMQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 80
 RESULT 12
JE0243
Lig kappa chain NIG93 precursor - human
CiSpecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Spacies: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 EIVMTQSPATLSVSPGERATLSCRASQSVATNVVWYMQKLGQAPRLLIYDASTRATGVPA
 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 EI VMTQSPATLSVSPGERATLSCRASQS I SNNFAWYQQKPGQAPRLLI FGASTRATGI PA
 Gaps
 Gaps
 ö
 .
0
 RFSGSGGTEFTLTISSLOSEDFAIYYCQHNNAWPPTFGQGTKVETK 107
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 A;Residues: 1-115 <110>
A;Residues: 1-115 <110>
A;Note: the sequence was determined from the differentiated gene (S. Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <1MM>
 Query Match 85.3%; Score 474; DB 2; Length 215; Best Local Similarity 85.0%; Pred. No. 1e-33; Matches 91; Conservative 5; Mismatches 11; Indels
 Length 115;
 A Accession: PL0106
A, Molecule type: mRNA
A, Medicule type: mRNA
A, Residues: 1-144 < SILD
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heteroctetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VRE>
 A;Molecule type: protein
A;Residudes: 1-215 <ALI:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
 3; Indels
 81 RFSGSGSGTEFTLTISRLOSEDFAVYYCOOYNNWP 115
 Score 474; DB 2;
Pred. No. 5.9e-34;
2; Mismatches 3;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 95
 F;36-110/Domain: immunoglobulin homology <IMM>
 Query Match
Best Local Similarity 94.7%;
Matches 90; Conservative
 A;Status: preliminary A;Molecule type: DNA
```

ద

g ò

```
C; Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin F:1-20/Domain: signal sequence #status predicted <SIG> F:1-129/Product: Ig kappa chain V-III region (Hah) #status predicted <WAT> F:21-117/Region: V segment F:31-111/Domain: immunoglobulin homology <IMM> F:34-111/Domain: immunoglobulin homology <IMM> F:34-55/Region: complementarity-determining 1 F:71-77/Region: complementarity-determining 2 F:110-117/Region: complementarity-determining 3 F:110-117/Region: Josephanentarity-determining 3 F:110-117/Region: Segment (JKI) F:43-109/Disulfide bonds: #status predicted
 Gaps
 1;
 Query Match
Best Local Similarity 83.3%; Pred. No. 2.9e-33;
Matches 90; Conservative 10; Mismatches 7; Indels 1.
 Search completed: November 16, 2005, 22:04:10 Job time: 13.7849 secs
 g
 ò
 q
 ઠે
```

ų.

1100 1000 00000

```
43
129
129 AA;
711.2
701.0
700.0
700.7
700.7
700.7
700.7
700.0
699.6
699.2
 NCBI_TaxID=9606;
 21
21
21
21
70
70
 20-MAR-1987 (
01-NOV-1990 (
15-JUL-1999 (
 KV3H HUMAN
ID KV3H HUMAN
DOMAIN
DISULFID
NON_TER
 NON TER
SEQUENCE
 Query Match
 SIGNAL
CHAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
 RESULT 1
 homo sapien
homo sapien
homo sapien
homo sapien
 sapien
sapien
sapien
 sapien
sapien
 sapien
sapien
 homo sapien
homo sapien
 sapien
 sapien
 sapien
 sapien
 sapien
 sapien
 sapien
 sapien
 sapien
 sapien
 homo sapien
 ; Search time 59.9908 Seconds (without alignments) 913.348 Million cell updates/sec
 Pred. No. is the number of cresults predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 EIVMTQSPATLSVSPGERAT......CQQYNNWPRTFGQGTKVEIK 107
 рошо
 homo
 homo
 homo
homo
 homo
 homo
 homo
 homo
 homo
 homo
 homo
 homo
 homo
 Description
 P01610 |
Q6pih7 |
Q6pit5 |
 Q9u183
Q9u185
Q6gmw0
P18135
 P01620
P01622
P01623
P01623
P01623
P01619
P04206
P01619
P06433
P06433
P06433
P06433
P06433
P06433
P06433
 Q9ul79
P06314
P04434
Q9ul70
 Q6gmw1
P01625
P01621
 1612378
 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1612378 segs, 512079187 residues
 SUMMARIES
 KV3M_HUMAN
Q9UL78
 Q6GMV9
KV3I HUMAN
KV3K HUMAN
 Q6PILB
KV1M HUMAN
Q9ULB6
 Q6P5S8
Q9UL79
KV4C_HUMAN
KV3J_HUMAN
Q9UL70
Q6GMW1
KV3A_HUMAN
KV3C_HUMAN
KV3C_HUMAN
 2005, 21:36:13
 QGGMWO
KV3L HUMAN
KV3B HUMAN
 KV3G HUMAN
KV3A HUMAN
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 KV3H HUMAN
KV3F HUMAN
 sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Q9ULB3
Q9ULB5
 Q6PIĤ7
Q6PITS
 UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
 - protein search, using
 seq length: 0
seq length: 200000000
 US-10-660-357A-34
556
 Query
Match Length DB
 November 16,
 1109
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
11110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
1110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
110
 Copyright
 77.4
 77.0
 76.0
 71.9
 71.6
71.6
71.6
 ii ii
 Perfect score:
Sequence:
 Scoring table:
 504
498.5
 422.5
 415
411
409.5
400
 398.5
398.5
398
398
 Score
 429
 Minimum DB Maximum DB M
 OM protein
 Searched:
 Database
 Run on:
 Result
 8
8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@ib.ch).
 mus musculu
homo sapien
homo sapien
homo sapien
 sapien
sapien
sapien
sapien
sapien
sapien
 sapien
sapien
 SEQUENCE FROM N.A.
MEDLINE=8617570; PubMed=3083417;
MINITIAE=8617570; PubMed=3083417;
Goldfien R., Carson D.A.;
"Cloning and sequence determination of a human rheumatoid factor light-chain gene."; O.S.A. 83:2195-2199(1986).
 homo
homo
homo
homo
homo
homo
homo
 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
 01-NOV-1990 (Rel. 16, Last sequence update)
15-VUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
Homo sapians (Human).
 O69mx8
O652c9
O6kb05
P01609
P80362
 DB 1; Length 129;
 Q723y4
Q65zc8
P01604
 P01598
P04430
 Ig kappa chain V-III region CLL
 Framework-1.
Complementarity-determining-1.
 Complementarity-determining-2.
 Complementarity-determining-3. JK1 segment.
 14275 MW; 5C13B411BE60CC14 CRC64;
 129 AA
 JK1 segment.
By similarity.
 Score 515.5;
 ALIGNMENTS
 Framework-3.
 Framework-2.
072473
KVIG HUMAN
KV1F—HUMAN
KV1V—HUMAN
QV23<u>Y</u>4
Q652CB
Q66XCB
Q66XCB
Q66XCB
Q66XCB
 KV1Q HUMAN
KV1Y HUMAN
KV1H HUMAN
 HSSP; P01625; 1LVE.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG_v.
 PRT;
 Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
 (Rel. 04, Created)
 Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
 EMBL; M12740; AAA58992.1; -.
 92.7%;
 STANDARD;
11088
11088
11088
11088
11088
11088
11088
11088
 20
129
43
43
54
69
69
108
118
118
129
```

셤 ò 엄

```
1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60
 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 ö
 ä
 SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Length 109;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYXCQQYNNWPRTFGQGTKVEIK 107
 Length 108;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
 'Match 90.6%; Score 504; DB 2; Length 10 Local Similarity 90.7%; Pred. No. 8.8e-47; Local Si, Conservative 4; Mismatches 6; Indels
 Indels
 109 109
109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;
 / Match 89.7%; Score 498.5; DB 2; Local Similarity 90.7%; Pred. No. 3.5e-46; hes 98; Conservative 5; Mismatches 4;
 Ciin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035031; AAD56267.1; -.
PIR; B30609; B30609.
PIR; C30609; C30609.
PIR; S34099; S34099.
HSSP; P01625; ILVE.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
 109 AA
 PRT;
 EMBL, AF015029, AAD56265.1; -. PIR, D30609, D30609. HSSP, P01625, 1EK3. InterPro; IPR007110; Ig-like. InterPro; IPR001596; Ig-v. SMART; SM0406; IGV; 1. PR05ITE; PS50815; IG_LIKE; 1.
 PROSITE; PS50835; IG_LIKE; 1.
 PRELIMINARY;
 108
NCBI_TaxID=9606;
 Q9UL85;
01-MAY-2000 (
01-MAY-2000 (
 Young D.C.;
 NON TER
NON TER
SEQUENCE
 NON TER
NON TER
SEQUENCE
 Query Match
 Query Match
 fetus."
 09UL85
 Best Loca
Matches
 RESULT 4
Q9UL85
 d
 ð
 g
 M. Klapper D.G., Capra J.D.;

"The amino acid sequence of the variable regions of the light chains of from two idiotypically cross reactive IgM anti-gamma globulins.";

"The amino acid sequence of the variable regions of the light chains diotypically cross reactive IgM anti-gamma globulins.";

"In mumunol. (Paris) 127C:361-271 (1976).

"In MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma globulin activity.

"The PIR, A01897; K3HUPM.

"RSP; PO1625; 1LVE.

"GO; GO:0005576; C:extracellular; NAS.

"GO; GO:0005576; F:antigen binding; NAS.

"GO; GO:0006955; F:immune response; NAS.

"InterPro; IPR00310; Ig-1ike.

"InterPro; IPR00310; Ig-V.
 ä
 1 EIVMTÖSPVTLSVSPGERATLSCRASOSISNSYLAMYQÖKPSGSPRLLIYGASTRATGIP 60
 9
 21 EIVWTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQXPQCPPRLLIYGASTRATGIPA 80
 1 EIVMTOSPATLSVSPGERATLSCRASOSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP 59
 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1; Gaps
 Gaps
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Homo Bapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 1;
 Ouery Match 90.7%; Score 504.5; DB 1; Length 109; Best Local Similarity 90.7%; Pred. No. 7.9e-47; Matches 98; Conservative 5; Mismatches 4; Indels 1;
 60 ARFSGSGSGTEFTLTISSLOSEDFAVYZCQOYNNWPRTFGQGTKVEIK 107
 61 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPTFGQCTRVEIK 108
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPR-TFGQGTKVEIK 107
 81 RFSGSGSGTEFTLTISRLQSEDFAVYYCQQYNNWPPWTFGQGTRVEIK 128
 4; Indels
 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;
 PEAM; PF0047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DISULED 23 89
NON_TER 109 109
 Pred. No. 6.1e-48;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
22-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-III region POM.
 3; Mismatches
 108 AA
 109 AA
 PRT;
 PRT;
 SEQUENCE
MEDLINE=76276460; Pubmed=60899;
 92.6%;
 Matches 100; Conservative
 PRELIMINARY;
 STANDARD;
 Best Local Similarity
 NCBI_TaxID=9606;
 KV3F HUMAN
P01624;
 (Fragment).
 61
 SEQUENCE
 Q9UL83
Q9UL83;
 KV3F HUMAN

ID KV3F HUMAN

YC 21-JUL

DT 21-JUL

DE IG ADID

OS HOMO BIO

OC MAMMAI

OX NCBL

RN KLAPPE

RA MAN

DR GO; GC

RA KLAPPE

RA MAN

RA RASSP;

RA MAN

RA SNART;

DR
 RESULT 3
29UL83
1D 09UL
AC 09UL
DT 01-M
DT 01-
```

ò ద ò g ij

Gaps

ö

Gaps

```
RFSGSGSGTEFTLTISSLQSEDFAVYXCQQYNNW-PRTFGQGTKVBIK
 (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 44, Last annotation update)
 HSSP, POIGES, IEEQ.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Ffam; PR0047; ig_1 1.
FRANT; SW00406; IGy; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
 Framework-1.
 Framework-3.
 Framework-2.
 MEDLINE=88171307; Pubmed=3127527;
 83.98;
 83.3%;
 90; Conservative
 STANDARD;
 STANDARD;
 43
55
70
77
77
1109
1129
1109
 leukemia.
PIR; PL0022; K3HUHA.
 129 1
129 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 21-JUL-1986
21-JUL-1986
05-JUL-2004
 KV3B HUMAN
P01620;
 KV3L_HUMAN
 NON TER
SEQUENCE
 61
 DISULFID
 Query Match
 DOMAIN
 DOMAIN
 KV3B HUMAN
ID KV3B HC
AC P01620;
DT 21-JUL-
DT 21-JUL-
DT 05-JUL-
 SIGNAL
 DOMAIN
 DOMAIN
 Matches
 RESULT 7
 셤
 ò
 ò
 셤
 ð
 g
 **X. Table State Continue F.S., Wagner L.H., Derge J.G., Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., A Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Brichards S., Worley K.C., Hals, S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Hilling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Green E.D., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.
EIVWTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 21 EIVMTQSPATLSVSPGERATLSCRASQSISNNLAWYQQRPGQAPRLLIYGASSRVTGIPG 80
 Gaps
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ;
 Score 488.5; DB 2; Length 235;
Pred. No. 1.1e-44;
7; Mismatches 5; Indels 1;
 61 RFSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLJFGGGTKVEIK 108
 RFSGSGSGTEFTLIISSLQSEDFAVYYCQQYNNW-PRIFGQGTKVEIK 107
 A Strausberger R.;
L Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL; BGO73792; AAH73792.1; -.
R InterPro; IPR003599; Ig-like.
R InterPro; IPR003599; Ig-like.
R InterPro; IPR003599; Ig-like.
R InterPro; IPR003596; Ig-like.
R InterPro; IPR003596; Ig-like.
R InterPro; IPR003596; Ig-like.
R InterPro; IPR003596; Ig-like.
R Ffam; PF07654; CI-set; I.
R SMART; SM00409; IG-2; I.
R SMART; SM00409; I.
R SMART; SM0
 ll protein.
235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;
 Last sequence update)
Last annotation update)
 Sci. U.S.A. 99:16899-16903 (2002)
 Created)
 PRT;
 87.9%;
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 95; Conservative
 PRELIMINARY;
 Hypothetical protein.
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Proc. Natl. Acad.
 NCBI_TaxID=9606;
 _
 19
 SEQUENCE
 Query Match
 Q6GMW0
 Matches
 g
 ઢ
 ò
 8
```

```
80
 23
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP
 21 EIVLTÓSÞGTLSLSÞGERATLSCRASÓSVSSSYLAWYQQKÞGQAPRLLIYGASSRATGIÞ
 1; Gaps
 Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for retiology and immunotherapy.";
J. Exp. Med. 167:840-852 (1988).
-!- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
81 RFSGSGSGTEFTLSISSLQSEDFAVYFCQQYNDWLLYTFGQGTKLEIK 128
 81 DRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGTSPRTFGQGTKVBIK 128
 DB 1; Length 129;
 60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Ig kappa chain V-III region HAH
 Complementarity-determining-1.
 Complementarity-determining-2.
 Complementarity-determining-3.
 Indels
 14073 MW; D3C55292772774D0 CRC64;
 Score 466.5; DB 1;
Pred. No. 1.3e-42;
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RAppa chain V-III region HAH precursor.
Homo sapiens (Human)
 Ş
 Ź
 By similarity.
 10; Mismatches
```

ä

```
Query Match
Best Local Similarity 81.5%
Matches 88; Conservative
 Local Similarity 82.4
hes 89; Conservative
 STANDARD;
 NCBI_TaxID=9606;
 HUMAN
 DISULFID
NON TER
SEQUENCE
 NON TER
SEQUENCE
 Query Match
 SEQUENCE
 group."
 Best Loca
Matches
 KV3E_HUMAN
 RESULT 10
 SO DE RELEVANTE DE LA DESTRETA LA PRESENTA DE LA PRESENTA LA PRESE
 g
 ð
 SETTER
 8
 8
 MEDLINE=72188439; PubMed=5027703;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
Hoppe-Seylar's Z. Physiol. Chem. 33:189-208 (1972).
HISCELLANEOUS: This is a Bence-Jones protein.
PRS, PO1625; This is a Bence-Jones protein.
PRSP, PO1625; Cextracellular; NAS.
Co; GO:0005576; Cextracellular; NAS.
Co; GO:0005576; P:immune response; NAS.
RO; GO:0006955; P:immune response; NAS.
RICEPTO; IFR007110; Ig-like.
RICEPTO; IFR007110; Ig-like.
 Typoup. Typoup
 29
 9
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP
 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSYLAWYQQKPGQAPRLLIYGASSRATGIP
 MEDIINE-82046598; PubMed-6794615;
Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from two idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 1;
 61 DRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGSSPQTFGQGSKVEIK 108
 83.0%; Score 461.5; DB 1; Length 109; 81.5%; Pred. No. 3.6e-42;
 60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 6; Indels
 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
18 Appa chain V-III region Ti.
 109 AA
 81.5%; Pred. .v..
 PRT;
Ig kappa chain V-III region SIE Homo sapiens (Human).
 88; Conservative
 STANDARD;
 Local Similarity
 KV3D_HUMAN
P01622;
 SEQUENCE
 SEQUENCE
 Query Match
 SEQUENCE
 NON TER
 | MARCO | MARC
 Matches
 g
 ò
 ò
 g
```

```
1 EIVMTQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP 59
 29
 9
 Biochemistry 20:5816-5822(1981).
-!- MISCELLANGOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
PIR; A01896; K3HUWL.
 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSFLAWYQQKPGQAPRLLIYVASSRATGIP
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP
 Gaps
 Gaps
 the
 chains from
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 1;
 Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains fri
idiotypically cross-reactive human IgM anti-gamma-globulins of
 1;
 60 ARFSGSGSGTEFILIISSLQSEDFAVYCQQYNNWPRTFGQGTKVEIK 107
 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGRTFGQGTKVEIK 108
 82.5%; Score 458.5; DB 1; Length 109; 82.4%; Pred. No. 7.7e-42; tive 10; Mismatches 8; Indels 1
 Length 109;
 81.7%; Score 454.5; DB 1; Leugum.
81.5%; Pred. No. 2.1e-41;
 HSPS; POLGES; ALDUM.
HSPS; POLGES; ALDUM.
HSPS; POLGES; ALDUM.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; F:antigen binding; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Fam; PF00047; Ig' 1.
SMART; SM00406; IGv; 1.
PROSTIE; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
DiSULPID
 109 AA; 11746 MW; 566C115E6B9CBEEE CRC64;
 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
By similarity.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
15 kappa chain V-III region WoL.
Homo sapiens (Human).
 109
 MEDLINE=82046598; PubMed=6794615;
```

S

```
Homo sapiens (Human).
 PIR; PH0965; PH0965.
PIR; S33988; S33988.
PIR; S34096; S34096.
 A30608.
B30601.
B30607.
 PIR; A30601; A30601
 D30608
 F30607
 F30608
 H30608
 PH0964
 130601
 SEQUENCE FROM N.A.
 A30608;
 PIR; H44151;
PIR; I30601;
 PH0964;
 HSSP; P01625;
 C30601;
 H30608;
 PH0963;
 D30601;
 D30607;
 F30608;
 C30608;
 D30608;
 G30608;
 SEQUENCE
 61
 SEQUENCE
 Young
 KV3G HUMAN
 PIR;
PIR;
PIR;
PIR;
 PIR; 1
PIR; 1
 PIR;
 PIR;
 PIR;
PIR;
PIR;
 PIR;
 PIR;
 RESULT 12
 ਨੇ
 셤
 ò
 셤
 1 EIVMTOSPATLSVSPGERATLSCRASOSISNNF-AWYQOKPGOAPRLLIFGASTRATGIP 59
 21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80
 Gaps
 MEDLINE=88171307; PubMed=3127527;

MEDLINE=8871307; PubMed=3127527;

Mippe T.J., Tomhave E., Chen P.P., Carson D.A.;

Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";

J. Exp. Med. 167:840-852(1988).

-!- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic
 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1,
 / Match 81.6%; Score 453.5; DB 1; Length 129; Local Similarity 81.5%; Pred. No. 3.3e-41; nes 88; Conservative 11; Mismatches 8; Indels 1
 60 ARFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Ig kappa chain V-III region HIC.
 Complementarity-determining-2. Framework-3.
 Complementarity-determining-1.
 Complementarity-determining-3.
 7395528EA2BB74D6 CRC64;
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
RADPA chain V-III region HIC precursor.
Homo sapiens (Human)
 129 AA.
 109 AA
 By similarity.
 Framework-2
 PIR; PLO021; K3HUHI.
HSSP; P01625; IEBQ.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR005596; Ig_v.
 Pfam, PF00047; ig; 1.
SMARY; SM00406; IGy; 1.
PROSITE; PSS0035; IG LIKE; 1.
Immunoglobulin V region; Signal.
 14070 MW;
 STANDARD;
 PRELIMINARY;
 129 1
129 AA;
 NCBI_TaxID=9606;
 leukemia.
 KV3M HUMAN
 DISULFID
NON TER
 SEQUENCE
 Query Match
 DOMAIN
 DOMAIN
 218136
 09UL78
KV3M_HUMAN
ID KV3M_HUMAN
ID KV3M_HUMAN
ID 01-NOV
DT 01-NOV
DT 15-NOV
DT 15-NOV
DE 19 AUTO
CC BUMBLII
RX MEDLII
RX MET
RX
 SIGNAL
 DOMAIN
 DOMAIN
 DOMAIN
 Matches
 RESULT 11
 09UL78
 ઠ
 쉽
 ò
 ద
```

```
29
 9
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP
 MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0; Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.; "Amino acid sequence of a light chain variable region of a human rheumatoid factor of the Wa idiotypic group, in part predicted by its reactivity with antipeptide antibodies.";
 1; Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 Query Match 80.1%; Score 445.5; DB 2; Length 109; Best Local Similarity 80.6%; Pred. No. 2e-40; Matches 87; Conservative 11; Mismatches 9; Indels 1
 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLFFGGGTKVEIK 108
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 109 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
 KV3G HUMAN STANDARD; PRT; 109 AA.
P04206;
20-MAR-1987 (Rel. 04, Created)
52-MAR-1987 (Rel. 04, Last sequence update)
55-UTL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-III region GOD (Rheumatoid factor).
 Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035036; AAD56272.1; -.
 Mol. Immunol. 23:239-244 (1986).
 InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig v.
SMART; SM00406; IGv; 1.
 PROSITE, PS50835; IG LIKE; 1
```

ï

```
Query Match
 RESULT 15
 RESULT 14
 OGGMV9
 Q6PJF2
 셤
 ð
 g
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP 59
 1 ZIVLTZSPGTLSLSPGZRAALSCRASQSLSGNYLAWYQQKPGQAPRLLMYGVSSRATGIP 60
 1 BIVWIQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP 59
 Milstein C.; "The basic sequences of immunoglobulin kappa chains: sequence studies of Rence Jones proteins Rad, Fr4 and B6.";
 1; Gaps
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
12 kappa chain V-III region B6.
13 kappa chain V-III region B6.
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 1;
 60 ARFSGSGSGTEFILTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRSFGQGTKVEIK 108
 DB 1; Length 108;
 60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 78.7%; Score 437.5; DB 1; Length 109; 78.7%; Pred. No. 1.5e-39;
 78.3%; Score 4.5...
75.0%; Pred. No. 2.4e-39;
rive 15; Mismatches 11; Indels
 11; Indels
 11635 MW; 8BC14FF07A419E3D CRC64;
 HESP, POIGS, 1873.

HISP, POIGS, 1873.

GO; GO: 0005576; C: extracellular; NAS.

GO; GO: 0003823; F: antigen binding; NAS.

GO; GO: 0003823; F: antigen binding; NAS.

GO; GO: 0005555; P: immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

Fam: PF00047; Ig-1.

PROSTITE; PSS: 0835; IG_LIKE; 1.

PROSTITE; PSS: 0835; IG_LIKE; 1.

Direct protein sequencing; Immunoglobulin V region.

DISULPID
 109 AA; 11830 MW; 9349A5B1D9358BB6 CRC64;
 PIR; A01891; K3HUB6.
HSSP; P01625; 1EEQ.
InterPro; IPR003196; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF0047; ig: 1.
PKOSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
Bence-Jones protein; Direct protein sequencing; Immunoglobulin v region.
BISULFID 23 89 similarity.
 of Bence Jones proteins Rad, Fr4 and B6.";
FEBS Lett. 2:301-304(1969).
-!- MISCELLANEOUS: This is a Bence-Jones protein.
 108 AA
 11; Mismatches
 PRT;
 Query Match
Best Local Similarity 75.09
 Local Similarity 78.79
nes 85; Conservative
 STANDARD;
 108 17
108 AA;
 PubMed=11946339;
 KV3A_HUMAN
 NON TER
SEQUENCE
 NON TER
SEQUENCE
 SEQUENCE.
 Query Match
 Matches
 셤
 ð
셤
 ઠે
 8
```

```
MEDINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachar R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
A patchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,
A Hilalon D.K., Maray D.M., Sodergen B.J., Lu X., Gibbs R.A.,
A Hilalon D.K., Maray D.M., Sodergen B.D., Dickson M.C.,
A Hilaceley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Marra M.A.,
A Jones S.J., Marra M.A.,
 59
 1 EIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80
 1 BIVMTOSPATLSVSPGERATLSCRASOSISNNF-AWYQOKPGQAPRLLIFGASTRATGIP
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1,
 81 DRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFGPGTKVDIK 128
 60 ARFSGSGSTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Length 235;
 Indels
 Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016380; AAH16380.1; -.
 Hypothetical protein.
SEOURNCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;
us-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein.
Hypothetical protein.
Eukaryota; Martin
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 / Match 78.3%; Score 435.5; DB 2; Local Similarity 78.7%; Pred. No. 5.9e-39; les 85; Conservative 12; Mismatches 10;
 PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 InterPro; IPR003599; Ig.
InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF07654; Cl-set; I.
 SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
 SEQUENCE FROM N.A.
 HSSP; P01837; 1KCU
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 rISSUE=Lung;
```

```
Straubberg R.L., Feingold E.A., Grouse L.H., Derge JG.

Strausberg R.L., Feingold E.A., Grouse L.H., Derge JG.

Klausner R.D., Colling F.S., Wagner L.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopking R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Willand D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Gromutz D., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

""" FProc. Natl. Acad. Sci. U.S.A. 99:16809-16803(2002).
 21 BIVLTQSPGTLSLSPGERAALSCRASQSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP 80
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNF-AWYQQKPGQAPRLLIFGASTRATGIP 59
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 1;
 TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 77.4%; Score 430.5; DB 2; Length 235; 76.9%; Pred. No. 2.1e-38; Live 12; Mismatches 12; Indels 1
 DRFSGSGSGTDFTLTISRLESEDFALYFCQQYGTSPLTFGGGTKVEIK 128
 60 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Straubberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BC073793; AMH73793.1; -.
InterPro; IPR003599; IG.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR003106; Ig-MC.
InterPro; IPR003066; Ig-MC.
InterPro; IPR003596; Ig-V.
Pfam; PP07654; Cl-Set; I.
 Hypothetical protein.
SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;
 Last sequence update)
Last annotation update)
 235 AA
 SMART; SM00409; ĬĞ; 2.
SMART; SM00407; IĞC1; 1.
SMART; SM00406; IĞY, 1.
PROSITE; PS50835; IĞ LIKE; 2.
PROSITE; PS00290; IĞ MHC; UNKNOWN_1.
 Created)
 PRT;
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 Best Local Similarity 76.9
Matches 83, Conservative
PRELIMINARY;
 Hypothetical protein.
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606
 IISSUE=Spleen;
 Query Match
 DD BREEF BRE
 g
 ò
 ò
```

Search completed: November 16, 2005, 22:01:54 Job time : 59.9908 secs 

```
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 101; Conserv
 US-09-456-090A-82
 US-09-203-768A-4
 US-09-203-768A-4
 ò
 g
 November 16, 2005, 21:41:29; Search time 18.1939 Seconds (without alignments) 439.017 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 30,
Sequence 47,
 556
1 EIVMTQSPATLSVSPGERAT......CQQYNNWPRTFGQGTKVEIK 107
 Description
 Sequence
Sequence
Sequence
Sequence
 Sequence Sequence S
 Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
 Sequence
 Sequence
 Sequence
 Sequence
 Sequence
 Sequence
 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 US-09-203-768A-4
US-09-456-090A-82
US-09-456-090A-98
US-09-456-090A-98
US-09-453-234-82
US-09-453-234-98
US-09-453-234-98
US-09-453-234-98
US-09-453-234-98
US-09-453-234-98
US-09-453-234-84
US-09-025-769B-16
US-09-025-769B-16
US-09-490-153-16
 Total number of hits satisfying chosen parameters:
 US-09-490-324-37
US-09-490-324-47
 513545 segs, 74649064 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-10-660-357A-34
 DB
 Query
Match Length
 106
109
109
109
 Copyright
 833.883.883.883.88383.88383.88383.88383.88383.88383.88383.88383.88383.88383.88383.88383.88383.88383.88383.8838
 83.7
83.7
83.7
83.7
83.5
 Perfect score:
 Scoring table:
 Score
 OM protein
 Sequence:
 Database
 Run on:
 Result
No.
```

```
Sequence 4, Application US/09203768A
Sequence 4, Application US/09203768A
Patent No. 6787638
GENERAL INFORMATION:
APPLICAMT: Huse, William D.
APPLICAMT: Watkins, Jeffry D.
TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
TITLE OF INVENTION: Of Use
FILE REFERENCE: P-1X 2947
CURRENT APPLICATION NUMBER: US/09/203,768A
CURRENT FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 117
 9
 1 EIVMTOSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Sequence 150,
Sequence 63, 7
Sequence 87, 7
 Gaps
 Sequence ï
 Sequence 82, Application US/09456090A

Sequence 82, Application US/09456090A

Patent No. 668209

GENERAL INFORMATION:

APPLICANT: Buechler, Joe

APPLICANT: Gary, Jeff

APPLICANT: Lonberg, Nils

TITLE OF INVENTION: HWAN ANTIBODIES AS DIAGNOSTIC REAGENTS

TITLE OF INVENTION: HWAN ANTIBODIES

CURRENT APPLICATION NUMBER: US/09/456,090A

CURRENT FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 110

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 82

LENGTH: 224
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIK 116
 Length 117;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNW-PRTFGQGTKVEIK 107
 Indels
 Score 520.5; DB 4;
Pred. No. 5.6e-41;
4; Mismatches 2;
 US-07-634-276-86
US-08-477-028-86
US-08-487-200-86
US-08-487-200-86
US-08-487-200-86
US-08-487-4813B-150
US-08-646-360-150
US-08-839-765-150
US-09-839-765-150
US-09-839-765-150
US-09-839-765-150
 1-09-472-087-14
1-09-472-087-65
1-08-232-081B-42
 US-09-610-838-150
US-09-711-485-150
 US-07-634-278-63
US-07-634-278-87
 ALIGNMENTS
 tch 93.6%; al Similarity 93.5%; 101; Conservative
```

```
TYPE: PRT
ORGANISM: Homo sapiens
US-09-456-090A-90
 JS-09-453-234-88
 US-09-453-234-82
 Query Match
 ઠ
 ઠ
 엄
 ò
 1 EIVLIQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVMTOSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
 Gaps
 Gaps
 .;
0
 ö
 Sequence 90, Application US/09456090A
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
APPLICANT: Weachler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Unberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; TITLE OF INVENTION: 1000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SEQ ID NO 90
; LENGTH: 224
 Sequence 88, Application US/09456090A
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
; APPLICANT: Unoberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; TITLE OF INVENTION: HUMAN ANTIBODIES, AS DIAGNOSTIC REAGENTS
; TITLE OF INVENTION: HUMAN ANTIBODIES, AS DIAGNOSTIC REAGENTS
; CURRENT APPLICATION NUMBER: 185/09/456,090A
; CURRENT FILIATION NUMBER: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SEQ ID NO 88
; LENGTH: 224
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRINWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Score 489; DB 4; Length 224;
Pred. No. 9e-38;
7; Mismatches 7; Indels
 DB 4; Length 224;
 Score 489; DB 4; Leus-Pred. No. 9e-38; 7; Indels
 7; Mismatches
 87.9%;
 86.9%;
 Query Match
Best Local Similarity 86.9
Matches 93; Conservative
 Query Match
Best Local Similarity 86.9
Matches 93; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-35L
; TYPE: PRT
OGNISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82
 ORGANISM: Homo sapiens
COTHER INFORMATION: M2-34L
US-09-456-090A-88
 RESULT 4
US-09-456-090A-90
 RESULT 3
US-09-456-090A-88
 TYPE: PRT
 d
 셤
 8
 8
```

```
ö
 1 EIVLIQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIXDASNRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 0; Gaps
 Gaps
 ö
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RPSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPRTFGGGTKVBIK 107
 61 RFSGSGGTEFTLTISSLQSEDFAVYYCOOYNNWPRTFGGGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPRTFGQGTKVEIK 107
 DB 4; Length 224;
 DB 4; Length 224;
 7; Indels
87.9%; Score 489; DB 4;
86.9%; Pred. No. 9e-38;
tive 7; Mismatches
 Query Match

87.9%; Score 489; DB 4;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches
 GENERAL INFOGRATION:
GENERAL INFOGRATION:
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genebarm International
TITLE OF INVENTION: Human Antibodies
TITLE REFERENCE: 020015-0001100S
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SENGTH: 224
 APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nil
APPLICANT: Lonberg, Nil
APPLICANT: Blosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT PTLING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
 Sequence 82, Application US/09453234
Patent No. 6794132
GENERAL INFORMATION:
 Sequence 88, Application US/09453234
Patent No. 6794132
 GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
 Best Local Similarity 86.5
Matches 93; Conservative
 ; OTHER INFORMATION: M2-31L
US-09-453-234-82
```

```
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 224
 US-09-453-234-36
 US-09-453-234-36
 셤
 ઠે
 셤
 ò
 g
 ઠ
 ઠ
 g
 9
 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVLIQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIXDASNRATGIPA 60
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 ö
 ..
0
 Sequence 36, Application US/09456090A
Fatent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gary, Jeff
APPLICANT: Lonberg, Nils
TILE OF INVENTION: HOWAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT FALPLICATION NUMBER: US/09/456,090A
CURRENT FILIOR DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPRTFGGGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 DB 4; Length 224;
 DB 4; Length 224;
 Query Match 87.9%; Score 489; DB 4; Length 22 Best Local Similarity 86.9%; Pred. No. 9e-38; Matches 93; Conservative 7; Mismatches 7; Indels
 7; Indels
 Query Match
87.9%; Score 489; DB 4;
Best Local Similarity 86.9%; Pred. No. 9e-38;
Matches 93; Conservative 7; Mismatches
 APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
 PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SEG ID NO 90
LENGTH: 224
 Sequence 90, Application US/09453234 Patent No. 6794132 GENERAL INFORMATION:
 TYPE: PRT
OCANISM: Homo sapiens
CTHER INFORMATION: M2-34L
US-09-453-234-88
 ; OTHER INFORMATION: M2-35L
US-09-453-234-90
 ORGANISM: Homo sapiens
 RESULT 8
US-09-456-090A-36
 RESULT 7
US-09-453-234-90
SEQ ID NO 88
LENGTH: 224
 g
 ò
 g
 ઠે
 ઠે
 셤
 δ
 g
```

```
ö
 9
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 0; Gaps
 ö
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVBIK 107
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPRTFGQGTKVEIK 107
 Length 224;
 Length 224;
 APPLICANT: Bucchler, Joe
APPLICANT: Valkire, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
IIILE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REPRESENCE: 020015-00020000US
CURRENT APPLICATION WUMBER: US/09/456,090A
CURRENT PILING DATE: 1999-12-06
 87.4%; Score 486; DB 4; Length 22
86.0%; Pred. No. 1.7e-37;
tive 8; Mismatches 7; Indels
 87.4%; Score 486; DB 4; Length 22
86.0%; Pred. No. 1.7e-37;
iive 8; Mismatches 7; Indels
 Sequence 36, Application US/09453234
Fatent No. 6794132
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: General International
ITIER BOF INVENTION: Human Antibodies
ITIER EPFERENCE: 020015-000110US
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARR: PatentIn Ver. 2.1
SENGTH: 224
 US-09-456-090A-84; Sequence 84, Application US/09456090A; Patent No. 6680209; GENERAL INFORMATION:
 Query Match
Best Local Similarity 86.09
Matches 92; Conservative
 92; Conservative
 CTHER INFORMATION: M1-1L US-09-456-090A-36
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
 TYPE: PRT
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 92; Conserv
```

a

ઠે 셤

```
ORGANISM: Homo sapiens
OTHER INFORMATION: M1-10L
 Query Match
Best Local Similarity
 RESULT 13
US-09-453-234-46
 US-09-453-234-46
 US-08-635-109-8
 PRT
 Matches
 g
 à
 ð
 g
 g
 ò
 ö
 9
 1 EIVLIQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIPA 60
 1 EIVLIQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVMTOSPATLSVSPGERATLSCRASOSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 Gaps
 0
 ö
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRNNWPLTFGGGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRIFGQGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRNNWPLTFGGGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Query Match 85.6%; Score 476; DB 4; Length 224; Best Local Similarity 85.0%; Pred. No. 1.4e-36; Matches 91; Conservative 7; Mismatches 9; Indels
 ch 85.6%; Score 476; DB 4; Length 224; Similarity 85.0%; Pred. No. 1.4e-36; 91; Conservative 7; Mismatches 9; Indels
 RESULT 12
US-09-456-090A-46
Sequence 46, Application US/09456090A
Patent No. 6680209
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Caray, Jeff
APPLICANT: Conberg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REPERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
 APPLICANT: Buechler, Joe
APPLICANT: Buechler, Gunars
APPLICANT: Glay, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nis
APPLICANT: GenPharm International
APPLICANT: GenPharm International
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-0001100S
GURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR APPLICATION NUMBER: US 60/157,415
NUMBER OF SEQ ID NOS: 112.
 ; Sequence 84, Application US/09453234; Patent No. 6794132; GENERAL INFORMATION:
; NUMBER OF SEQ ID NOS: 110
; SOTWARE: Patentin Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84
 ; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84
 Query Match
Best Local Similarity
Matches 91; Conserval
 RESULT 11
US-09-453-234-84
 SEQ ID NO 84
LENGTH: 224
```

d ò

8

```
ô
 9
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1. DVVWTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 Gaps
 .
0
 ö
 Sequence 8, Application US/08635109
; Patent No. 6538114
; GENERAL INFORMATION:
 APPLICANT: Persson, Mats A. A.
 APPLICANT: Allander, Tobias E.
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
 TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPTFGGGTKVBIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPTFGGGTKVEIK 107
 ch 85.4%; Score 475; DB 4; Length 224; 1 Similarity 84.1%; Pred. No. 1.8e-36; 9; Mismatches A. Talana
 Length 224;
 Query Match 85.4%; Score 475; DB 4; Length 22 Best Local Similarity 84.1%; Pred. No. 1.8e-36; Matches 90; Conservative 9; Mismatches 8; Indels
 GENERAL INCORNATION:
APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Lonberg, Wils
APPLICANT: Lonberg, Wils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: OSEDATE DIAGNOSTICS, Inc.
APPLICANTON NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 46
LENGTH: 224
 Sequence 46, Application US/09453234 Patent No. 6794132
; CURRENT FILING DATE: 1999-12-06; NUMBER OF SEQ ID NOS: 110; SEQ ID NO 46; LENGTH: 224; LENGTH: 224; TYPE: PRT: PROMOSAJION: M1-10L US-09-456-090A-46
```

```
Search completed: Novem
Job time : 19.1939 secs
 d
 ð
 4 MTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPARFS 63
 Gaps
 Sequence 11, Application US/08844215
Fatent No. 6747136
GENERAL INCRNATION:
GENERAL INCRNATION:
APPLICANT: PERSSON, MATS AXEL
APPLICANT: ALLANDER, TOBIAS ERIK
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: 0A
COUNTRY: USA
COUNTRY: USA
STATE: AB COMPATER REABBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PROPEN GENERALING
COMPATIER: 1DAPP GENERALING
COMPATIER: 1DAPP COMPATIBLE
COMPATIER: 1DAPP COMPATIBLE
COMPATIER: 1DAPP COMPATIBLE
CLASSIFICATION DATA:
FILING DATE: 17-APR-1997
FILING DATE: 19-APR-1996
FILING DATE: 19-APR-1996
 ő
 Query Match
83.8%; Score 466; DB 4; Length 106;
Best Local Similarity 83.7%; Pred. No. 5.4e-36;
Matches 87; Conservative 7; Mismatches 10; Indels
 63 GSGSGTEFTLTISSLQSEDFAVYFCQHYSTWPLTFGGGTKVEFK 106
 64 GSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
APPLICATION DATA:
APPLICATION NUMBER: US/08/635,109
FILING DATE: 19-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCTACKEN, Thomas P
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 38,548
REGISTRATION FORCET UNMBER: 320-6146
TELEFHONE: (415) 327-3331
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDENESS: single
TOPPLOGY: linear:
COMPUTER: Innear:

 STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: California
REED & ROBINS
 , MOLECULE TYPE: protein US-08-635-109-8
 STATE: Ca
 ద
 ઠે
 g
```

```
4 MTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPARFS 63
 3 LTQSPATLSVSPGERASLSCRASQSVGNNLAWYQQKPGQAPRLLIYGGNTRATGTPDRFS 62
 Gaps
 ö
 Query Match
83.8%; Score 466; DB 4; Length 106;
Best Local Similarity 83.7%; Pred. No. 5.4e-36;
Matches 87; Conservative 7; Mismatches 10; Indels
 64 GSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 GSGSGTEFTLTISSLQSEDFAVYFCQHYSTWPLTFGGGTKVEFK 106
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 80146.002
TELECOMULNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFRAX: (650) 325-7813
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 anino acids
TTYPE: amino acids
 November 16, 2005, 22:07:22
 single
 MOLECULE TYPE: peptide
 STRANDEDNESS:
TOPOLOGY: lin
 US-08-844-215-11
```

The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s

Sequence 1 Sequence 1 Sequence 3 Sequence

Sequence

Sequence

19, App 114, App 107, App 29, Appl

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence S

Sequence

115, App 115, App 4, Appli

Sequence 1 Sequence 1 Sequence 4

US-10-251-085B-123 US-10-737-252-109 US-10-737-252-109 US-10-727-155-313 US-10-251-085B-117 US-10-251-085B-117 US-10-251-085B-117 US-10-251-085B-119 US-10-737-252-119 US-10-737-252-119 US-10-737-252-119 US-10-737-252-119 US-10-737-252-119 US-10-737-252-119 US-10-737-252-115 US-10-737-253-146 US-10-737-252-146 US-10-737-252-146 US-10-737-755-146 US-10-737-755-146 US-10-737-755-146 US-10-737-755-146 US-10-737-755-146 US-10-737-755-146 US-10-737-755-146 US-10-737-755-146 US-10-737-755-177

1268, Ap 1268, Ap

Sequence Sequence Sequence S

Sequence

Sequence

Appl Appl Appl Appli Appli

> Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

```
US-10-330-613-34
 521
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
520.5
52
 61
 N
 RESULT
 셤
 ઠે
 6, Appli
6, Appli
6, Appli
122, App
 November 16, 2005, 22:02:09; Search time 65.6949 Seconds (without alignments) 681.481 Million cell updates/sec
 Sequence 122,
Sequence 126,
Sequence 126,
Sequence 109,
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 US-10-660-357A-34
556
1 BIVMTQSPATLSVSPGERAT.......CQQYNNWPRTFGQGTKVEIK 107
 Sequence 3
Sequence 3
Sequence 3
Sequence 6
Sequence 6
Sequence 6
Sequence 6
 Description
 Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT TBW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT TBW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
 US-10-330-613-34
US-10-330-34
US-10-660-357-34
US-10-330-613-6
US-10-660-357-6
US-10-660-357-6
US-10-651-0858-122
US-10-737-252-122
US-10-737-252-126
US-10-251-0858-126
US-10-251-0858-126
US-10-251-0858-126
 Total number of hits satisfying chosen parameters:
 1867879 segs, 418409474 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 seq length: 0
seq length: 200000000
 DB
 Length
 107
107
107
107
107
107
107
 Copyright
 100.0
100.0
98.2
98.2
98.2
96.0
96.0
96.0
 Title:
Perfect score:
 Scoring table:
 Score
 Minimum DB
Maximum DB
 OM protein
 Sequence:
 Searched:
 Database
 2643978611
 Run on:
 Result
No.
```

```
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
 ð
 셤
 ò
 g
 ઠે
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVMTÖSPATLSVSPGERATLSCRASOSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPQQAPRLLIFGASTRATGIPA 60
 Gaps
 Gaps
 ;
0
 ;
0
US-10-330-530-34
; Sequence 34, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR APPLICATION NUMBER: US 60/346414
; RILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 34
; LENGTH: 107
 Query Match
100.0%; Score 556; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 107; Conservative 0; Mismatches 0; Indels 0
 Length 107;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYCQQYNNWPRTFGQGTKVEIK 107
 Sequence 34, Application US/10660357

Sequence 34, Application US/10660357

Publication No. US20040115205A1

GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe

TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUCL8

TITLE OF INVENTION: WHEREN
FILE REFERENCE: ABGENIX.030C1

CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: US/10/660,357

CURRENT FILING DATE: 2002-12-26

NUMBER OF SEQ ID NOS: 40

SEQ ID NO 34

LENGTH: 107
 0; Indels
 100.0%; Score 556; DB 16; 100.0%; Pred. No. 1.4e-40;
 0; Mismatches
 Sequence 6, Application US/10330613
Publication No. US20030147809A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
 Matches 107; Conservative
 TYPE: PRT
ORGANISM: Homo Sapiens
 ORGANISM: Homo Sapiens
 Query Match
Best Local Similarity
 RESULT 3
US-10-660-357-34
 US-10-330-530-34
 US-10-660-357-34
 g
 유
 ò
 Ω
 ઠે
```

```
9
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 0; Gaps
 Sequence 6, Application US/10330530;
Publication No. US20030152514A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORMATION WETHOUS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: ABGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT APPLICATION NUMBER: US 60/346414
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 107
 61 RFSGSGSGTEFTLTISSLOSEDFAVYYCOOYNNWPRTFGOGTKVEIK 107
 98.2%; Score 546; DB 14; Length 107; 97.2%; Pred. No. 1e-39; tive 2; Mismatches 1; Indels
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGGGTKVEIK 107
 DB 14; Length 107;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Sequence 6, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
 APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUCI8
; TITLE OF INVENTION: ANTIGEN
; TITLE OF INVENTION: ANTIGEN
; CURRENT FILING DATE: 20303-09-10
; RRIOR APPLICATION NUMBER: 10/330,580
 Query Match 98.2%; Score 546; DB 14; Length 1 Best Local Similarity 97.2%; Pred. No. 1e-39; Matches 104; Conservative 2; Mismatches 1; Indels
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
 Best Local Similarity 97.2
Matches 104; Conservative
 , ORGANISM: Homo Sapiens
US-10-330-530-6
 TYPE: PRT
CRGANISM: Homo Sapiens
US-10-330-613-6
 JS-10-660-357-6
 US-10-330-530-6
 Query Match
```

ö

ઠે g ò g

```
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, mark
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
 APPLICANT: Frederickson, Shana APPLICANT: Renshaw, Mark APPLICANT: Renshaw, Mark APPLICANT: Lin, Ying-Chi APPLICANT: Lin, Ying-Chi APPLICANT: Maruyama, Toshiaki APPLICANT: Maruyama, Toshiaki TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION FILLE PERERENCE: 1087-21 CURRENT APPLICATION NUMBER: US/10/251,085B PRIOR PILING DATE: 2002-09-19 PRIOR FILING DATE: 2001-09-19
 ö
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 Gaps
 ö
 ö
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLÓSEDFAVYYCQOYNNWPGTFGOGTKVEIK 107
 96.0%; Score 534; DB 16; Length 107; 95.3%; Pred. No. 1.1e-38;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 Length 107;
 Indels
 95.3%; Score 530; DB 15;
94.4%; Pred. No. 2.5e-38;
tive 3; Mismatches 3;
 3; Mismatches
PRIOR APPLICATION NUMBER: US 10/251,085 PRIOR PILING DATE: 2002-09-19 PRIOR PELING DATE: 2002-09-19 PRIOR APPLICATION NUMBER: US 60/323,455 PRIOR FILING DATE: 2001-09-19 NUMBER OF SEQ ID NOS: 309 SOFTWARE: Patentin version 3.2 SEQ ID NO 122
 Sequence 126, Application US/10251085B; Publication No. US20040072164A1
GENERAL INFORMATION: APPLICANT: Bowdish, Katherine S.
 ; Sequence 126, Application US/10737252; Publication No. US20040175736A1; GENERAL INFORMATION:
 SOFTWARE: PatentIn version 3.2
SEQ ID NO 126
LENGTH: 107
 Query Match
Best Local Similarity 95.3%;
Matches 102; Conservative
 Best Local Similarity 94.4%;
Matches 101; Conservative
 NUMBER OF SEQ ID NOS: 278
 ORGANISM: human
 ORGANISM: human
 RESULT 9
US-10-251-085B-126
 US-10-251-085B-126
 US-10-737-252-126
 US-10-737-252-122
 TYPE: PRT
 Query Match
 TYPE: PRT
 δ
 g
 셤
 ò
 셤
 APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruping Tobliaki
TITLE OF INVENTION: BOGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21
CURRENT APPLICATION NUMBER: US/10/251,085B
CURRENT FILING DATE: US 60/323,455
PRIOR FILING DATE: 2001-09-19
 APPLICANT: Bowdish, Katherine S.
APPLICANT: Brederickson, Shana
APPLICANT: Renshaw, Mark
APPLICANT: Renshaw, Mark
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
FILE REFERENCE: 1087-21 CIP
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
 1 EIVWTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaps
 Gaps
 ö
 ö
 Query Match 98.2%; Score 546; DB 16; Length 107; Best Local Similarity 97.2%; Pred. No. 1e-39; Matches 104; Conservative 2; Mismatches 1; Indels
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYCQQYNNWPPTFGQGTKVEIK 107
 Length 107;
 2; Indels
 96.0%; Score 534; DB 15;
95.3%; Pred. No. 1.1e-38;
tive 3; Mismatches 2;
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
 CURRENT APPLICATION NUMBER: US/10/737,252 CURRENT FILING DATE: 2003-12-15
 ; Sequence 122, Application US/10251085B; Publication No. US20040072164A1; GENERAL INFORMATION; APPLICANT: Bowdish, Katherine S.
 Sequence 122, Application US/10737252
Publication No. US20040175736A1
GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
 Query Match 96.0
Best Local Similarity 95.3
Matches 102; Conservative
 LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-660-357-6
 TYPE: PRT
ORGANISM: human
 RESULT 7
US-10-251-085B-122
 US-10-251-085B-122
 US-10-737-252-122
 SEQ ID NO 122
```

ઠે g ò g

```
Page 4

APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
CURRENT APPLICATION NUMBER: US/10/251,0858
CURRENT FILING DATE: 2002-09-19
FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patentin version 3.2
SEQ ID NO 123
LENGTH: 107
TYPE-
 Sequence 109, Application US/10737252

Sequence 109, Application US/10737252

Sequence 109, Application US/20040175736A1

GENERAL INFORMATION:

APPLICANT: Bondiah, Katherine S.

APPLICANT: Breaking Carlon

APPLICANT: Languama, Toshiaki

TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION

FILE REFERENCE: 1087-21.CIP

CURRENT FILING DATE: 2003-12-15

FRIOR APPLICATION NUMBER: US 60/251,085

FRIOR APPLICATION NUMBER: US 60/323,455

FRIOR PILING DATE: 2001-09-19

FRIOR PILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 309

SOFTWARE: PatentIn version 3.2

SEQ ID NO 109

LENGTH: 107
 ö
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 BIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 Gaрв
 Gaps
 ;
0
 ö
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPITFGQGTRLEIK 107
 Query Match

94.8%; Score 527; DB 16; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 5; Mismatches 2; Indels
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPNTFGPGTKVDIK 107
 Length 107;
 Indels
 Query Match
94.8%; Score 527; DB 15;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 4; Mismatches 3;
 US-10-737-252-123
; Sequence 123, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
 , ORGANISM: human
US-10-737-252-109
 ORGANISM: human
US-10-251-085B-123
 US-10-737-252-109
 RESULT 14
 ð
 ò
 g
 8
 US-10-251-0858-109
Sequence 109, Application US/10251085B
Sequence 109, Application US/10251085B
Sequence 109, Application US/002040072164A1
Sequence 109, Application No. US20040072164A1
APPLICANT: Bredarickson, Shana
APPLICANT: Renchaw, Mark
APPLICANT: Renchaw, Mark
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
FILE REFERENCE: 1087-21
CURRENT PRIJECTON NUMBER: US/10/251,085B
CURRENT FILING DATE: 2002-09-19
PRIOR PILING DATE: 2002-09-19
PRIOR PILING DATE: 2001-09-19
SPRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 278
SEQ ID NOS: 278
SEQ ID NOS: 278
FEMALE.
 9
 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
 1 EIVWTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGTSTRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA
 1 EIVMTOSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGOAPRLLIFGASTRATGIPA
 Gaps
 ö
 ö
 94.8%; Score 527; DB 15; Length 107; 93.5%; Pred. No. 4.5e-38;
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 RFSGSGSGTEFTLTISSLOSEDFAVYYCQQYNNWPITFGQGTRLEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPGTFGQGTKVEIK 107
 Length 107;
 3; Indels
 Score 530; DB 16;
Pred. No. 2.5e-38;
3; Mismatches 3;
 5; Mismatches
 FILE REFERENCE: 1087-21 CIP
CURRENT APPLICATION NUMBER: US/10/737,252
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 10/251,085
PRIOR PELING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn version 3.2
 Sequence 123, Application US/10251085B; Publication No. US20040072164Al; GENERAL INFORMATION: APPLICANT: Bowdish, Katherine S.; APPLICANT: Frederickson, Shana APPLICANT: Renshaw, Mark
 Query Match
Best Local Similarity 94.4%;
Matches 101; Conservative
 Matches 100; Conservative
 Best Local Similarity
 ORGANISM: human
 TYPE: PRT
ORGANISM: human
 US-10-251-085B-123
 US-10-251-085B-109
 US-10-737-252-126
 SEQ ID NO 126
LENGTH: 107
 Query Match
 g
 Q
 ò
 g
 ò
 8
```

```
61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPITFGGGTRLEIK 107
 61 RFSGSGSGTEFTLTISSLOSEDFAVYYCOOYNNWPRTFGQGTKVEIK 107
 Search completed: November 16, 2005, 23:05:45 Job time : 66.6949 secs
 셤
 ઠે
 임
 APPLICANT: Enchas, Mark
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Lin, Ying-Chi
APPLICANT: Maruyama, Toshiaki
TITLE OF INVENTION: BNGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
CURRENT APPLICATION NUMBER: US/10/737,252
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 60/2251,085
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR APPLICATION NUMBER: US 60/323,455
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.2
SEQ ID NO 123
LENGTH: 107
 ö
 ö
 1 EIVWTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
 1 EIVMTQSPATLSVSPGERATLSCRASQSISNNFAWYQQKPGQAPRLLIFGASTRATGIPA 60
 Gaps
 ö
 ö
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPNTFGPGTKVDIK 107
 Query Match

94.8%; Score 527; DB 16; Length 107;
Best Local Similarity 93.5%; Pred. No. 4.5e-38;
Matches 100; Conservative 4; Mismatches 3; Indels.
 61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPRTFGQGTKVEIK 107
 94.8%; Score 527; DB 17; Length 107; 93.5%; Pred. No. 4.5e-38; tive 5; Mismatches 2; Indels
 APPLICANT: Meina Liang
APPLICANT: Meina Liang
APPLICANT: Rathy Manchulencho
APPLICANT: Rathy Manchulencho
APPLICANT: Rathy Manchulencho
APPLICANT: Rathy Manchulencho
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
TITLE OF INVENTION: ANTIBODIES
FILE REPREMENTE: ABGENIX: 073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT PILING DATE: 2003-12-02
PRIOR FILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3100
 Larry Green
Xiao Feng
Scott Klakamp
Mary Haak-Frendscho
Palaniswami Rathanaswami
 Sequence 310, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcook
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
Bowdish, Katherine S.
Frederickson, Shana
 Best Local Similarity 93.5
Matches 100; Conservative
 Craig Pigott
Meina Liang
 LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: human
 RESULT 15
US-10-727-155-310
 US-10-727-155-310
 US-10-737-252-123
 APPLICANT:
APPLICANT:
APPLICANT:
 g
 ઠે
```

11.10 Part 12.11.17 (127.70)

Н

```
November 16, 2005, 21:35:48; Search time 64.2353 Seconds (without alignments) 674.351 Million cell updates/sec
 1 DIVMTQSPLSLPVIPGEPAS..........CMQALQIPLTFGGGTKVEIK 112
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2105692 seqs, 386760381 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 A_Geneseq_16Dec04:*
1: geneseqp1980s:*
 geneseqp1980s:*
geneseqp1990s:*
 geneseqp2001s:*geneseqp2002s:*
 geneseqp2000s:*
 US-10-660-357A-38
 seq length: 0 seq length: 2000000000
 Title:
Perfect score:
 Scoring table:
 OM protein -
 DB
DB
 Sequence:
 Database
 Minimum Maximum Maximum
 Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003as:\* geneseqp2003bs:\*

geneseqp2004s:\*

|           | Description           | Adc99809 Anti-huma | Add05413 Anti-MUC1 | Adf09851 Human ant | Abr55794 Kappa cha | G        |          | 0        | Adg96897 Single ch |          | Aay82615 Human PTH | Abr55770 Kappa cha | 0        | -        | Adi22122 Anti-plat |          | Adl93576 Human CD4 | Ad193653 Human CD4 |          | Adk18796 Anti-huma | N        | Adk18855 Anti-huma | Adl25402 Human mAb | Ad193564 Human CD4 | Ad193649 Human CD4 | Adj76892 Anti-IGF- |
|-----------|-----------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|----------|--------------------|--------------------|----------|----------|--------------------|----------|--------------------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | CI                    | ADC99809           | ADD05413           | ADF09851           | ABR55794           | ABR55786 | ADP03893 | ABP46070 | ADG96897           | ADP03892 | AAY82615           | ABR55770           | ABR55812 | ADI22119 | ADI22122           | ABR55796 | ADL93576 .         | ADL93653           | ADK18830 | ADK18796           | ADK18592 | ADK18855           | ADL25402           | ADL93564           | ADL93649           | ADJ76892           |
|           | DB                    | 7                  | 7                  | 7                  | 9                  | 9        | 7        | ß        | 7                  | 7        | ٣                  | 9                  | 9        | æ        | ω                  | 9        | 8                  | œ                  | 7        | 7                  | 7        | 7                  | ω                  | œ                  | œ                  | 7                  |
|           | Query<br>Match Length | 112                | 112                | 112                | 112                | 112      | 112      | 262      | 262                | 112      | 239                | 112                | 112      | 112      | 112                | 112      | 112                | 238                | 111      | 111                | 111      | 111                | 111                | 112                | 238                | 112                |
| d         | Query<br>Match        | 100.0              | 100.0              | 100.0              | 95.2               | 95.2     | 95.2     | 94.5     | 94.5               | 94.3     | 94.1               | 94.0               | 93.8     | 93.8     | 93.8               | 93.1     | 93.1               | 93.1               | 93.0     | 93.0               | 93.0     | 93.0               | 93.0               |                    | 92.9               | 5                  |
|           | Score                 | 580                | 580                | 580                | 552                | 552      | 552      | 548      | 548                | 547      | 546                | 545                | 544      | 544      | 544                | 540      | 540                | 540                | 6        | 539.5              | 539.5    | ۳.                 | 539.5              | m                  | 539                | m                  |
|           | Result<br>No.         | -                  | 8                  | ٣                  | 4                  | 2        | 9        | 7        | œ                  | 6        | 10                 | 11                 | 12       | 13       | 14                 | 15       |                    | 17                 | 18       | 19                 | 20       | 21                 | 22                 | 23                 | 24                 | 25                 |

| Ado07297 Human pro Adj80417 Hybrid hu Abg76926 Humanised Adr88410 Human pro Adj22112 Anti-plat Adj22111 Anti-plat Adj22111 Anti-plat Adj22111 Anti-plat Adj2211 Anti-plat Adj2211 Anti-plat Adj2211 Anti-plat Adg28451 Human PTH Ade28453 Human ant Ade28451 Human ant Ade28477 Human ant Ade284847 Human ant Ade284848 Adg2847 Human ant Ade284848 Adg2847 Human ant | Ade28445 Human ant<br>Ade28409 Human ant<br>Adp47097 Human pho<br>Ade28405 Human ant<br>Ade28469 Human ant |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|
| ADO07297 ADJ80417 ABG76926 ADR88410 ADR47297 AD122111 AD122111 AD122114 AAY82611 ADB28453 ADE28521 ADR38477 ADE28477 ADE28477 ADE28477 ADE28477 ADE28487                                                                                                                                                                                                              | ADE28445<br>ADE28409<br>ADE47097<br>ADE28405<br>ADE28469                                                   |
| 87777788888887777                                                                                                                                                                                                                                                                                                                                                     | 7 7 8 7 7                                                                                                  |
| 1112<br>1112<br>1112<br>1112<br>1112<br>1112<br>1122<br>112                                                                                                                                                                                                                                                                                                           | 112<br>112<br>113<br>239<br>239                                                                            |
| 99999999999999999999999999999999999999                                                                                                                                                                                                                                                                                                                                | 91.9<br>91.9<br>91.9<br>91.9                                                                               |
| 0                                                                                                                                                                                                                                                                                                                                                                     | 23333333333333333333333333333333333333                                                                     |
| 2000 10 10 10 10 10 10 10 10 10 10 10 10                                                                                                                                                                                                                                                                                                                              | 4 4 4 4 4<br>1 52 52 4 52                                                                                  |
|                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                            |

## ALIGNMENTS

anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast; Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 38 ADC99809 standard; protein; 112 AA (first entry) lung cancer; human. 01-JAN-2004 ADC99809; 

Homo sapiens.

WO2003057838-A2.

17-JUL-2003.

26-DEC-2002; 2002WO-US041581.

28-DEC-2001; 2001US-0346299P

(ABGE-) ABGENIX INC.

Gudas J;

WPI; 2003-587113/55. N-PSDB; ADC99811.

New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.

Claim 3; SEQ ID NO 38; 78pp; English.

a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to WUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithal neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the anti-human MUC18 monoclonal antibody The invention relates to a novel isolated monoclonal antibody comprising

õ

Gape

ô

Indels

9 9

SXS

셤 ò 8

```
1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQXPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGBNRA
 cell proliferation inhibition; MUC18 tumour antigen; anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour; carcinoma; cancer; malignancy; light chain; human.
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 Human anti-MUC18 monoclonal antibody light chain #10
Pred. No. 7.6e-44;
Mismatches 0;
 Ź
 ADF09851 standard, protein; 112
Local Similarity 100.0%; P. nes 112; Conservative 0;
 28-DEC-2001; 2001US-0346414P.
 26-DEC-2002; 2002WO-US041580.
 Conservative
 WPI; 2003-598367/56
 (ABGE-) ABGENIX INC
 monoclonal antibody
 Best Local Similarity
Matches 112; Conserv
 N-PSDB; ADF09853,
 Sequence 112 AA;
 WO2003057837-A2
 12-FEB-2004
 17-JUL-2003
 ADF09851;
 Query Match
 61
 61
 Gudas J;
 Best Loc
Matches
 ADF0985
 RESULT
 셤
 ò
 g
 ò
 셤
 ò
 ö
 The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the amonoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in linhibited proliferation of the cells. The monoclonal antibody has cytostetic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and
 treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or tumour metastasis), inhibiting cell invasion associated with melanoma, or increasing survival of an animal hatib an estastatic tumour. This sequence represents an anti-MCC18 antibody light chain, variable region,
 09
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine; antigen; tumour metastasis; melanoma; metastatic; human; light chain.
 Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metascatic tumor.
 Anti-MUC18 antibody light chain variable region protein, SEQ ID No 38.
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLIFGGGTKVEIK 112
 ó,
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK
 Length 112;
 Indels
 ö
 Score 580; DB 7;
Pred. No. 7.6e-44;
 0; Mismatches
light chain protein of the invention.
 Claim 3; SEQ ID NO 38; 87pp; English
 ADD05413 standard; protein; 112 AA
 100.0%;
 26-DEC-2002; 2002WO-US041582
 28-DEC-2001; 2001US-0346460P
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 112; Conservative
 protein of the invention.
 Gudas J, Bar-Eli M;
 WPI; 2003-577496/54.
 (ABGE-) ABGENIX INC.
 N-PSDB; ADD05415
 Sequence 112 AA;
 Sequence 112 AA;
 WO2003057006-A2
 01-JAN-2004
 Homo sapiens
 17-JUL-2003
```

ADD05413;

```
ö
 9
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61
 61
 셤
 à
```

The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastessis. The method is useful for inhibiting tumour metastessis. The method carcinomas, cancer and other malignancies. The present amino acid sequence represents a light chain from an MUC18 tumour antigen-specific Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-MUC18 monoclonal antibody. Claim 3; SEQ ID NO 38; 83pp; English.

Gaps ó 100.0%; Score 580; DB 7; Length 112; 100.0%; Pred. No. 7.6e-44; ive 0; Mismatches 0; Indels

Query Match

Length 112; DB 7; 100.0%; Score 580; us-10-660-357a-38.rag

61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 112

셤

```
The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease, inflammatory disease, inflammatory disease, atherosclerosis, endometriosis, neoplastic disease, bone-related disease, or psoriasis) in a mammal. The present sequence represents a kappa chain variable region of an anti-Ang-2
 New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
 Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer; angiogenesis; antibody.
 "complementarity determining region (CDR) 1"
 5
 (CDR) 3"
 Kappa chain variable region of anti-Ang-2 antibody 551 kappa.
 95.2%; Score 552; DB 6; Length 112; 94.6%; Pred. No. 2.3e-41;
 "complementarity determining region
 /note= "complementarity determining region
 Location/Qualifiers
 ABR55794 standard; protein; 112 AA.
 Claim 1; Page 93; 161pp; English.
 11-OCT-2002; 2002WO-US032613
 2001US-0328604P
2002US-00269805
 (first entry)
 .102
 54. .62
 /note=
93. .10
 /note=
 WPI; 2003-504963/47.
 (AMGE-) AMGEN INC.
 Sequence 112 AA;
 WO2003030833-A2
 11-OCT-2001;
10-OCT-2002;
 Homo sapiens
 02-SEP-2003
 17-APR-2003
 Oliner JD;
 ABR55794;
 Query Match
 antibody
 Region
 Region
 Region
RESULT 4
 ABR55794
```

```
The invention relates to a specific binding agent, which comprises at fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, heamangioblastoma, heamangioma, arteriosclerosis, inflammatory disease, inflammatory disease, inflammatory disease, inflammatory disease, bone-related disease, or psoriaeis) in a mammal. The present sequence represents a kappa chain variable region of an anti-Ang-2
 New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
 9
 9
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antinflammatory; osteopathic; antipsoriatic; cancer; angiogenesis; antibody.
 Gaps
 <u>-</u>
 Ē
 (CDR) 1"
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVBIK 112
 (CDR)
 ö
 Kappa chain variable region of anti-Ang-2 antibody 543 kappa.
 "complementarity determining region
 .62
.e= "complementarity determining region
 /note= "complementarity determining region
 Length 112;
 4; Indels
 Score 552; DB 6;
Pred. No. 2.3e-41;
 2; Mismatches
 Location/Qualifiers
 Ŗ
 Claim 1; Page 93; 161pp; English.
 ABR55786 standard; protein; 112
 11-OCT-2001; 2001US-0328604P.
 11-OCT-2002; 2002WO-US032613
 Query Match
Best Local Similarity 94.6%;
Matches 106; Conservative
 02-SEP-2003 (first entry)
 23. .40
/note= "
 /note=
 WPI; 2003-504963/47.
 (AMGE-) AMGEN INC.
 Sequence 112 AA;
 WO2003030833-A2
 Homo sapiens.
 17-APR-2003
 Oliner JD;
 ABR55786;
 Región
 Region
 Region
RESULT 5
 ABR55786
 셤
 ò
 ò
```

ö

ö

Gaps

ö

Indels

2; Mismatches

Best Local Similarity 74.0 Matches 106; Conservative

Similarity

9 9

DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA

Н

셤 ð

ઠ

61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112

61

```
The invention relates to a novel isolated monoclonal antibody (mAb) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as coloractal nooplasm, renal cell carcinoma, cervical arreaphith and antibody of the invention of tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VL (light chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into
 monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal call carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast cancer; gene therapy; murine; mouse; human; light chain variable domain.
 Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 33.
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors
 Gaps
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQALQTPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 .
 95.2%; Score 552; DB 7; Length 112; 94.6%; Pred. No. 2.3e-41; ive 2; Mismatches 4; Indels
 Gallo M;
 Claim 3; SEQ ID NO 33; 89pp; English.
 Ź
 ADP03893 standard; protein; 112
 02-DEC-2002; 2002WO-US038550
 03-DEC-2001; 2001US-0337275P
 Gudas J, Foltz I, Handa M,
 (first entry)
 Query Match
Best Local Similarity 94.6
Matches 106; Conservative
 cransgenic mouse strain.
 WPI; 2003-523295/49.
 (ABGE-) ABGENIX INC
 Sequence 112 AA;
 WO2003048328-A2
 29-JUL-2004
 Unidentified
 12-JUN-2003
 61
 61
 ADP03893;
RESULT 6
ADP03893
ID ADP03893
ADP03893
ADP03893
DT 29-4
AC ADP
AC
 셤
 δ
 g
```

```
This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (CVID) and immunodeficiency (CVID) and interpretation interpret
 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulati; immunombulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
 acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 Length 262;
 Indels
 Hilbert D;
 Score 548; DB 5; Le
Pred. No. 1.3e-40;
 Vaughan T,
 3; Mismatches
 Claim 1; Page 2880-2881; 3148pp; English.
 CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 Human BLyS binding scFv SEQ ID 2081.
ABP46070 standard; protein; 262 AA.
 Choi GH,
 17-OCT-2000; 2000US-0240B16P.
16-MAR-2001; 2001US-027624BP.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
 94.5%;
 15-JUN-2001; 2001WO-US019110.
 16-JUN-2000; 2000US-0212210P.
 HUMA-) HUMAN GENOME SCI INC
 Matches 105; Conservative
 Barash SC,
 WPI; 2002-114799/15.
 Local Similarity
 Sequence 262 AA;
 WO200202641-A1
 the invention
 Homo sapiens.
 19-AUG-2002
 10-JAN-2002.
 210
 Ruben SM,
 Query Match
 ABP46070;
셤
 8
 ઠ
 g
```

ö

ö

9 9

RESULT 7 ABP46070

9

of

61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112 210 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK

ò a

Ŋ

```
This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single contain antibody molecules (ecfevs) derived, preferably, from the variable contains region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The correct invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple solerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallersgic and cytostatic. This polypeptide sequence las a single chain antibody that binds BLyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
 Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
 antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor; B cell proliferation; differentiation; scFv; myasthenia gravis; multiple sclerosis; asthma; rheumatodi arthritis; AIDS; leukaemia; carcinoma; lymphoma; antirheumatic; antiathritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 Single chain antibody that immunospecifically binds BLyS SeqID 2081.
 directely from WIPO at ftp.wipo.int/pub/published pct_sequences
 Hilbert
 Vaughan TJ,
 Example 1; SEQ ID NO 2081; 394pp; English.
ADG96897 standard; protein; 262 AA
 Choi GH,
 14-NOV-2002; 2002WO-US036496
 16-NOV-2001; 2001US-0331469P.
 (HUMA-) HUMAN GENOME SCI INC
 (first entry)
 Barash SC,
 WPI; 2003-505530/47.
 Sequence 262 AA;
 WO2003055979-A2
 Unidentified
 11-MAR-2004
 10-JUL-2003,
 Ruben SM,
 ADG96897;
```

```
The invention relates to a novel isolated monoclonal antibody (mAb) ecomprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VL (light chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a
 cancer;
 Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 32.
 9
 9
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQCPQLLIYLGSNRA
 New anti-CA IX monoclonal antibody, useful for treating a tumor e.g., colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia or esophageal tumors.
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Сарв
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVBIK 112
 monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen; cytostatic; colorectal neoplasm; renal call carcinoma; cervical intraepithelial squamous neoplasia; cervical intraepithelial glandular neoplasia; oesophageal; breast gene therapy; murine; mouse; human; light chain variable domain.
 112
 Length 112;
 Score 547; DB 7; Length 11.
Pred. No. 6.4e-41;
Tref. 5; Indels
 2; Mismatches
 Ξ
 Claim 3; SEQ ID NO 32; 89pp; English
 Gallo
 ADP03892 standard; protein; 112 AA
 94.3%;
 02-DEC-2002; 2002WO-US038550.
 03-DEC-2001; 2001US-0337275P.
 Foltz I, Handa M,
 (first entry)
 Matches 105; Conservative
 transgenic mouse strain.
 WPI; 2003-523295/49.
 (ABGE-) ABGENIX INC.
 Query Match
Best Local Similarity
 Sequence 112 AA;
 WO2003048328-A2
 Unidentified
 29-JUL-2004
 12-JUN-2003.
 Gudas J,
 ADP03892;
 61
ADP03893
 g
 ઠ
 ઠે
```

ö

RESULT 10

1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA

94.5%; Score 548; DB 7; Length 262; 93.8%; Pred. No. 1.3e-40; ive 3; Mismatches 4; Indels

Best Local Similarity 93.8 Matches 105; Conservative

ઠ 요

Query Match

9

Gaps

.; 0

"complementarity determining region (CDR) 1"

Location/Qualifiers

(first entry)

"complementarity determining region

"complementarity determining

.102

/note= note=

. .62 23. .46 /note= "

5 <u>-</u>

```
Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer; angiogenesis; antibody.
 Kappa chain variable region of anti-Ang-2 antibody 526 kappa.
 11-OCT-2001; 2001US-0328604P.
 11-OCT-2002; 2002WO-US032613
 WPI; 2003-504963/47.
 (AMGE-) AMGEN INC
 WO2003030833-A2
 Homo sapiens.
 02-SEP-2003
 17-APR-2003
 Oliner JD;
 ABR55770;
 Query Match
 Region
 Region
 Region
 Best Loca
Matches
 g
 8
 셤
 ₽
 ö
 The present invention describes a human monoclonal antibody to parathyroid hormone related protein (PTHrP). The monoclonal antibody or lite fragments, following the stimulation of PTHrP has the following properties: (a) inhibits intracellular elevation of CAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypophosphateaemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human PTHRP monoclonal antibody clone protein sequence from the present
 9
 80
 Human; parathyroid hormone related protein; PTHrP; monoclonal antibody; hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain; farcture; cachexia; tooth disease; periodontal disease; gingiva; sepsis; systemic inflammatory response syndrome; SIRS; hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 A human monoclonal antibody to parathyroid hormone related protein. - useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone including metastasis, and pain.
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.
 ó
 94.1%; Score 546; DB 3; Length 239; 93.8%; Pred. No. 1.8e-40; ive 2; Mismatches 5; Indels
 /note= "possible Ala"
 Claim 31; Page 45-46; 88pp; Japanese.
 Location/Qualifiers
155
 AAY82615 standard; protein; 239 AA.
 98JP-00304793
 98JP-00188196
 98JP-00196729
 (first entry)
 NISB) JAPAN TOBACCO INC
 105; Conservative
 WPI; 2000-286723/25.
N-PSDB; AAA13925.
 Local Similarity
 Sequence 239 AA;
 Misc-difference
 JP2000080100-A
 12-OCT-1998;
 17-JUN-1998;
 26-JUN-1998;
 02-AUG-2000
 Homo sapiens
 21-MAR-2000
 invention
 21
 61
 Query Match
 Matches
셤
 ò
 g
```

```
ö
New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
 The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease, inflammatory disease, inflammatory disease, or psoriasis) in a mammal. The present sequence represents a kappa chain variable region of an anti-Ang-2
 9
 9
 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gарв
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 ö
 94.0%; Score 545; DB 6; Length 112; 93.8%; Pred. No. 9.7e-41; ive 2; Mismatches 5; Indels
 Claim 1; Page 93; 161pp; English.
 Conservative
 Local Similarity
es 105; Conserv
 Sequence 112 AA;
 61
 61
```

RESULT 12 **ABR55812** 

ABR55770 standard; protein; 112 AA

RESULT 11 ABR55770 ID ABR55

ò

thrombus; platelet adhesion inhibition; thrombotic thrombocytopenic purpura; platelet aggregation inhibition; idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;

thrombolytic; human

sapiens,

Synthetic

03-JUL-2003; 2003WO-US021304. 03-JUL-2002; 2002US-0394352P 18-SEP-2002; 2002US-0411694P

WO2004005890-A2.

15-JAN-2004

(UYPE-) UNIV PENNSYLVANIA.

WPI; 2004-142998/14.

Siegel DL;

N-PSDB; ADI22066

Anti-platelet autoantibody related light chain amino acid L43 SEQ:82. anti-platelet autoantibody; autoantibody; blood clotting inhibition;

(first entry)

22-APR-2004

ADI22119;

ADI22119 standard; protein; 112 AA.

ADI22119

```
The invention relates to a specific binding agent, which comprises at fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating cancers, inhibiting undesired angiogenesis, modulating or inhibiting disease. The example of activity modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease, inflammatory disease, or psoriasis) in amammal. The present sequence represents a kappa chain variable region of an anti-Ang-2.
 New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
 Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;
gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
 /note= "complementarity determining region (CDR) 2" 93. .102
/note= "complementarity determining region (CDR) 3"
 "complementarity determining region (CDR) 1"
 54. .62
/note= "complementarity determining region (CDR)
 Kappa chain variable region of anti-Ang-2 antibody FE-B7 kappa.
 Location/Qualifiers
ABR55812 standard; protein; 112 AA.
 Claim 1; Page 94; 161pp; English
 11-OCT-2002; 2002WO-US032613
 11-OCT-2001; 2001US-0328604P
10-OCT-2002; 2002US-00269805.
 (first entry)
 /note= "C
 angiogenesis; antibody.
 WPI; 2003-504963/47.
 (AMGE-) AMGEN INC.
 Sequence 112 AA;
 WO2003030833-A2.
 12-SEP-2003
 Homo sapiens
 17-APR-2003
 Oliner JD;
 ABR55812;
 antibody
 Region
 Region
 Region
```

```
The present invention describes a method (M1) for identifying an antiport platelet autoantibody (I) in a mammal. The autoantibody is detected by producing an antibody plage display library from B-lymphocytes obtained from the mammal, and screening the library from B-lymphocytes obtained from the mammal, and screening the library from B-lymphocytes obtained from the mammal, and screening the library to detect a phage that component, where the screening competitive can intact platelet using competitive cell-carriage panning the phage on intact platelet using competitive cell-carriage in a mammal having a thrombus or at risk of thrombus formation; (3) inhibiting (M2) blood clotting in a mammal having a thrombus or at risk of thrombus formation; (5) inhibiting (M5) platelet autoantibody with a platelet component; (6) inhibiting (M5) platelet autoantibody or its biologically active fragment with a contibuting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody, or its biologically active fragment with a contibuting (M9) platelet function; (11) inhibiting (M10) binding of an anti-platelet autoantibody with a platelet thrombocytopenic cut inhibiting defining platelet that specifically binds with an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody with a platelet. (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-platelet autoantibody with a platelet in a mammal; or a mammal of an anti-platelet activation compatibiling platelet cativation compatibiling platelet function compatibiling and mammal of a mammal or anti-platelet activation compatibiling and inhibiting platelet activation compatibility are interesting compatibility and (16) a kit for reversibly inhibiting platelet activation compatibility and inhibiting platelet activation compatibility are actived fragment that an anti-platelet activation compatibility and c
 platelet autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H4414 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagniant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (MG) and (M12) are useful for treating thromboty topenic purpura and idiopathic thrombocytopenic purpura and idiopathic thrombocytopenic conting. The present sequence is useful for inhibiting blood clotting. The present sequence is used in the exemplification of the
 Claim 12; SEQ ID NO 82; 232pp; English.
 clotting. The pres
present invention.
```

9

Gaps

ö

Score 544; DB 6; Length 112; Pred. No. 1.2e-40; 4; Mismatches 4; Indels

93.8%;

Matches 104; Conservative

Best Local Similarity

Query Match

1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60 

61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 112

61

g ઠ RESULT 13

```
angiogenesis; antibody.
 'note=
 WPI; 2003-504963/47.
 Query Match
Best Local Similarity
 present invention.
 (AMGE-) AMGEN INC.
 Sequence 112 AA;
 WO2003030833-A2
 11-OCT-2001;
10-OCT-2002;
 Homo sapiens.
 02-SEP-2003
 17-APR-2003
 Oliner JD;
 ABR55796;
 Region
 Region
 Region
 RESULT 15
 ABR55796
 $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
 8
 g
 ਨੇ
 The present invention describes a method (MI) for identifying an antipatelet autoantibody (I) in a mammal. The autoantibody is detected by producting an antibody plage display library from B-lymphocytes obtained from the mammal, and screening the library to detect a plage that comparises panning the phage on intact platelets using competitive cellomyries panning. Also described: (I) an autoantibody identified by (MI); (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3) inhibiting (M2) blood clotting in a mammal having a thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a mammal having a thrombus or at risk of thrombus formation (G) inhibiting (MS) platelet autoantibody with a platelet component; (M) thrombotic thrombocytopenic purpura in a mammal; (B) inhibiting (M3) platelet dension in a mammal; (B) inhibiting (M3) inhibiting (M3) platelet function; (1) inhibiting (M3) inhibiting (M3) platelet function; (1) inhibiting (M3) binding of an anti-platelet autoantibody, or its biologically active fragment with a platelet; (12) identifying (M1) a peptide that inhibite binding of an anti-platelet autoantibody with a platelet; (13) a peptide identified by the method of (12); (14) a peptide that specifically binds with an anti-
 ö
 9
 9
 1 DIVMTÓSPLSLPVTPGEPASISCRSSÓSLLHSNGYNYLDWYLQKPGOSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 Anti-platelet autoantibody related light chain amino,acid L46 SEQ:85.
 autoantibody; blood clotting inhibition;
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQSPPTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 thrombus; platelet adhesion inhibition;
thrombotic thrombocytopenic purpura; platelet aggregation inhibit
idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
thrombolytic; human.
 .
0
 Length 112;
 Score 544; DB 8; Length 11 Pred. No. 1.2e-40; 2; Mismatches 5; Indels
 Claim 12; SEQ ID NO 85; 232pp; English.
 ADI22122 standard; protein; 112 AA.
 03-JUL-2003; 2003WO-US021304.
 03-JUL-2002; 2002US-0394352P.
18-SEP-2002; 2002US-0411694P.
 93.8%;
 autoantibody;
 (first entry)
 (UYPE-) UNIV PENNSYLVANIA
 Best Local Similarity 93.8
Matches 105; Conservative
 WPI; 2004-142998/14.
N-PSDB; ADI22069.
 Sequence 112 AA;
 WO2004005890-A2.
 anti-platelet
 03-JUL-2002;
 sapiens
 22-APR-2004
 15-JAN-2004
 Siegel DL;
 Synthetic.
 ADI22122;
 Query.Match
 Homo
 RESULT 14
 × S
 g
 g
 ठ
```

```
platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood clotting, inhibiting platelet aggregation, inhibiting platelet function or inhibiting platelet activation comprising an amount of an anti-completed activation comprising an amount of an anti-completed autoantibody, or its biologically active fragment that specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or its fragment comprises an antigen binding region derived from an H44L4 anti-platelet autoantibody, the kit further comprising a peptide inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator and an instructions for use. (I) has haemostatic, anticoagulant and thrombolytic activities. The autoantibodies (I) are useful for diagnosing and for developing therapeutics for diseases mediated by autoantibody binding with platelet antigens. (M6) and (M12) are useful for treating thrombocytopenic purpura had (M3) are useful for inhibiting blood clotting. The present sequence is used in the exemplification of the
 ô
 New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful
 9
 9
 1 DIVMTÓSPLSLPVTPGEPASISCRSSQSLLHSNGNNYLDWYLQKPGQSPQLLIYLASNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic; gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
 Gaps
 ۳,
 ~
 -
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEPEDVGLYYCWQALQTPLIFGGGSKVEIK 112
 "complementarity determining region (CDR)
 (CDR)
 (CDR)
 .
0
 Kappa chain variable region of anti-Ang-2 antibody 553 kappa
 region
 /note= "complementarity determining region
 Length 112;
 5; Indels
 "complementarity determining
 Score 544; DB 8;
Pred. No. 1.2e-40;
3; Mismatches 5;
 Location/Qualifiers
 ¥.
 ABR55796 standard; protein; 112
 2001US-0328604P.
2002US-00269805.
 93.8%;
 11-OCT-2002; 2002WO-US032613
 (first entry)
 .102
 Matches 104; Conservative
 54. .62
 23. .40
/note= "
```

```
for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity, hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
```

Claim 1; Page 93; 161pp; English

The invention relates to a specific binding agent, which comprises at least one peptide selected from any of 62 peptides (ABR55769-830) or its fragment. The binding agents are antibodies that recognize and bind to angiopoietin-2 (Ang-2). The specific binding agent, particularly the antibody, is useful for inhibiting undesired angiogenesis, treating 2 activity, modulating vascular permeability or plasma leakage, or treating a disease (e.g. ocular neovascular disease, obesity, haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease, inflammatory disease, or psoriasis) in amammal. The present sequence represents a kappa chain variable region of an anti-Ang-2 

Sequence 112 AA;

Gaps ; Query Match
93.1%; Score 540; DB 6; Length 112;
Best Local Similarity 92.0%; Pred. No. 2.7e-40;
Matches 103; Conservative 4; Mismatches 5; Indels 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60

1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60

g

ઠે

ò

Search completed: November 16, 2005, 21:51:43 Job time : 64.2353 secs

with the time to the second

.

```
GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 16, 2005, 21:37:48 ; Search time 13.3824 Seconds

(without alignments)

805.260 Million cell updates/sec
```

(without alignments)
 805.260 Million cell updates/
Title:
 US-10-660-357A-38
Perfect score: 580
Sequence: 1 DIVMTQSPLSLPVIPGEPAS.......CMQALQIPLTFGGGTKVEIK 112

Sequence: 1 DIVMTQSPLSLPVIPGEPAS...
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

kappa chain - h
kappa chain - h
kappa chain V r
kappa chain V r
light chain V r
kappa chain V r
kappa chain P r chain - h chain - h chain V-I Fab Jel 1 chain V r chain pre chain V r Description 19 kappa 19 light 19 light 19 kappa SUMMARIES 838715 838715 838719 E27887 D29380 \$40371 \$03876 \$40319 \$40321 \$24681 \$24681 \$27887 \$40375 S58206 S58207 S26882 S40342 S40357 KZHUGM S40339 K2HUML S40372 K2HUTW S53750 PT0359 B34904 S40341 DB Query Match Length 92.8 92.8 90.7 89.6 86.4 86.4 84.5 84.0 881.0 880.3 880.2 880.2 779.8 779.8 779.7 779.7 88.4 548 538 538 538 538 538 526 510.5 490 487 478.5 478 Result Š.

Length 112;

DB 2;

94.5%; Score 548;

Query Match

F;16-95/Domain: immunoglobulin homology <IMM>

| Ig kappa chain V r |              | Ig kappa chain (mo |        | chain  | chain  | chair  | chair  | kappa chain | kappa chain | kappa chain | kappa chain | kappa  | kappa chair | Ig kappa chain V-I |
|--------------------|--------------|--------------------|--------|--------|--------|--------|--------|-------------|-------------|-------------|-------------|--------|-------------|--------------------|
| A31807             | 842611       | · PC4203           | PL0203 | C27887 | B31485 | B39276 | C34904 | S32189      | G34903      | A27887      | B30577      | S40340 | S26335      | K2HUFR             |
| 2.0                | N 60         | ~                  | 0      | ~      | 0      | 0      | ~      | 0           | ~           | 7           | 7           | 0      | 7           | н                  |
| 112                | 133          | 219                | 113    | 112    | 112    | 131    | 131    | 112         | 131         | 112         | 131         | 114    | 110         | 113                |
| 79.3               | 79.3         | 79.3               | 79.1   | 79.0   | 79.0   | 79.0   | 79.0   | 78.8        | 78.8        | 78.6        | 78.6        | 78.5   | 78.4        | 78.4               |
| 460                | 4 60<br>4 60 | 460                | 459    | 458    | 458    | 458    | 458    | 457         | 457         | 456         | 456         | 455.5  | 455         | 455                |
| 30                 | 35           | 33                 | 34     | 35     | 36     | 37     | 38     | 39          | 40          | 41          | 42          | 43     | 44          | 45                 |

| _    |  |
|------|--|
| Ę    |  |
| ~    |  |
| E SE |  |
| ◛    |  |
| ₽:   |  |
| ~    |  |
| U    |  |
| Ē    |  |
| ä    |  |
| ч    |  |
| ⋖    |  |
|      |  |

```
Ig light chain V region anti-F(ab')2 - human (fragment)
C)species: Homo sapiens (man)
C)Accession: S58206
R,Welschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitling, F submitted to the EMBL Data Library, July 1995
R,Welschon: Characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization of heavy and light chain immunoglobulin variable region characterization characterization of heavy and light chain immunoglobulin variable region characterization characterizatio
 ö
 9
 69
 Species: Homo sapiens (man)
Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 10 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHNNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 A/Accession: S40356
A/Status: preliminary; translation not shown
A/Molecule type: manA
A/Residues: 1-125 < KLIB-
A/Cross-references: EMBL:X72466; NID:g441400; PIDN:CAA51134.1; PID:g441401
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Reywords: heterotetramer; immunoglobulin
F;25-104/Domain: immunoglobulin homology < IMM>
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 C;Accession: S40356
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
 Gaps
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVBIK 112
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQVLQIPLTFGGGTKVEIK 121
 ö
 Length 125;
 4; Indels
 Score 550; DB 2;
Pred. No. 9.3e-46;
3; Mismatches 4.
 Query Match
Best Local Similarity 93.8%;
Matches 105; Conservative
Ig kappa chain - human
 61
 20
 RESULT 2
 셤
 ଚ
 ò
 요
```

```
14 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 73
 Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 Ig Kappa chain - human
C.Species: Homo sapiens (man)
C.Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 21 DIVMTÓSPLSLÞVTÞGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 C;Accession: S40357
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Fitle: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40357
A;Status: preliminary; translation not shown
 C'Accession: $40342

*Klein, R.; Jaenichen, R.; Zachau, H.G.

Bur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: $40312; MUID:94080891; PMID:8258341
 A;Cross-references: UNIPROT:QBNEKO; EMBL:X72452; NID:g441372; PID:g441373 (S.buperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;29-108/bomain: immunoglobulin homology <IMM>
 74 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPRTFGQGTKVEIK 125
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPWTFGQGTKVBIK 132
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 81 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPQTFGQGTKVBIK 132
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK
 Length 136;
 Length 135;
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;36-115/Domain: immunoglobulin homology <IMM>
 Ig kappa chain precursor V-II region (GM607) - human (fragment)
C;Species: Homo sapiens (man)
 Query Match 92.8%; Score 538; DB 2; Length 13
Best Local Similarity 92.9%; Pred. No. 1.4e-44;
Matches 104; Conservative 2; Mismatches 6; Indels
 6; Indels
 Score 538; DB 2;
Pred. No. 1.4e-44;
 Query Match
92.8%; Score 538; DE
Best Local Similarity 92.9%; Pred. No. 1.4e
Matches 104; Conservative 2; Mismatches
 A; Cross-references: UNIPROT: Q8NEK0; EMBL: X72467
 A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-135 <KLE>
 A; Molecule type: mRNA
A; Residues: 1-136 <KLE>
 A;Accession: S40342
 81
 61
 RESULT 7
 RESULT 6
 K2HUGM
 g
 8
 요
 8
 셤
 g
 8
 ò
 g
 δ
 RESULT 3
S58207
Graph thain V region anti-F(ab')2 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C;Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C;Accession: S58207
R;Welstend to the EMBL Data Library, July 1995
A;Description: Characterization of heavy and light chain immunoglobulin variable region
A;Reference number: S58207
A;Status; preliminary
 ö
 ö
 ö
 9
 9
 21 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 80
 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIYLGSNRA 60
 9
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 RESULT 4
S26882
[19 kappa chain V region (V607) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: S26882
R;Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A;Title: Megabase inversions in the human genome as physiological events.
A;Accession: S26882
A;Status: Preliminary; translation not shown
A;Mesedues: 1-132 <WEI>
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 DIVMTQSPLSLPUTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 A;Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C;Genetics:
C;Ghritcons:
A;Introns: 17:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
 A;Residues: 1-112 <WEL-
A;Residues: 1-112 <WEL-
A;Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-95/Domain: immunoglobulin homology <NMM>
 Gaps
 Gaps
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPWTFGQGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 .
 .
 ;
0
 Score 538; DB 2; Length 132;
Pred. No. 1.4e-44;
2; Mismatches 6; Indels
 92.8%; Score 538; DB 2; Length 112; 92.9%; Pred. No. 1.2e-44;
 6; Indels
 Indels
 Pred. No. 1.3e-45;
2; Mismatches 5;
 2; Mismatches
 F;36-115/Domain: immunoglobulin homology <IMM>
 Query Match
Best Local Similarity 92.9%;
Matches 104; Conservative
 93.8%;
 Best Local Similarity 92.9
Matches 104; Conservative
 105; Conservative
Best Local Similarity
Matches 105; Conserv
 A; Molecule type: mRNA
 61
 61
 Query Match
 g
 ð
 셤
 ò
 g
 셤
 ઠે
 g
 ò
 ò
```

ö

0; Gaps

ö

0; Gaps

```
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01887
R;Dreyer, W.J.; Gray, W.R.; Hood, L.
R;Dreyer, W.J.; Gray, W.R.; Hood, L.
A;Title: The genetic, molecular, and cellular basis of antibody formation: some facts and A;Title: The genetic, molecular, and cellular basis of antibody formation: some facts and A;Title: The genetic, molecular, and cellular basis of antibody formation: some facts and A;Accession: A01887
A;Accession: A01887
A;Accession: A01887
A;Accession: U112 cARE>
A;Cross-references: UNIPROT:P01616
A;Cross-references: UNIPROT:P01616
C;Comment: This is a Bence Jones protein.
 A)Cross-references: GDB:136265
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp complex: An immunoglobulin heterotetramer subunit some cases, such as IgA and IgM, the subunits associate into last c;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
 C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40372
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
 Ig kappa chain V-II region (Tew) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 21 DIVMTQSPLSLPVTPGESASFSCKTSQSLLHSNGHNYLDWYLQKPGQSPQLLIYLGSTRA
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 60 SGVPNRFSGSGSGTBFTLKISRVZAZBVGVYYCMQALQTPLTFGGGTNVEIK 111
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVBI 111
 Length 112;
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMOPLOTPYTFGOGTKLEI
 Length 131;
 Cross-references: EMBL:X72482; NID:g441432; PIDN:CAA51150.1; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
 Indels
 ģ
 DB 1;
 88.4%; Score 512.5; DB 1
83.9%; Pred. No. 3.2e-42;
tive 14; Mismatches 3
 DB 2;
 87.1%; Score 505; DB 2;
86.5%; Pred. No. 2e-41;
iive 6; Mismatches
 F;36-115/Domain: immunoglobulin homology < IMM>
 F_16-94/{\rm Domain}: immunoglobulin homology <1MM>F_123-92/{\rm Disulfide} bonds: #status predicted
 A,Accession: S40372
A,Status: preliminary, translation not shown
A,Molecule type: mRNA
 Ig kappa chain V-J region - human
 94; Conservative
 Best Local Similarity 86.5
Matches 96; Conservative
 Best Local Similarity
 A; Residues: 1-131 < KLE>
 A; Gene: GDB: IGKV2
 Query Match
 Query Match
 :Genetics:
 RESULT 11
KZHUTW
 Matches
 S40372
 ઠે
 d
 ò
 d
 ે
 유
 Š
 요
 A;Cross-references..GDB:136265
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>F;1-1/Product: Ig kappa chain VII region (GM607) #status predicted <MAT>F;20-99/Domain: immunoglobulin homology <IMM>F;20-99/Domain: immunoglobulin homology <IMM>F;27-97/Disulfide bonds: #status predicted
 to light-chain diversity.
 ö
 9
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 75
 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 64
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004 C;Accession: A01889; B24452
R;Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Mature 309, 73-76, 1984
A;Title: Contribution of human V-kappall germ-line genes to light-chain dive A;Accession: A01889; MUID:84191506; PMID:6325927
A;Accession: A01889
A;Molecule type: mRNA
A;Residues: 1-117 <-KLO
A;Coss-references: UNIPROT:P06309
A;Coss-references: UNIPROT:P06309
A;Coss-references: UNIPROT:P06309
A;Cost: the sequence was determined from the differentiated gene
 Grappa chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40339
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40339
A;Status: preliminary; translation not shown
 A; Molecule type: mRNA
A; Residues: 1-126 «KLE>
A; Residues: 1-126 «KLE>
A; Cross-references: EMBL: X72449; NID: g441366; PIDN: CAAS1117.1; PID: g441367
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer, immunoglobulin
F; 31-110/Domain: immunoglobulin homology «IMM»
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 16 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHINGYNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 Gaps
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFGQGTKVEIK 116
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCMQALQ-PWTFGQGTKVEIK 126
 1,
 .
0
 Query Match 89.6%; Score 519.5; DB 2; Length 126; Best Local Similarity 91.1%; Pred. No. 7.9e-43; Matches 102; Conservative 3; Mismatches 6; Indels 1
 Score 526; DB 1; Length 117;
Pred. No. 1.7e-43;
2; Mismatches 8; Indels
 KZHUML
Ig kappa chain V-II region (Mil) - human (tentative sequence)
C;Species: Homo sapiens (man)
 Query Match 90.7%;
Best Local Similarity 91.1%;
Matches 102; Conservative
 A; Gene: GDB: IGKV2
 61
 94
 r)
 61
 C, Genetics
```

RESULT 8 S40339

a

g

ઠે

ð

ö

Gaps

ö

PID:9441433

၀

131

RESULT 9

g

8

d

ઢ

-

Gaps

1;

```
Cipacession: S03876
Riferri, G.; Stoppini, M.; Iadarola, P.; Bellotti, V.; Merlini, G.
Biochim. Biophys. Acta 995, 103-108, 1989
Airlie: Structural characterization of kappa II Inc, a new amyloid immunoglobulin. A; Reference number: S03876; MUID:89194238; PMID:2495028
Aircession: S03876; MUID:89194238; PMID:2495028
Airocession: S03876; MUID:89194238; PMID:2495028
Airolecule type: protein
A; Residues: 1-124 *FER>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
 C'Species: Homo sapiens (man)
C'Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C'Accession: S40321
R'Klein, R.; Jaenichen, R.; Zachau, H.G.
 Ig kappa chain V-II region (Inc) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
 11 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYDYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVITQSPLSLPVTPGEPASISCKSSQSLMHSSGDNYLDWYLQKPGQSPQIVIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 A,Cross-references: EMBL:X72429; NID:g441326; PIDN:CAA51097.1; PID:g441327 C,Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDTFSGSGSGTDFTLISSVGAEDVGVYYCMQALQTPWTFGQGTKVGIK 112
 ö
 ö
 61 PDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPTTFGQGTKLEIK 109
 Length 124;
 Length 123;
 Indels
 Indels
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIP 100
 4
 10;
 84.0%; Score 487; DB 2;
94.0%; Pred. No. 1e-39;
 Query Match
Best Local Similarity 83.0%; Pred. No. 5.2e-40;
Matches 93; Conservative 9; Mismatches 10.
 2; Mismatches
 ;26-105/Domain: immunoglobulin homology <IMM>
 Ig kappa chain V region - human
 94; Conservative
 Query Match
Best Local Similarity
 Ig kappa chain - human
 g
 용
 g
 임
 ò
 ò
 셤
 ò
 ò
C;Accession: A90370; A92764; A01888
R;Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N.
Biochemistry 12, 3763-3780, 1973
A;Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary amylc A;Reference number: A90370; MUID: 74148480; PMID: 4556149
A;Contents: Bence Jones protein Tew
A;Accession: A90370
A;Molecule type: protein
A;Residues: 1-113 <a href="https://documber.no.number.num
 A; Cross-references: GDB:136265
A; Map position: 2p12-2p12
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keyworfs: amyloid; heterotetramer; immunoglobulin
F; 16-95/Domain: immunoglobulin homology < IMM>
F; 23-93/Disulfide bonds: #status predicted
 RESULT 12
$40371
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: 840371
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Fitle: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40371
A;Accession: $40371
A;Accession: $40371
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-121 «KLE>
A;Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroretramer; immunoglobulin
F;13-92/Domain: immunoglobulin homology <IMM>
 ö
 ö
 9
 63
 9
 9
 1 MTQSPLSLPVTPGEPASISCRSSQSLLYSTGYNYLDWYLQKPGKSPQLLIYLGSKRASGV
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 4 MTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRASGV
 Gaps
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMZALQAPITFGQGTRLEIK 112
 ö
 .;
0
 64 PDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 86.4%; Score 501; DB 1; Length 113; 84.8%; Pred. No. 4.1e-41; rive 10; Mismatches 7; Indels
 Length 121;
 Query Match

86.4%; Score 501; DB 2; Length 12
Best Local Similarity 88.1%; Pred. No. 4.5e-41;
Matches 96; Conservative 4; Mismatches 9; Indels
 95; Conservative
 Local Similarity
 Query Match
```

g ઠે g

ô 9

Gaps

70

유

ò

ð

ö

Gaps

09

```
Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: 840312; MUID:94080891; PMID:8258341

A;Accession: S40321

A;Status: preliminary: translation not shown

A;Molecule type: mRNA

A;Residues: 1-130 «KLE>

A;Cross-references: EmBL:X72431

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

C;Keywords: heterotetramer; immuno
```

Search completed: November 16, 2005, 22:04:10 Job time : 13.3824 secs

sand the sand of the sand

.

.

```
November 16, 2005, 21:36:13; Search time 62.7941 Seconds (without alignments) 913.348 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 OM protein - protein search, using sw model
 US-10-660-357A-38
 Copyright
 580
 Perfect score:
 Run on:
```

1 DIVMTQSPLSLPVIPGEPAS.......CMQALQIPLTFGGGTKVEIK 112 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| SUMMAKIES |        | tion            | Q8nek0 homo sapien | P06309 homo | P01616 homo | Q6pih6 homo | P01617 homo | P01614 homo | 0652q7 mus s    | P01615 homo | P01631 mus n |            | Q65zc0 mus musculu |        |        | P01630 mus m |            | Q9u180 homo sapien | mus m  | JSE P01629 mus musculu |            | P01626   |         | MAN P06314 homo sapien | P06313 homo | P01625 homo | Q6kb05 mus musculu | Q9ul78 homo sapien | P01627 mus m | P01620 homo | omod 6vm690 | P01622 homo |
|-----------|--------|-----------------|--------------------|-------------|-------------|-------------|-------------|-------------|-----------------|-------------|--------------|------------|--------------------|--------|--------|--------------|------------|--------------------|--------|------------------------|------------|----------|---------|------------------------|-------------|-------------|--------------------|--------------------|--------------|-------------|-------------|-------------|
| MWOS.     |        | ΩI              | QBNEKO             | KV2E HUMAN  | KV2C_HU     | Q6PIH6      | KV2D HUMAN  | KV2A HU     | 0652 <u>0</u> 7 | KV2B HUP    | KV2G MOUSE   | KV2F HUMAN | 0652 <u>C</u> 0    | Q6P491 | QBTCD0 | KV2F MOUSE   | KV2E MOUSE | OBULEO<br>OBULEO   | Q6LEM8 | KV2D MOUSE             | KV2C MOUSE | KV2A MOI | KV1 CAN | KV4C HUMAN             | KV4B HUMAN  | KV4A HUMAN  | Q6KB05             | Q9UL78             | KV2B MOUSE   | KV3B HUMAN  | Q6GMV9      | KV3D HUMAN  |
|           |        | DB              | 8                  |             |             |             | ٦           |             |                 | -           | -            | Н          |                    | ~      |        | Н            | Н          | 7                  | ~      |                        | ~          | -        | -       | ٦                      | Н           |             | 7                  | •                  |              | <b>н</b>    |             | -           |
|           |        | Match Length DB | 239                | 117         | 112         | 240         | 113         | 115         | 248             | 113         | 113          | 133        | 219                | 239    | 239    | 113          | 113        | 114                | 112    | 112                    | 113        | 112      | 108     | 134                    | 133         | 114         | 255                | 109                | 120          | 109         | 235         | 109         |
| æ         | Query  | Match           | 90.9               | 90.7        | 88.4        | 96.6        | 86.4        | 81.8        | 78.6            | 78.4        | 78.4         | 9.92       | 9.9/               | 75.9   | 75.7   | 74.0         | 73.6       | 73.5               |        | 72.4                   | 70.0       | 69.7     | 68.5    | 66.8                   | 66.4        | 65.3        | 64.9               | 64.5               | 64.0         | •           |             | 62.8        |
|           |        | Score           | 527                | 526         | 512.5       | 502.5       | 501         | 474.5       | 456             | 455         | 455          | 444        | 444                | 440    | 439    | 429          | 427        | 426.5              | 424    | 420                    | 406        | 404      | 397.5   | 387.5                  | 385         | 378.5       | 376.5              | 374                | 371          | 365         | 365         | 364         |
|           | Result | No.             | 1                  | 7           | ٣           | 4           | Ŋ           | φ           | 7               | 60          | o.           | 10         | 11                 | 12     | 13     | 14           | 15         | 16                 | 17     | 18                     | 19         | 20       | 21      | 22                     | 23          | 24          | 25                 | 56                 | 27           | 28          |             | 30          |

| Q920e9 mus musculu | P18135 homo sapien | P01670 mus musculu | P01673 mus musculu | P18136 homo sapien | P01662 mus musculu | P01671 mus musculu | P01661 mus musculu | P01623 homo sapien | P83593 homo sapien | P01663 mus musculu | P01664 mus musculu | P01656 mus musculu | P01666 mus musculu |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |
|                    | Z,                 | SE                 | 38                 | A.                 | 38                 | 38                 | 38                 | . 3                | 7                  | 38                 | SE                 | 38                 | SE                 |
| Q920E9             | KV3L HUM           | KV3R MOU           | KV3U MOU           | KV3M HUM           | KV3J MOU!          | KV3S MOU           | KV3I MOUR          | KV3E HUM           | KV4D HUM           | KV3K MOUS          | KV3L_MOU           | KV3C_MOU           | KV3N_MOU           |
| ~                  | -                  | -                  | ч                  | Н                  | -                  | ч                  | -                  | -                  | -1                 | -                  | _                  | ч                  | ч                  |
| 111                | 129                | 111                | 111                | 129                | 111                | 111                | 131                | 109                | 109                | 111                | 111                | 111                | 111                |
| 62.0               | 61.9               | 61.8               | 61.6               | 61.6               | 61.5               | 61.5               | 61.3               | 61.2               | 6.09               | 60.9               | 60.9               | 8.09               | 8.09               |
|                    | _                  | 'n                 | s.                 | 357                | 9.5                | 36.5               | 55.5               | 355                | 53.5               | 53.5               | 53.5               | 52.5               | 52.5               |
| 359.5              | 35                 | 358                | 357                |                    | 35                 | ç                  | m                  |                    | m                  | m                  | m                  | m                  | ñ                  |

## ALIGNMENTS

```
RECURENCE FROM N.A.

RECURENCE FROM N.A.

TISSUE-Prostate;

RA TISSUE-Prostate;

RA MIDINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;

RA MIDINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;

RA Altechul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

RA Altechul S.F., Jordan H., Moore I., Max S.I., Wang J., Haieh N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Maramson R.D., Mullahy S.J.,

Robards S., McEwan P.J., McKernan K.J., Matek J.A., Gunarathe P.H.,

RA Boask S.A., McEwa P.J., McKernan K.J., Lu X., Gibbs R.A.,

RA Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Grands S.J., Marra M.A.,

RA Marian M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA "Generation and initial analysis of more than 15,000 full-length human
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 the EMBL/GenBank/DDBJ databases.
 01-00T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 239 AA.
 PRT;
 PIR, $22638; $23638.

PIR; $34091; $34091.

PIR; $40342; $40342.

PIR; $40357; $40342.

HSSP; PO1834; 1172.

InterPro; IPR007110; Ig-like.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003596; Ig_WC.

PERM; $7007654; C1-set; I.

SWART; $8004406; IGY; I.

PROSITE; PS50835; IG_LIKE; 2.
 Strausberg R.;
Submitted (JUN-2002) to the
EMBL; BC030814; AAH30814.1;
 PRELIMINARY;
 Hypothetical protein.
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 IISSUE=Prostate;
 NCBI_TaxID=9606;
 QBNEKO
RESULT 1
 QBNEKO
```

```
102; Conservative
 NCBI_TaxID=9606;
 KV2C HUMAN P01616;
 NON TER
SEQUENCE
 61
 65
 SEQUENCE
 Query Match
 беріне;
 DOMAIN
 DOMAIN
 9ні де
 DOMAIN
 DOMAIN
 HUMAN
Matches
 RESULT 4
 RESULT
 9ні 490
 δ
 à
 셤
 ò
 g
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ;
0
 9
 21 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRA 80
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 81 SGVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQGLQTPQTFGQGTKVEIK 132
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SEQUENCE FROM N.A.
MEDILIES-84191506; PubMed-6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
 ö
 Ig kappa chain V-II region GM607.
 Length 117;
 Length 239;
 Complementarity-determining-1.
 Complementarity-determining-2
 Complementarity-determining-3
 90.9%; Score 527; DB 2; Length 23 91.1%; Pred. No. 5.8e-47; ive 3; Mismatches 7; Indels
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human)
 12664 MW; 92C57DC719E558B1 CRC64;
 Hypothetical protein.
SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;
 Score 526; DB 1;
Pred. No. 3.1e-47;
 117 AA
 By similarity.
 GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; Ig-like.
 PS00290; IG MHC; UNKNOWN 1
 EMBL; Z00009; -; NOT ANNOTATED CDS.
PIR; A01889; K2HUGM.
 Pfam, PF00047, ig; 1. —
SMARY; SM0406; IGv; 1. —
PROSITE, PS50835; IG LIKE; 1.
Immunoglobulin V regIon; Signal.
 90.7%;
91.1%;
 Best_Local Similarity 91.1
Matches 102; Conservative
 STANDARD;
 Nature 309:73-76(1984).
 43
58
65
97
106
 27
117
117 AA;
 HSSP; Q99M37; 1191
 NCBI_TaxID=9606;
 KV2E HUMAN
 DOMAIN
DISULFID
 NON TER
SEQUENCE
 diversity
 Query Match
 Immunoglo
NON TER
SIGNAL
 PROSITE;
 Query Match
 DOMAIN
DOMAIN
DOMAIN
 DOMAIN
 DOMAIN
 DDT THE LETT THE PART OF THE P
 SW
 ઠે
 셤
 ò
 셤
```

Best Local Similarity

```
ä
ō
 59
 60
 64
 1 DIVLTQSPLSLPVTPGEPASISCRSSQNLLZSBG-BYLDWYLZKPGZSPZLLIYLGSNRA
 5 DIVMTOSPLSLPVTPGEPASISCRSSOSLLHSNGYNYLDWYLOKPQOSPQLLIYLGSNRA
 1 DIVMTOSPLSLPVIPGEPASISCRSSOSLLQSNGNNYLDWYLQKPGOSPOLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Dreyer W.J., Gray W.R., Hood L.E.;
"The genetic, molecular, and cellular basis of antibody formation:
some facts and a unifying hypothesis.";
clod Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
 Gaps
0; Gaps
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFGQGTKVEIK 116
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 60 SGVPNRFSGSGSGTBFTLKISRVZAZBVGVYYCMQALQTPLTFGGGTNVEIK 111
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 ;
 Length 112;
 Pramework-1.
Complementarity-determining-1.
Framework-2.
 Complementarity-determining-2.
 Complementarity-determining-3.
 Indels
8; Indels
 12055 MW; E5B22E2FA7ABE481 CRC64;
 Last sequence update)
Last annotation update)
 88.4%; Score 512.5; DB 1;
83.9%; Pred. No. 7.7e-46;
iive 14; Mismatches 3;
 PIR; A01887; K2HUML.
HSSP; Q99M37; I191.
InterPro; IPR007110; Ig-like.
InterPro; IPR003156; Ig-v.
Pfam; PF00047; ig; 1.
PRORITE; PSS0835; IGv; 1.
PROSITE; PSS0835; IG LIKE; 1.
Bence-Jones protein; Direct protein sequencing;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
 240 AA.
 Æ
 By similarity.
2; Mismatches
 Framework-3
 Framework-4
 Created)
 g kappa chain V-II region MIL.
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypochetical protein. Homo sapiens (Human).
 Local Similarity 83.9
les 94; Conservative
 PRELIMINARY;
 STANDARD;
 [mmunoglobulin V region]
 23
38
53
60
60
101
111
 Homo sapiens (Human).
 112 1
112 AA;
 DE DIT DE OS
```

m

```
marker.
 NON TER
SEQUENCE
 SEQUENCE
 DISULFID
 DOMAIN
DOMAIN
DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 RESULT 6
KV2A_HUMAN
 Matches
 ద
 ò
 셤
 Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
A plokins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Frange C.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Frange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Makek J.A., Ghabararne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Dones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
 7
 9
 80
 DIVMAQSPLSLSVTPGEPASISCRSSQSLLHSNGYNYFDWYLQKPGQSPQLLIYWGSNRA
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQI-PLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPYTFGQGTKLEIK 133
 05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-II region TEW.
Ig homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 Score 502.5; DB 2; Length 240; Pred. No. 2.2e-44;
 10; Indels
 Strausberg^{R.;}
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
 113 AA
 (Rel. 01, Created)
(Rel. 01, Last sequence update)
 3; Mismatches
 InterPro; IPR00359; IG.
InterPro; IPR00359; IG.
InterPro; IPR00359; IG.
InterPro; IPR003596; IG_MHC.
InterPro; IPR003596; IG_MHC.
InterPro; IPR003596; IG_W.
Pfam; PF07654; C1-set; I.
SWART; SW00409; IG; 2.
SWART; SW00406; IG', I.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00250; IG_MHC; UNKNOWN_I.
 86.6%;
 EMBL; BC034142; AAH34142.1;
HSSP; P01837; 1KB5.
 and mouse cDNA sequences."
 99, Conservative
 STANDARD;
 Hypothetical protein
 SEQUENCE FROM N.A.
TISSUE=Lung;
 Local Similarity
 FROM N.A.
 NCBI TaxID=9606;
 NCBI_TaxID=9606;
 21-JUL-1986
21-JUL-1986
 KV2D HUMAN
P01617;
 SEOUENCE
 Query Match
 RESULT 5
KV2D HUMAN
1D KV2D HU
1D KV2D HU
1D 21-JUL
1D 21-JUL
1D 10-JUL
1D 1
 Matches
 ò
 음
 ð
 g
```

```
1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 MEDILINE-7166688, CALLILLE AND ADDRESS AND
 Gaps
 õ
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N., "Amino acid sequence of a kappa Bence Jones protein from a case
 ..
0
 Complementarity-determining-1.
 Complementarity-determining-3.
Framework-4.
 Length 113;
 Complementarity-determining-2.
 86.4%; Score 501; DB 1; Length 11.84.8%; Pred. No. 1.3e-44;
 Pfam; PF00047; ig; i. SMART; SM00406; IGv; l. PROSITE; PS50835; IG LIKE; l. Amyloid; Bence-Jones protein; Direct protein sequencing;
 12316 MW; 0C3C38F81F1843CA CRC64;
 KV2A_HUMAN STANDARD; PRT, 115 AA. P01614; 21-JUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
 By similarity.
 Framework-3.
 Framework-1.
 Framework-2
 SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 HSSP, Q99M37, 1191.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; Ig_v.
 MEDLINE=68242259; PubMed=5586923;
Hilschmann N.;
PubMed=4596149;
 Ig kappa chain V-II region Cum.
Homo sapiens (Human).
 primary amyloidosis.";
Biochemistry 12:3763-3780(1973)
 95; Conservative
 23
39
54
61
112
112
113
 Immunoglobulin V region
DOMAIN 1 23
 PIR; A90370; K2HUTW.
HSSP; Q99M37; 1191.
 113 AA;
 Query Match
Best Local Similarity
MEDLINE=74148480;
 NCBI_TaxID=9606;
```

ô

0; Gaps

9

```
1 DIVMTOSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Biochemistry 15:3829-3833(1976).
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVBAEDLGVYYCPQGSHVPFTFGSGTKLEIK 247
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 -I. MISCELLANBOUS: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.

PIR, A01886, KZHUFR.

HSSP, Q99M37; I191.

GO, GO:0005576, C:extracellular; NAS.

GO, GO:0005826, P:antigen binding; NAS.

GO, GO:0005825, P:immune response; NAS.

InterPro; IPR00110; Ig-like.

InterPro; IPR00110; Ig-like.

Pfam; PP00047; Ig-l.
 Match 78.4%; Score 455; DB 1; Length 113; Local Similarity 75.0%; Pred. No. 8.3e-40; es 84; Conservative 13; Mismatches 15; Indels
 Complementarity-determining-1.
 Complementarity-determining-2.
 Framework-3.
Complementarity-determining-3.
15; Indels
 12660 MW; OCODA39E46DB96BE CRC64;
 Immunoglobulin V region.
 21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig kappa chain V-II region FR. Home sapiens (Human).
85; Conservative 12; Mismatches
 FYZG_MOUSE STANDARD; PRT; 113 AA P01631; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update)
 Ą
 By similarity.
 Framework-1.
 Framework-2.
 Framework-4
 SEQUENCE.
MEDLINE=76253627; PubMed=821524;
 21-JUL-1986 (Rel. 01, Created)
 SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Im
 STANDARD;
 23
39
54
61
102
112
113
 113 AA;
 NCBI_TaxID=9606;
 KV2B HUMAN P01615;
 196
 DISULFID
 SEQUENCE
 Query Match
 KV2G MOUSE
ID KV2G MC
AC P01631;
DT 21-JUL-
DT 21-JUL-
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 KV2B_HUMAN
 Matches
 RESULT 9
 셤
 ₽
 셤
 8
 ઠે
 g
 à
 g
 Hilschmann N.;

Hilschmann N.;

Wholecular basis of antibody formation.";

Lautuwiseanschaften 56:195-25(1969).

Lautuwiseanschaften 56:195-25(1969).

C. -! MISCELLANEOUS: The C region of this chain has the INV (3) marker.

J. MISCELLANEOUS: This is a Bence-Jones protein.

DR FIR B916-39; KRHUCK.

BR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR00110; Ig_1ke.

DR FIRE PROSITE; PS50835; IG_LIKE; 1.

ENART; SW00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region.

MAN Immunoglobulin V region.

MAN Immunoglobulin V region.
 29
 61
 MEDLINE=92020904; PubMed=1924323;

A Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;

BSI(FV) PESSRDEL, a single-chain immunotoxin that causes complete

regression of a human carcinoma in mice.,

Proc. Nacl. Acad. Sci. U.S.A. 88:8616-8620(1991).

E EMBL; S57990; ABB19971.2; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR00359; Ig.

R InterPro; IPR00359; Ig.

R Pfam; PF00047; Ig; 2.

SWART; SW00409; IG; 2.

SWART; SW0066; IGv; 2.

R PROSITE; PS50835; IG LIKE; 2.

R PROSITE; PS50835; IG LIKE; 2.
 DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSGDGNTYLNWYLQKAGQSPQLLIYTLSYR
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQS-NGNNYLDWYLQKPGQSPQLLIYLGSNR
 Gaps
complete amino acid sequence of Bence Jones protein Cum (kappa-
 60 ASGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 62 ASGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCMQRLEIPYTFGQGTKLEIR 114
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10095;
 1;
 Score 474.5; DB 1; Length 115;
Pred. No. 7.7e-42;
9; Mismatches 10; Indels 1
 Length 248;
 26634 MW; 7A3759B43E570950 CRC64;
 115 AA; 12676 MW; 59E9F90A379569EC CRC64;
 Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967)
 Last sequence update)
Last annotation update)
 Score 456; DB 2;
Pred. No. 1.7e-39;
 248
 Created)
 PRT;
 [2]
REVISIONS TO 50; 52; 96 AND 97.
MEDLINE=70063440; PubMed=4188189;
 78.6%;
 Query Match 81.8%;
Best Local Similarity 82.3%;
Matches 93; Conservative
 25-0CT-2004 (TrEMBLrel. 28,
25-0CT-2004 (TrEMBLrel. 28,
25-0CT-2004 (TrEMBLrel. 28,
33 (FV) - PE40 (Fragment).
Name=B3 (FV) - PE40;
 PRELIMINARY;
 248 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NON TER
SEQUENCE
 DISULFID
NON TER
SEQUENCE
 Q652Q7
Q652Q7;
```

g ò a

ò

Mus sp

RESULT 7
065207
065207
07 0652
07 0652
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0
07 25-0

ö

0; Gaps

```
DISULFID
NON TER
SEQUENCE
 Query Match
Best Local
 CHAIN
 DOMAIN
 SIGNAL
 DOMAIN
 DOMAIN
 DOMAIN
 Q652C0
 RESULT 11
Q65ZC0
 g
 8
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
 Novotny J., Margolies M.N.;

"Amino acid sequence of the light chain variable region from a mouse arti-digoxin Mybridoma antibody.",

Biochemistry 22:1153-1158 (1981).

-!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma protein that binds digoxin.

PIR; A01914; KVM256.

R HSSP; Q99M37; 1191.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.

R RSP; Q99M37; 1191.

R InterPro; IPR0047; 19; 1.

R PFOM PEAM; PRO040; 19; 1.

R PROSITE; PS50835; IG_LIKE; 1.

R PROSITE; PS50835; IG_LIKE; 1.
 9
 DIVMIQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.; "Human immunoglobulin kappa light chain genes of subgroups II and
 Length 113;
 Framework-1.
Complementarity-determining-1.
Framework-2.
 Complementarity-determining-2.
Framework-3.
 Complementarity-determining-3
 14; Indels
 12273 MW; F9F39CE949A84C2A CRC64;
 78.4%; Score 455; DB 1; 77.7%; Pred. No. 8.3e-40; ive 11; Mismatches 14;
 Ig kappa chain V-II region RPMI 6410 precursor. Homo sapiens (Human).
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-II region 26-10.
Mus musculus (Mouse).
 133 AA
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update
 By similarity.
 Framework-4.
 Nucleic Acids Res. 13:6499-6513(1985).
 SEQUENCE FROM N.A.
MEDLINE=86041852; PubMed=2997711;
 MEDLINE=83178921; PubMed=6404298;
 87; Conservative
 STANDARD;
 Monoclonal antibody.
 113 AA;
 Local Similarity
 NCBI_TaxID=10090;
 NCBI_TaxID=9606;
 STRAIN=A/J;
 KV2F HUMAN P06310;
 DOMAIN
DISULFID
 NON TER
SEQUENCE
 Query Match
 SEQUENCE
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 셤
 g
 ò
```

```
ö
 STRAINE-Balb/c; TISSUE-Spleen;

MEDLINE-95319505; PubMed-9768802;

Kipp B., Schlaak M., Becker W.M.;

Kipp B., Schlaak M., Becker W.M.;

Cloning and expression of a recombinant mouse Fab-fragment

recognizing a defined linear epitope of Chironomus thummi major

T allergen Chi t I.,

Int. Arch. Allergy Immunol. 110:348-353(1996).

R EMBL; Z37499; CAA85724.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.

R InterPro; IPR003506; Ig.

R InterPro; IPR003506; Ig.

R Pfam; PF07654; C1-8et; I.
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 21 DVVWTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRD 80
 0; Gaps
 Ig kappa chain V-II region RPMI 6410. Framework-1.
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Length 133;
 Complementarity-determining-1.
 Complementarity-determining-2.
 Complementarity-determining-3.
 16; Indels
 14707 MW; 513CCAF3673009EB CRC64;
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 76.6%; Score 444; DB 1;
76.8%; Pred. No. 1.4e-38;
tive 10; Mismatches 16;
 By similarity.
 EMBL, 200020; CAA77315.1; -.
PTR, AOLB90; KZHURP.
HSSP; Q99M37; 1191.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
 Framework-4.
 Framework-3.
 Kappa light chain C region (Fragment).
 SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
 86; Conservative
 PRELIMINARY;
 133
59
74
113
113
113
113
 SMART; SM00409; IG; 2.
SMART; SM00407; IGC1;
 Pfam; PF00047; ig; 2.
 Pfam; PF00047; ig; 1.
 133 1
133 AA;
 Similarity
 NCBI_TaxID=10090;
 SEQUENCE FROM N.A
```

ö

```
01-JUN-2002
01-JUN-2002
 TISSUE=Lung
 QSTCD0
 RESULT 13
Q8TCD0
 SAN
 g
 ò
 MEDLINE=22188157; PubMed=12477912; DOI=10.1073/pnas.242603899;
A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagner L., Shaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
B chartchenko L., Marusina B., Branddo M.F., Casavant T.L., Scheetz T.E.,
B connecein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A marka M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A marka M.J., Marka M.J.,
A marka M.J., Shalska U., Smailus D.E., Schnerch A., Schein human
 9
 9
 1 DIVMTOSPLSLPVIPGEPASISCRSSQSLLOSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 Length 219;
 Query Match 76.6%; Score 444; DB 2; Length 21 Best Local Similarity 75.0%; Pred. No. 2.6e-38; Matches 84; Conservative 14; Mismatches 14; Indels
 Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0635999; AAH63599.1; -.
HSSP; P01817; 1KCU.
 219 219
219 AA; 23944 MW; 7EIBB2A14EAF8445 CRC64;
 (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
 Sci. U.S.A. 99:16899-16903(2002)
 Z
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 Created)
 Interpro; IPR003599; Ig.
Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig cl.
Interpro; IPR003506; Ig_MHC.
Interpro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; I.
 SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
 05-JUL-2004 (TrEMBLrel. 27,
 cDNA sequences.
 PRELIMINARY;
 Hypothetical protein.
 Homo sapiens (Human).
 SEQUENCE FROM N.A.
TISSUE=Skin;
 SEQUENCE FROM N.A.
 Proc. Natl. Acad.
 NCBI_TaxID=9606;
 05-JUL-2004
 and mouse
 NON TER
NON TER
SEQUENCE
 Query Match
 Q6P491
Q6P491;
 RESULT 12
 SO FT SO
 g
 ð
 g
```

```
Attaubberg R. L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul R. P., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S. P., Zeeberg B. Buetow K.H., Schafer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Blakebey J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Blakebey B. W., Touchman J.W., Green E.D., Dickson M.C.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Generation and initial malysis of more than 15,000 full-length human
 9
 80
 21 DIVMTQTPLSSPVTLGQPASISCRSSESLLHSNGNTYLSWLHQRPGQPPRLLIYKISNRF
 1 DIVMTOSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 81 SGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVSHFPRTFGQGTRVEIK 132
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
 ö
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 Length 239;
 18; Indels
 the EMBL/GenBank/DDBJ databases
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Last sequence update)
Last annotation update)
 75.9%; Score 440; DB 2; 75.9%; Pred. No. 7.7e-38; iive 9; Mismatches 18.
 Created)
 PRT;
 HSSP, P01834; 1722.
InterPro; IPR007110; Ig-like.
InterPro; IPR001359; Ig_c1.
InterPro; IPR001596; Ig_WHC.
InterPro; IPR001596; Ig_WHC.
InterPro; IPR001596; Ig_WHC.
SWART; SM00406; IGY; I.
PROSITE; PS50815; IG_LIKE; 2.
 Strausberg R.;
Submitted (FEB-2002) to the E
EMBL, BC023362; AAH22362.1;
PIR; S22658; S22658.
PIR; S34095; S34095.
PIR; S40324; S40324.
PIR; S40324; S40324.
PIR; S4267; S42267.
 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein. Homo sapiens (Human).
 and mouse cDNA sequences.
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
```

```
NON TER
SEQUENCE
 DISULFID
 SEQUENCE
 Query Match
 Local
 DOMAIN
 DOMAIN
 Best Loc
Matches
 d
 ò
 ö
 ö
 9
 9
 21 DVVMTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRD 80
 1 DIVMTOTAPSALVTPGESVSISCRSSKSLLHSNGNTYLYWFLORPGOCPOLLIYRMSNLA 60
 MEDLINE=83256427; PubMed=6409088; Chang J.Y., Herbst H., Aebersold R., Braun D.G.; Chang J.-Y., Herbst H., Aebersold R., Braun D.G.; Chang J.-Y., Herbst H., Aebersold R., Braun D.G.; In the wallest be sequence (V kappa 27) of the variable region of kappa-light chains from a mouse hybridoma-derived anti-(streptococcal group A polysaccharide) antibody containing an additional cysteine residue. Application of the dimethylaminoazobenzene isothiocyanate technique for the isolation of peptides."; Biochem. J. 211:173-180(1983).

--- MISCELLANGOUS: This chain is from a hybridoma-derived monoclonal antibody against the streptococcal group A polysaccharide.
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 Gaps
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 81. SGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQCTHWPSTFGQGTKLEIK 132
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQQREYPYTFGGGTKLEIK 112
 ö
 Hybridoma; Immunoglobulin V region;
 Length 239;
 Framework-1.
Complementarity-determining-1.
Framework-2.
 74.0%; Score 429; DB 1; Length 113; 75.0%; Pred. No. 4.4e-37; ive 9; Mismatches 19; Indels
 Complementarity-determining-2.
 Framework-3.
Complementarity-determining-3.
 15; Indels
PROSITE; PS00290; 19 Pmc, Hypothetical protein.
eFOHENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
 12496 MW; 42C019D10ADA3C91 CRC64;
 ; Score 439; DB 2;
; Pred. No. 9.8e-38;
14; Mismatches 15,
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
22-JUL-2004 (Rel. 44, Last annotation update)
1g kappa chain V-II region 7534.1.
 113 AA
 By similarity.
 Framework-
 HSSP, 099M37, 1191.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig v.
Pfam; PP00047; ig; 1.
SMART; SM0406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Direct protein sequencing; Hybr:
Monoclonal antibody.
 75.7%;
 83; Conservative
 84; Conservative
 STANDARD;
 Mus musculus (Mouse).
 Query Match
Best Local Similarity
Matches 83; Conserv
 Similarity
 113
 KV2F MOUSE
P01630;
 DISULFID
NON TER
SEQUENCE
 61
 SEQUENCE
 Query Match
 Local
 RESULT 14

KV2F_MOUSE

AC PO1630,
DT 21-UUL.
DT 21-UUL.
DT 21-UUL.
DT 21-UUL.
DE 16 WARPO

OC MAMMALI.

RN MEDLINI
RA MEDLINI
RA MEDLINI
RA TAPDIIC.
RT 119ht,
RT 119ht,
RT APDIIC.
RT APDIIC.
CC -1- MI.
RT APDIIC.
RT DOMAIN.
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 Matches
 ઠે
 쉱
 8
 g
 ò
 셤
 ò
 g
```

```
9
 A Abbersold R., Herbet H., Cutter T., Chang J.Y., Braun D.G.;

"Murine V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6

origin: monoclonal antibodies 17829.1 and 22825.1 specific for the
Torigin: monoclonal antibodies 17829.1 and 22825.1 specific for the
Torigin: monoclonal antibodies 17829.1 and 22825.1 specific for the
T group A-streptococcal polysaccharide.";
HOPPE-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).

-! FUNCTION: Anti-streptococcal group A carbohydrate antibody.
R PIR, 909847; 1191.

R InterPro; IPR007110; Ig-like.
R InterPro; IPR007110; Ig-like.
R Pfam; PF00047; ig; 1.

R Pfam; PF00047; ig; 1.

R PROSITE; PS50835; IG_LIKE: 1.
 1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 ö
 PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin V region.
 Complementarity-determining-1. Framework-2.
 Framework-3.
Complementarity-determining-3.
Framework-4.
By similarity.
 Complementarity-determining-2.
 Length 113;
 19; Indels
 12390 MW; 4E93797046F8DB33 CRC64;
 73.6%; Score 427; DB 1;
llarity 75.0%; Pred. No. 7.2e-37;
Conservative 9; Mismatches 19
 23-0CT-1986 (Rel. 02, Created)
23-0CT-1986 (Rel. 02, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-II region 17829.1.
 113 AA
 Framework-1
 TISSUE=Hybridoma;
MEDLINE=85128968; PubMed=6441768;
 STANDARD;
 23
39
54
102
112
93
 Mus musculus (Mouse).
 103 1
23
113 1
113 AA;
 Similarity
 NCBI_TaxID=10090
LT 15
MOUSE
KV2E MOUSE
P03976;
 84;
 61
```

Search completed: November 16, 2005, 22:01:55 Job time : 63.7941 secs

ö

1151 1151 1161, 1 110, 1 1115, 1 666, 1 666, 1 666, 1

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq

Run on:

```
Length 113;
 COMPUTER TREADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-40G-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: AN ORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
 Indels
 GENERAL INCEMATION:

APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 1940, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
 92.4%; Score 536; DB 3; L
1larity 92.0%; Pred. No. 1.7e-46;
Conservative 3; Mismatches 6;
US-08-107-669D-15
US-08-477-78RA-15
US-08-477-51B-15
US-08-646-36-151
US-08-819-765-151
US-09-1136-389-151
US-09-610-818-151
US-09-610-818-151
US-09-610-818-151
US-08-478-039-88
US-08-478-039-88
US-08-478-039-88
US-08-478-039-88
US-08-478-039-88
US-08-482-882-66
US-08-487-1150-66
US-08-487-1150-66
US-08-487-1150-66
 ALIGNMENTS
 Sequence 15, Application US/09025769B Patent No. 6300064
 TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TOPOLOGY: linear
MOLECULE TYPE: protein
 amino acid
 Query Match
Best Local Similarity
Matches 103; Conserv
 \begin{array}{c} 66.6 \\ 6.6
 STRANDEDNESS
 10021
 US-09-025-769B-15
 US-09-025-769B-15
 LENGTH:
 RESULT 1
 Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 9, Appli
Sequence 49, Appl
Sequence 45, Appl
Sequence 178, Appl
Sequence 178, Appl
 Sequence 178, App
Sequence 178, App
Sequence 8, Appli
Sequence 2, Appli
 Sequence 151, App
Sequence 151, App
 November 16, 2005, 21:41:29; Search time 19.0441 Seconds (without alignments) 439.017 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 US-10-660-357A-38
580
1 DIVMTQSPLSLPVIPGEPAS........CMQALQIPLTFGGGTKVEIK 112
 Description
 Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 3-09-025-769B-178
3-09-490-070A-178
3-09-490-153-178
 US-09-025-769B-15
US-09-490-153-15
US-09-490-153-15
US-09-490-153-15
US-08-331-39R8-49
US-08-331-39R8-49
US-08-331-39R8-49
US-09-225-693-49
US-09-225-769B-29
US-09-025-769B-29
US-09-490-070R-29
US-09-490-070R-29
US-09-490-153-45
US-09-490-153-45
US-09-490-153-45
US-09-490-153-45
US-09-490-153-178
US-09-490-153-178
US-09-490-153-178
US-09-490-153-178
US-09-490-153-178
US-09-490-153-178
US-09-490-153-178
 US-09-000-088-2
US-08-488-113B-151
US-08-477-484B-151
 Total number of hits satisfying chosen parameters:
 513545 segs, 74649064 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 Gapop 10.0 , Gapext 0.5
 seq length: 0
seq length: 200000000
 Length
 BLOSUM62
 Query

 Scoring table:
 Perfect score:
 OM protein
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Database
```

Result No.

ö

Gaps

ö

```
US-09-490-153-15
 g
 ð
 g
 9
 1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGGGTXLEIK 112
 COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
PILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 14-Jan-2000
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 14-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: COlin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
 ö
 Length 113;
 Sequence 15, Application US/09490070A
Patent No. 6696248

GENERAL INFORMATION:
Pack, Peter
11ag, Vic
Ge, Liming
Moroney, Simon
Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
 6; Indels
 92.4%; Score 536; DB 4;
92.0%; Pred. No. 1.7e-46;
tive 3; Mismatches 6;
) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-070A-15
 TELEFAX: (202) 912-2020 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
 LENGTH: 113 amino acida TYPE: amino acid
 STRANDEDNESS: <Unknown>
 ZIP: 20006
COMPUTER READABLE FORM:
 CITY: Washington
STATE: D.C.
COUNTRY: USA
 TOPOLOGY: linear
 Query Match
Best Local Similarity 92.0
Matches 103; Conservative
 RESULT 2
US-09-490-070A-15
 61
 61
 유
 ò
 요
 g
 ઠે
 à
 셤
```

RESULT 3

```
9
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYIFGQGTKLEIK 112
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COFERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: B-55 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
CARRESPER: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 151 Avenue of the Americas
CITY: New York
 Query Match 92.4%; Score 536; DB 4; Length 113; Best Local Similarity 92.0%; Pred. No. 1.7e-46; Matches 103; Conservative 3; Mismatches 6; Indels
 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
 NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REPERENCE/DOCKET NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-153-15
 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Go. Liming
Moroney, Simon
Plueckthun, Andreas
 TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
 Sequence 15, Application US/09490324; Patent No. 6828422; GENERAL INFORMATION:
Sequence 15, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
 LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
 STATE: New York
 COUNTRY: USA
 US-09-490-324-15
```

```
ö
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHNNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPYTFGQGTKLEIK 112
 APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FirzGerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Brinkmann, Ulrich
APPLICANT: Brinkmann, Ulrich
APPLICANT: Slingle Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
 Length 112;
 Query Match
91.9%; Score 533; DB 4; Length 11.
Best Local Similarity 91.1%; Pred. No. 3.4e-46;
Matches 102; Conservative 4; Mismatches 6; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-0CT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/56,289
FILING DATE: 12-0CT-1990
ATTONNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
 015280-126110US
 COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 49, Application US/08331398A Patent No. 5608039 GENERAL INFORMATION:
 NAMB: Hunter, Tom
REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
 PRIOR FILING DATE: 1996-09-02
NUMBER OF SEQ ID NOS: 183
SOFWARE: Patentin version 3.1
SEQ ID NO 9
 MOLECULE TYPE: protein FEATURE:
 LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
 NAME/KEY: Protein
 amino acid
 linear
 STRANDEDNESS
 US-08-331-398A-49
 US-09-254-180C-9
 ò
 셤
 ò
 g
 APPLICANT: CANADAY, VESUVUKI
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAEDA, Hiroaki
APPLICANT: WISHIO, YOSHILTAN
APPLICANT: HIGUGHI, Hirofumi
APPLICANT: HIGUGHI, Hirofumi
APPLICANT: NAKATA, Motomi
APPLICANTON HUMBIRE (US/09/254,180C
FILE REFERENCE: 050006-0055
FILE REFERENCE: 050006-0055
FILE REFERENCE: 1999-04-15
PRIOR APPLICATION NUMBER: PCT/JP97/02983
PRIOR FILING DATE: 1997-08-27
PRIOR PAPLICATION NUMBER: 271546/1996
PRIOR FILING DATE: 1996-09-20
PRIOR PLING DATE: 1996-09-20
PRIOR PLING DATE: 1996-09-20
 9
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMOALOTPYTFGOGTKLEIK 112
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
OFBRATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
 ö
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSES: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
 Query Match 92.4%; Score 536; DB 4; Length 113; Best Local Similarity 92.0%; Pred. No. 1.7e-46; Matches 103; Conservative 3; Mismatches 6; Indels
 NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27, 794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-324-15
 TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
 Sequence 9, Application US/09254180C
Patent No. 6777540
 LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
APPLICANT: OKUMURA, KO
 ZIP: 10021
 RESULT 5
US-09-254-180C-9
```

g ઠે

ઠે

```
RESULT 8
 셤
 ð
 ò
 RESULT 7
US-08-331-397B-49
is Sequence 49, Application US/08331397B
is Patent No. 5981726
is GENERAL INFORMATION:
is APPLICANT: Benhar, Ital
is APPLICANT: Pastan, Iral
is APPLICANT: Pastan, Iral
is APPLICANT: Pastan, Iral
is APPLICANT: Specific Antibody Fragments, Fusion Proteins, and Uses
is TITLE OF INVENTION: Thereof
is TITLE OF INVENTION: Thereof
is TITLE OF INVENTION: About the Application of Townsend and Townsend and Crew
is ADDRESSEE: Townsend and Townsend and Crew
is STREET: One Market Plaza, Steuart Street Plaza
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 60
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFGQGTKVEIK 112
 ö
 90.7%; Score 526; DB 1; Length 112; 91.1%; Pred. No. 1.7e-45; tive 2; Mismatches 8; Indels
 /note= "Human IgM antibody GM607
Variable Light chain (V-L)"
 /note= "Human IgM antibody GM607
Variable Light chain (V-L)"
 CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-0CT-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/56,289
FILING DATE: 12-0CT-1990
FILING DATE: 12-0CT-1990
ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REPERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acids
STRANDEDNESS:
 COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Query Match
Best Local Similarity 91.13
Matches 102; Conservative
 MOLECULE TYPE: protein
 NAME/KEY: Protein LOCATION: 1..112 OTHER INFORMATION: OTHER INFORMATION:
; LOCATION: 1..112
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-331-398A-49
 linear
 US-08-331-397B-49
 d
 ò
```

90.7%; Score 526; DB 2; Length 112;

Query Match

```
ô
 1 DIVMTOSPLSLPVIPGEPASISCRSSOSLLOSNGNNYLDWYLQKPGOSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA 60
 0; Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGLQTPQTFGQGTKVEIK 112
 Score 526; DB 2; Length 112;
Pred. No. 1.7e-45;
Best Local Similarity 91.1%; Pred. No. 1.7e-45;
Matches 102; Conservative 2; Mismatches 8; Indels
 APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Prink
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
 /note= "Human IgM antibody GM607
Variable Light chain (V-L)"
 COUNTRY: USA
ZIP: 94111-3834
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUW TYPE: FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION NUMBER: US/08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/56,289
FILING DATE: 12-OCT-1990
ATTOMNEY/AGENT INFORMATION:
 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
 NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
 US-08-759-804A-49; Sequence 49, Application US/08759804A; Patent No. 5990296
 90.7%;
 112 amino acids
 MOLECULE TYPE: protein
 CITY: San Francisco
STATE: California
 ; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-759-804A-49
 NAME/KEY: Protein LOCATION: 1..112
 TYPE: amino acid STRANDEDNESS:
 TOPOLOGY: linear
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 ORGANISM: Homo sapiens
 94301
 US-09-240-274-30
 TYPE: PRT
 g
 ò
 g
 ò
ö
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPQQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
Gaps
 Gaps
 Sequence 49, Application US/09227693

Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: BENHAR, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMOGLOTPOTFGOGTKVBIK 112
ö
 Score 526; DB 3; Length 112;
Pred. No. 1.7e-45;
2; Mismatches 8; Indels
8; Indels
 LOCATION: 1..112
COTHER INFORMATION: /note= "Human IgM GM607 VL region"
US-09-227-693-49
 NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
Mismatches
 NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
..
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity 91.1%;
Matches 102; Conservative
 112 amino acids
Conservative
 TYPE: amino acid
STRANDEDNESS: single
 COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
 MOLECULE TYPE: peptide
 San Francisco
California
 NAME/KEY: Protein
 TOPOLOGY: linear
 FILING DATE:
 RESULT 9
US-09-227-693-49
102;
 LENGTH:
Matches
 ઠે
 셤
```

```
DD 1 DINNIQUE LEAF PRICE ASSOCIATION FROM THE PROPERTY OF ALL OF THE PROPERTY OF
```

```
(212)596-9090
 LENGTH:
 g
 1 DIVWIQSPLSLSVTPGEPASISCRSSQSLLHTNGYNYLDWYVQKPGQSPQLLIYLASNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 SGVPDRFSGSGSGTDFTLKISRVETEDVGVYYCMQALQIPRTFGQGTKVEIK 112
 Query Match 89.5%; Score 519; DB 1; Length 113; Best Local Similarity 89.3%; Pred. No. 8.6e-45; Matches 100; Conservative 4; Mismatches 8; Indels
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR DATE: 18-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 CTHER INFORMATION: /note= "The peptide sequence of the OTHER INFORMATION: V-1 region of SDZ MSL 109" US-08-082-623-4
 CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
 APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Lining
APPLICANT: Moroney, Simon
APPLICANT: Pluckkhun, Andreas
ITILE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INPORMATION:
NAME: SMITH, WILLIAIN
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-055-1
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
 Sequence 29, Application US/09025769B Patent No. 6300064
GENERAL INFORMATION:
 ORGANISM: Homo sapiens
 TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
 NAME/KEY: Peptide LOCATION: 1..113
 New York
: USA
 US-09-025-769B-29
 COUNTRY:
 STATE:
 엄
 ò
```

```
ö
 9
 9
 1 DIVATOSPLSLPVTPGEPASISCRSSQSLLHSNGYVYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQHYTTPPTFGQGTKVEIK 112
 ö
 Score 515; DB 3; Length 114;
Pred. No. 2.2e-44;
2; Mismatches 10; Indels
 Query Match 88.8%; Score 515; DB 3; Length 114; Best Local Similarity 89.3%; Pred. No. 2.2e-44; Matches 100; Conservative 2; Mismatches 10; Indels
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
 STREET: 121 Avenue of the Americas CONTRY: New York COUNTRY: New York COUNTRY: USA
 US-09-025-769B-45

Sequence 45, Application US/09025769B

Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Moroney, Simon
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
 NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REGISTRATION NUMBER: MORPHO/S TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: (212)596-9000
 88.8%;
 LENGTH: 114 amino acida
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
 amino acids
 (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity 89.3
Matches 100; Conservative
 TELEFAX: (212)596-909(
INFORMATION FOR SEQ ID NO:
 TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-025-769B-45
 , MOLECULE TYPE: protein US-09-025-7698-29
 CORRESPONDENCE ADDRESS: ADDRESSEE: James F. I
```

```
Sequence 45,
 ઠ
 ద
 ò
 1 DIVMIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 9
DIVMTOSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQHYTTPPTFGQGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNHBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 18-404-1995
ATTORNEY/AGENT INFORMATION:
 ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
 ö
 Query Match 88.8%; Score 515; DB 4; Length 114; Best Local Similarity 89.3%; Pred. No. 2.2e-44; Matches 100; Conservative 2; Mismatches 10; Indels
 NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-490-070A-29
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
 LENGTH: 114 amino acids TYPE: amino acid
 STRANDEDNESS: <Unknown>
 INFORMATION FOR SEC ID NO: 29
 SEQUENCE CHARACTERISTICS
 COMPUTER READABLE FORM:
 CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
 61
 g
 ò
 g
 δ
 g
```

```
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVWTQSPLSLPV1PGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 61 SGVPDRFSGSGGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & Moduliffe
 COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
 Length 114;
 Query Match
88.8%; Score 515; DB 4; Length 11.
Best Local Similarity 89.3%; Pred. No. 2.2e-44;
Matches 100; Conservative 2; Mismatches 10; Indels
 APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
 STREET: 1666 K Street, N.W., Suite 300
 Search completed: November 16, 2005, 22:07:22 Job time : 19.0441 secs
 MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-490-070A-45
quence 45, Application US/09490070A
tent No. 6696248
GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
 INFORMATION FOR SEQ ID NO: 45
 SEQUENCE CHARACTERISTICS
 COMPUTER READABLE FORM:
 CITY: Washington
 USA
 STATE: D.C.
 COUNTRY:
```

RESULT 15 US-09-490-070A-45

ô

المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران المستران الم

Sequence

Sequence 40, Appl Sequence 28, Appl Sequence 71, Appl Sequence 148, App Sequence 220, Appl Sequence 220, Appl Sequence 279, Appl Sequence 279, Appl Sequence 12, Appl Sequence 12, Appl Sequence 103, Appl Sequence 111, Appl Sequence 30, Appl Sequence 1177, Appl Sequence 177, Appl

Appli Appli Appli Appli Appli

Sequence (Sequence (Sequen

Sequence

Sequence

```
, ORGANISM: Homo Sapiens
US-10-330-613-38

 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...
 ...</td
 RESULT 1
US-10-330-613-38
 61
 TYPE: PRT
 61
 N
 RESULT
 g
 ò
 38, Appl
18, Appl
26, Appl
33, Appl
2081, Ap
 32, Appl
2, Appli
44, Appl
 November 16, 2005, 22:02:09; Search time 68.7647 Seconds (without alignments) 681.481 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 DIVMTQSPLSLPVIPGEPAS......CMQALQIPLTFGGGTKVEIK 112
 Sequence 3
Sequence 3
Sequence 2
 Description
 Published Applications Asia.

(gan2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
 5.1.6
Compugen Ltd.
 US-10-330-613-38
US-10-330-530-38
US-10-660-357-38
US-10-269-805-18
US-10-269-762-33
US-09-880-748-2081
US-10-293-418-2081
US-10-293-418-2081
US-10-269-805-44
 Total number of hits satisfying chosen parameters:
 1867879 seqs, 418409474 residues
 version 5
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Applications_AA:
 protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 GenCore (c) 1993
 12
 US-10-660-357A-38
580
 seq length: 0
seq length: 200000000
 В
 Length
 Copyright
 Published_
 Query
 1000.0
1000.0
95.2
95.2
94.5
94.5
94.3
93.0
 110...
111...
112...
113...
116...
119...
119...
 Title:
Perfect score:
 Scoring table:
 88
 OM protein
 Sequence:
 Searched:
 Database
 Minimum I
Maximum I
 110 8 4 8 9 7 11
 Run on:
 Result
 ģ
```

```
ö
 9
 9
 1 DIVWTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPQQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 Sequence
 Length 112;
 ; Sequence 38, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILLE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 38
; LENGTH: 112
 IndelB
 Query Match 100.0%; Score 580; DB 14; Best Local Similarity 100.0%; Pred. No. 7.6e-48; Matches 112; Conservative 0; Mismatches 0;
```

ó 9 9

```
셤
 g
 a
 ò
 ð
 δ
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVWTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA 60
 DIVMTOSPLSLPVIPGEPASISCRSSOSLLOSNGNNYLDMYLOKPGOSPQLLIYLGSNRA
 Gaps
 Gaps
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEADDVGTYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 ö
 ö
Sequence 38, Application US/10330530
| Publication No. US20030152514A1
| GENERAL INFORMATION:
| APPLICANT: Gudas, Jean
| TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
| FILE REPERENCE: ABGENIX.031A
| CURRENT APPLICATION NUMBER: US/10/330,530
| CURRENT APPLICATION NUMBER: US 60/346414
| PRIOR FILING DATE: 2001-12-18
| NUMBER OF SEQ ID NOS: 40
| SOFTMARE: FastSEQ for Windows Version 4.0
| LENGTH: 112
 Query Match 100.0%; Score 580; DB 14; Length 112; Best Local Similarity 100.0%; Pred. No. 7.6e-48; Matches 112; Conservative 0; Mismatches 0; Indels 0
 Length 112;
 APPLICANT: Barrelli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
TITLE OF INVENTION: ANTIGEN
TITLE OF INVENTION: ANTIGEN
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 112
 Indels
 100.0%; Score 580; DB 16;
100.0%; Pred. No. 7.6e-48;
ive 0; Mismatches 0;
 Sequence 38, Application US/10660357; Publication No. US20040115205A1; GENERAL INFORMATION;
 Best Local Similarity 100.
Matches 112; Conservative
 ORGANISM: Homo Sapiens
 ORGANISM: Homo Sapiens
 RESULT 4
US-10-269-805-18
 RESULT 3
US-10-660-357-38
 US-10-330-530-38
 US-10-660-357-38
 61
 Query Match
 g
 g
 ò
 ò
 ð
 ઠે
```

```
1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 0; Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 112
 RESULT 5
US-10-269-805-26

i Sequence 26, Application US/10269805

j Sequence 26, Application US/10269805

j Publication No. US20030124129A1

j GENERAL INFORMATION:

j APPLICANT: OLINER, JONATHAN D.

j TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

FILE REPERBNCE: A-722

CURRENT FILING DATE: 2002-10-10

pRIOR APPLICATION NUMBER: US/10/269,805

j CURRENT FILING DATE: 2001-10-11

NUMBER OF SEQ ID NOS: 76

j SOFTHARE: Patentin version 3.1

s SEQ ID NO 26

LENGTH: 112
 Query Match

95.2%; Score 552; DB 14; Length 112;
Best Local Similarity 94.6%; Pred. No. 3.7e-45;
Matches 106; Conservative 2; Mismatches 4; Indels
 Query Match 95.2%; Score 552; DB 14; Length 112; Best Local Similarity 94.6%; Pred. No. 3.7e-45; Matches 106; Conservative 2; Mismatches 4; Indels
 Sequence 33, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Foltz, Ian
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
TITLE OF INVENTION: (A IX) TUMOR ANTIGEN
TITLE OF INVENTION: (A IX) TUMOR ANTIGEN
CURRENT APPLICATION NUMBER: US/10/309,762
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS FILE REPERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 112
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 RESULT 6
US-10-309-762-33
 US-10-269-805-18
 US-10-269-805-26
```

ö

9

Sequence 18, Application US/10269805; Publication No. US20030124129A1; GENERAL INFORMATION: APPLICANT: OLINER, JONATHAN D.

```
Query Match
 ò
 ò
 셤
 ò
 셤
 ઠે
 셤
 ö
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPQQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 Gaps
 Gaps
 Sequence 2001, Application US/09880748

Sequence 2001, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:
APPLICATY: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT APPLICATION NUMBER: 000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/279,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-05-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0
 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 210 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 261
 ö
 ;
0
 APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
 Length 112;
 Length 262;
 4; Indels
 4; Indels
 Score 552; DB 15;
Pred. No. 3.7e-45;
2; Mismatches 4;
 Score 548; DB 10;
Pred. No. 2.3e-44;
 3; Mismatches
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 112
 Sequence 2081, Application US/10293418 Publication No. US20030223996A1 GENERAL INFORMATION:
 Query Match
Best Local Similarity 94.6%;
Matches 106; Conservative
 Query Match
Best Local Similarity 93.8%;
Matches 105; Conservative
 tryPE: PRT
CORGANISM: Homo sapiens
US-09-880-748-2081
 tyPE: PRT CAGANISM: Homo sapiens US-10-309-762-33
 US-10-293-418-2081
 US-09-880-748-2081
 ઠે
 5
 ઠ
 g
 임
 ઠે
 d
```

```
9
 9
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVWTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQCPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVBIK 112
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 112
 210 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPLTFGGGTKVEIK 261
 .
0
 Sequence 32, Application US/10309762

Sequence 32, Application US/10309762

Publication No. US20040018198A1

GENERAL INFORMATION:

APPLICANT: Gudae, Jean

APPLICANT: Handa, Masahisa

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX

TITLE OF INVENTION: ANTIBODIES

FILE REFERENCE: ABGENIX.027A

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/337275

PRIOR APPLICATION NUMBER: 60/337275

PRIOR APPLICATION NUMBER: 60/337275

WUMBER OF SEQ ID NOS: 246

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 324
 ö
 94.3%; Score 547; DB 15; Length 112; 93.8%; Pred. No. 1.1e-44; ive 2; Mismatches 5; Indele
 Length 262;
 4; Indels
 94.5%; Score 548; DB 15;
93.8%; Pred. No. 2.3e-44;
iive 3; Mismatches 4;
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-16
PRIOR PAPLICATION NUMBER: 60/276,248
PRIOR PAPLICATION NUMBER: 60/276,248
PRIOR PAPLICATION NUMBER: 60/210,816
PRIOR PILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
 Query Match
Best Local Similarity 93.8
Matches 105; Conservative
 Best Local Similarity 93.8
Matches 105; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2081
 ; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-32
```

ö

```
0
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSKGDNYLDMYLQKPGQSPQLLIXLGSHRA 60
 9
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVWTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPPTFGGGTKVEIK 112
 ;
0
 .;
0
Sequence 2, Application US/10269805;
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
SPRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin version 3.1
 Query Match
93.8%; Score 544; DB 14; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.1e-44;
Matches 104; Conservative 4; Mismatches 4; Indels
 Query Match
94.0%; Score 545; DB 14; Length 112;
Best Local Similarity 93.8%; Pred. No. 1.7e-44;
Matches 105; Conservative 2; Mismatches 5; Indels
 Sequence 44, Application US/10269805
PUblication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
FITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REPERBENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
 RESULT 12
US-11-021-715-82
is Sequence 82, Application US/11021715
is Publication No. US20050208596A1
igeneral INFORMATION:
 SOFTWARE: PatentIn version 3.1
 NUMBER OF SEQ ID NOS: 76
 TYPE: PRT
ORGANISM: Homo sapiens
 TYPE: PRT
ORGANISM: Homo sapiens
 RESULT 11
US-10-269-805-44
 JS-10-269-805-44
 SEQ ID NO 44
LENGTH: 112
 US-10-269-805-2
 셤
 ð
 ò
 유
 ò
 ઠ
```

```
US-11-021-715-85

US-11-021-715-85

Sequence 85, Application US/11021715

Publication No. US20050208596A1

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET

TITLE OF INVENTION: COMPOSITIONS, METHODS AND INHIBITORS THEREOF

FILE REPREMENCE: 053993-6050

CURRENT APPLICATION NUMBER: US/11/021,715

PRIOR APPLICATION NUMBER: E07/US03/21304

PRIOR PILING DATE: 2003-07-03

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-09-18

NUMBER OF SEQ ID NOS: 153

SOFTWARE: Patentin version 3.2

SEQ ID NO 85

LENGTH: 112
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET TITLE OF INVENTION: COMPOSITIONS, METHODS AND INHIBITORS THEREOF TITLE OF INVENTION: AUTOMATIBODIES AND INHIBITORS THEREOF CURRENT APPLICATION NUMBER: US/11/021,715
CURRENT FILING DATE: 2004-12-23
PRIOR PRIOR PAPLICATION NUMBER: ECT/US03/21304
PRIOR FILING DATE: 2003-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-07-03
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin Version 3.2
SEQ ID NO 92
 ô
 9
 1 DIVNTQSPLSLPVTPGEPASISCRSSQSLLHSNGNNYLDWYLDKFGQSPQLLIYLASNRA 60
 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTOSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 Gaps
 0; Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVBPEDVGLYYCMQALQTPLTFGGGSKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQSPPTFGGGTKVEIK 112
 .
0
 Query Match
93.8%; Score 544; DB 20; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.1e-44;
Matches 104; Conservative 3; Mismatches 5; Indels
 Length 112;
 Indels
 Query Match
93.8%; Score 544; DB 20;
Best Local Similarity 93.8%; Pred. No. 2.1e-44;
Matches 105; Conservative 2; Mismatches 5;
 TYPE: PRT
ORGANISM: Homo sapiens
US-11-021-715-82
 ; ORGANISM: Homo sapiens
US-11-021-715-85
 TYPE: PRT
 셤
 셤
 ò
 g
 à
 셤
 Š
```

US-10-638-265-40

RESULT 14

```
9
 9
 1 DIVWIQSPLSLPVIPGEPASISCRSSQSLLHSNGYKYLEWYLQKPGQSPQLLIYLGSNRA 60
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 1 DIVMTQSPLSLPVIPGEPASISCRSSQSLLQSNGNNYLDWYLQKPGQSPQLLIYLGSNRA
 0; Gaps
 Gaps
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQTLQIPLTFGGGTXVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEADDVGIYYCMQALQIPLTFGGGTKVEIK 112
 61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQTLQIPLTFGGGTKVEIK 112
 ;
0
 Query Match 93.6%; Score 543; DB 17; Length 112; Best Local Similarity 92.9%; Pred. No. 2.7e-44; Matches 104; Conservative 3; Mismatches 5; Indels
 93.6%; Score 543; DB 17; Length 112; 92.9%; Pred. No. 2.7e-44; Live 3; Mismatches 5; Indels
; Sequence 40, Application US/10638265;
; Publication No. US20050031614A1
; GENERAL INFORMATION:
; APPLICANT: Reskes, Lorin
; APPLICANT: Roltz, Ian
; APPLICANT: King, Chadwick
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID
; TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF
; FILE REFERENCE: ABGENIX: 092A
; CURRENT FILING DATE: 2003-08-08
; UNDBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homosapien
US-10-638-265-40
 RESULT 15
195-10-628-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
195-10-638-265-48
 Search completed: November 16, 2005, 23:05:45 Job time : 68.7647 secs
 Query Match
Best Local Similarity 92.99
Matches 104; Conservative
 ò
 셤
 ò
 g
 ઠે
 셤
 ઠે
 g
```

ţ

A Commission of the commission